

***Helicobacter pylori* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 8**

Catalog No. NR-19484

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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-19484.

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-19484 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 8, NR-19484."

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 8 (ZHPAH)¹

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	58871	A01	HP0347	conserved hypothetical protein	931	NP_207145.1	2
26695	58878	A02	HP0221	nifU-like protein	1015	NP_207019.1	1.59015
26695	58882	A03	HP1360	4-hydroxybenzoate octaprenyltransferase	919	NP_208152.1	1.99129
26695	58888	A04	HP0848	type I restriction enzyme S protein	931	NP_207640.1	1.75403
26695	58890	A05	HP1344	magnesium and cobalt transport protein	991	NP_208136.1	1.97679
26695	58894	A06	HP0727	transcriptional regulator, putative	1021	NP_207521.1	1.52693
26695	58898	A07	HP0960	glycyl-tRNA synthetase, alpha subunit	946	NP_207752.1	1.98943
26695	58902	A08	HP1412	hypothetical protein	961	NP_208203.1	1.9948
26695	58906	A09	HP1435	protease IV	913	NP_208226.1	2
26695	58910	A10	HP0393	chemotaxis protein	970	NP_207191.1	3.11443
26695	58922	A11	HP1084	aspartate transcarbamoylase	958	NP_207875.1	1.96764
26695	58926	A12	HP0576	signal peptidase I	907	-	2
26695	58931	B01	HP0163	delta-aminolevulinic acid dehydratase	1006	NP_206962.1	1.834
26695	58942	B02	HP0240	octaprenyl-diphosphate synthase	958	NP_207038.1	1.86326
26695	58946	B03	HP1583	pyridoxal phosphate biosynthetic protein A	958	NP_208374.1	1.80376
26695	58952	B04	HP0554	hypothetical protein	1000	NP_207349.1	1.534
26695	58955	B05	HP0577	methylene-tetrahydrofolate dehydrogenase	913	NP_207371.1	1.96386
26695	58958	B06	HP0929	geranyltranstransferase	946	NP_207721.1	1.91966
26695	58962	B07	HP1138	plasmid replication-partition related protein	907	NP_207929.1	1.98346
26695	58966	B08	HP1121	cytosine specific DNA methyltransferase	973	NP_207912.1	1.98972
26695	58979	B09	HP0538	cag pathogenicity island protein	955	NP_207334.1	1.99791
26695	58982	B10	HP0557	acetyl-coenzyme A carboxylase	973	NP_207352.1	1.95581
26695	58990	B11	HP1111	pyruvate ferredoxin oxidoreductase, beta subunit	979	NP_207902.1	4.03984
26695	58995	B12	HP0874	KapA protein	910	NP_207668.1	1.79341
26695	58998	C01	HP0158	hypothetical protein	991	NP_206957.1	1.72351

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	59003	C02	HP0889	iron(III) dicitrate ABC transporter, permease protein	1015	NP_207682.1	3.68768
26695	59007	C03	HP0328	conserved hypothetical protein	973	NP_207126.1	1.86536
26695	59010	C04	HP1234	conserved hypothetical integral membrane protein	931	NP_208026.1	2
26695	59014	C05	HP1407	YihY family protein	913	NP_208198.1	1.96605
26695	59020	C06	HP0833	lipoprotein, putative	913	NP_207626.1	2.14129
26695	59023	C07	HP0237	porphobilinogen deaminase	955	NP_207035.1	1.98953
26695	59027	C08	HP0825	thioredoxin reductase	970	NP_207618.1	1.84845
26695	59030	C09	HP1034	ATP-binding protein	919	NP_207824.1	3.69423
26695	59034	C10	HP1434	formyltetrahydrofolate hydrolase	916	NP_208225.1	1.99563
26695	59042	C11	HP0485	catalase-like protein	979	NP_207282.1	3.82125
26695	59046	C12	HP0709	conserved hypothetical protein	937	NP_207503.1	2
26695	59050	D01	HP0763	cell division protein	916	NP_207556.1	1.92467
26695	59054	D02	HP0176	fructose-bisphosphate aldolase	958	NP_206975.1	3.00522
26695	59064	D03	HP0160	conserved hypothetical secreted protein	955	NP_206959.1	1.57487
26695	59066	D04	HP1050	homoserine kinase	916	NP_207841.1	1.97707
26695	59070	D05	HP1421	conjugative transfer regulon protein	949	NP_208212.1	1.76396
26695	59076	D06	HP1055	hypothetical protein	979	NP_207846.1	1.90705
26695	59078	D07	HP0117	conserved hypothetical protein	961	NP_206917.1	2
26695	59082	D08	HP0583	hypothetical protein	916	NP_207378.1	2
26695	59090	D09	HP0432	protein kinase C-like protein	925	NP_207230.1	1.95568
26695	59095	D10	HP1098	conserved hypothetical secreted protein	907	NP_207889.1	2
26695	59102	D11	HP1399	arginase	1003	NP_208190.1	3.30508
26695	59106	D12	HP0107	cysteine synthetase	955	NP_206907.1	2
26695	59111	E01	HP0280	heat shock protein B	1021	NP_207078.1	3.71499
26695	59122	E02	HP1164	thioredoxin reductase	1009	NP_207955.1	1.79187
26695	59126	E03	HP0745	conserved hypothetical protein	1018	NP_207538.1	1.92043
26695	59130	E04	HP0854	GMP reductase	1018	NP_207648.1	1.86935
26695	59135	E05	HP0582	hypothetical protein	1009	NP_207375.1	3.78295
26695	59147	E06	HP1133	ATP synthase F1, subunit gamma	940	NP_207924.1	2
26695	59154	E07	HP0638	outer membrane protein	952	NP_207432.1	2
26695	59158	E08	HP1021	response regulator	931	NP_207811.1	2
26695	59164	E09	HP0045	nodulation protein	967	NP_206846.1	2.11686
26695	59168	E10	HP0517	GTP-binding protein	943	NP_207314.1	2.10817
26695	59174	E11	HP0726	hypothetical protein	952	NP_207520.1	1.93067
26695	59179	E12	HP0090	malonyl coenzyme A-acyl carrier protein transacylase	964	NP_206890.1	2
26695	59182	F01	HP1351	hypothetical protein	907	NP_208143.1	2
26695	59187	F02	HP1454	hypothetical protein	946	NP_208245.1	1.99154
26695	59195	F03	HP1052	UDP-3-O-acyl N-acetylglucosamine deacetylase	922	NP_207843.1	2.06182
26695	59198	F04	HP0489	hypothetical protein	922	NP_207286.1	2.84273
26695	59203	F05	HP1495	transaldolase	985	NP_208286.1	1.91878
26695	59208	F06	HP0616	chemotaxis protein	976	NP_207411.1	1.43852
26695	59210	F07	HP0175	cell binding factor 2	934	NP_206974.1	1.97859
26695	59215	F08	HP0757	beta-alanine synthetase homolog	913	NP_207550.1	1.90361
26695	59218	F09	HP0096	phosphoglycerate dehydrogenase	979	NP_206896.1	1.99081
26695	59224	F10	HP1013	dihydrodipicolinate synthetase	937	NP_207803.1	1.91035

Strain	Clone	Well Position	Locus ID	Description	ORF Length	Accession Number ²	Average Depth of Coverage
26695	59230	F11	HP0961	glycerol-3-phosphate dehydrogenase, NAD(P)+ dependent	973	NP_207753.1	1.97533
26695	59234	F12	HP0312	conserved hypothetical ATP-binding protein	1000	NP_207110.1	4.087
26695	59242	G01	HP0707	conserved hypothetical protein	961	NP_207501.1	1.99584
26695	59254	G02	HP1103	glucokinase	1045	NP_207894.1	1.79809
26695	59258	G03	HP0299	dipeptide ABC transporter, permease protein	1039	NP_207097.1	4.5409
26695	59265	G04	HP1251	oligopeptide ABC transporter, permease protein	1081	NP_208043.1	3.12581
26695	59276	G06	HP0362	conserved hypothetical integral membrane protein	1072	NP_207160.1	2.09422
26695	59278	G07	HP0729	hypothetical protein	1102	NP_207523.1	1.78221
26695	59286	G08	HP0077	peptide chain release factor RF-1	1093	-	3.20952
26695	59291	G09	HP0493	phospho-N-acetylmuramoyl-pentapeptide-transferase	1096	NP_207290.1	3.58759
26695	59295	G10	HP1346	glyceraldehyde-3-phosphate dehydrogenase	1027	NP_208138.1	2.06913
26695	59302	G11	HP0251	oligopeptide ABC transporter, permease protein	1051	NP_207049.1	4.04091
26695	59307	G12	HP0304	hypothetical protein	1024	NP_207102.1	2.75488
26695	59311	H01	HP1584	sialoglycoprotease	1057	NP_208375.1	4.19678
26695	59314	H02	HP0279	lipopolysaccharide heptosyltransferase-1	1057	NP_207077.1	1.67928
26695	59320	H03	HP0202	beta-ketoacyl-acyl carrier protein synthase III	1030	NP_207001.1	2.12136
26695	59324	H04	HP1293	DNA-directed RNA polymerase, alpha subunit	1069	NP_208085.1	2.40412
26695	59331	H05	HP0995	integrase/recombinase	1102	NP_207786.1	3.96733
26695	59334	H06	HP1077	nickel transport protein	1030	NP_207868.1	1.88738
26695	59343	H07	HP0283	3-dehydroquinate synthase	1066	NP_207081.1	4.14259
26695	59346	H08	HP1356	quinolinate synthetase A	1045	NP_208148.1	4.00957
26695	59356	H09	HP1555	translation elongation factor EF-Ts	1102	NP_208346.1	2.15426
26695	59362	H10	HP0660	hypothetical protein	1051	NP_207454.1	1.92293
26695	59366	H11	HP1265	hypothetical protein	1021	NP_208057.1	1.85113
26695	59371	H12	HP1253	tryptophanyl-tRNA synthetase	1054	NP_208045.1	4.10626

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).