Helicobacter pylori Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 5

Catalog No. NR-19481

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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-19481 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 5, NR-19481."

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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Tel: 800-359-7370
Fax: 703-365-2898

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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 5 (ZHPAE)[1]

Strain	Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
26695	57546	A01	HP1123	peptidyl-prolyl cis-trans isomerase, FKBP-type rotamase	592	NP_207914.1	1.868
26695	57550	A02	HP1497	peptidyl-tRNA hydrolase	595	NP_208288.1	1.983
26695	57554	A03	HP1473	hypothetical protein	610	NP_208264.1	2
26695	57558	A04	HP0692	3-oxoadipate coA-transferase subunit B	658	NP_207486.1	1.994
26695	57562	A05	HP0363	L-isoaspartyl-protein carboxyl methyltransferase	664	NP_207161.1	2
26695	57566	A06	HP0276	hypothetical protein	592	NP_207074.1	1.983
26695	57570	A07	HP0579	hypothetical protein	589	NP_207373.1	1.993
26695	57574	A08	HP0472	outer membrane protein	595	NP_207270.1	2
26695	57579	A09	HP1108	pyruvate ferredoxin oxidoreductase, gamma subunit	595	NP_207899.1	2
26695	57583	A10	HP0755	molybdopterin biosynthesis protein	667	NP_207548.1	2.936
26695	57586	A11	HP0794	ATP-dependent clp protease proteolytic component	625	NP_207587.1	2
26695	57590	A12	HP0061	hypothetical protein	604	NP_206861.1	2
26695	57594	B01	HP0991	hypothetical protein	664	NP_207782.1	2
26695	57598	B02	HP1130	biopolymer transport protein	604	NP_207921.1	1.993
26695	57603	B03	HP1281	anthranilate synthase component II	619	NP_208073.1	1.994
26695	57607	B04	HP0545	cag pathogenicity island protein	658	NP_207341.1	1.862
26695	57611	B05	HP0124	translation initiation factor IF-3	646	NP_206924.1	1.937
26695	57614	B06	HP1323	ribonuclease HII	664	NP_208115.1	2
26695	57622	B07	HP0718	conserved hypothetical integral membrane protein	667	NP_207512.1	2
26695	57626	B08	HP0652	phosphoserine phosphatase	658	NP_207446.1	1.758
26695	57630	B09	HP1256	ribosome releasing factor	592	NP_208048.1	1.986
26695	57634	B10	HP0813	conserved hypothetical protein	652	NP_207606.1	2
26695	57638	B11	HP1016	phosphatidylglycerophosphate synthase	637	NP_207806.1	1.987
26695	57642	B12	HP0806	hypothetical protein	655	NP_207599.1	2
26695	57646	C01	HP1485	conserved hypothetical protein	607	NP_208276.1	1.946
26695	57650	C02	HP0954	oxygen-insensitive NAD(P)H nitroreductase	667	NP_207746.1	2
26695	57655	C03	HP1127	hypothetical protein	616	NP_207918.1	1.994

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Strain	Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
26695	57658	C04	HP1574	riboflavin synthase alpha subunit	655	NP_208365.1	2
26695	57663	C05	HP0068	urease accessory protein	634	NP_206868.1	2
26695	57670	C06	HP1424	lipoprotein, putative	655	NP_208215.1	1.951
26695	57679	C07	HP0428	phage/colicin/tellurite resistance cluster terY protein	592	NP_207226.1	1.983
26695	57682	C08	HP0338	hypothetical protein	601	NP_207136.1	-
26695	57687	C09	HP0769	molybdopterin-guanine dinucleotide biosynthesis protein A	640	NP_207562.1	1.994
26695	57690	C10	HP0177	translation elongation factor EF-P	598	NP_206976.1	1.993
26695	57694	C11	HP1066	conserved hypothetical protein	637	NP_207857.1	2
26695	57698	C12	HP0933	hypothetical protein	637	NP_207725.1	2
26695	57703	D01	HP0802	GTP cyclohydrolase II	613	NP_207595.1	2
26695	57707	D02	HP0630	modulator of drug activity	619	NP_207424.1	2
26695	57714	D03	HP1169	glutamine ABC transporter, permease protein	688	NP_207960.1	1.994
26695	57718	D04	HP0920	conserved hypothetical integral membrane protein	727	NP_207712.1	3.1
26695	57722	D05	HP1115	hypothetical protein	721	NP_207906.1	2.99
26695	57727	D06	HP0507	conserved hypothetical protein	673	NP_207304.1	-
26695	57730	D07	HP0395	conserved hypothetical protein	703	NP_207193.1	2
26695	57735	D08	HP0761	hypothetical protein	682	NP_207554.1	2
26695	57738	D09	HP0939	amino acid ABC transporter, permease protein	748	NP_207731.1	2
26695	57743	D10	HP1365	response regulator	676	NP_208157.1	-
26695	57747	D11	HP0232	secreted protein involved in flagellar motility	682	NP_207030.1	2
26695	57751	D12	HP0851	conserved hypothetical integral membrane protein	718	NP_207644.1	-
26695	57754	E01	HP0166	response regulator	712	NP_206965.1	2
26695	57758	E02	HP1378	competence lipoprotein	697	NP_208169.1	2.703
26695	57763	E03	HP0674	hypothetical protein	721	NP_207468.1	1.635
26695	57766	E04	HP0369	hypothetical protein	745	NP_207167.1	2
26695	57770	E05	HP1268	NADH-ubiquinone oxidoreductase, NQO9 subunit	697	NP_208060.1	2
26695	57775	E06	HP0145	cytochrome c oxidase, monoheme subunit, membrane-bound	733	NP_206944.1	2.75
26695	57779	E07	HP0633	quinone-reactive Ni/Fe hydrogenase, cytochrome b subunit	709	NP_207427.1	2.691
26695	57785	E08	HP1537	hypothetical protein	721	NP_208328.1	1.594
26695	57790	E09	HP1318	ribosomal protein L4	682	NP_208110.1	2
26695	57795	E10	HP0606	membrane fusion protein	739	NP_207401.1	2
26695	57799	E11	HP0531	cag pathogenicity island protein	691	NP_207327.1	1.74
26695	57806	E12	HP1148	tRNA (guanine-N1)-methyltransferase	724	NP_207939.1	2.454
26695	57810	F01	HP0748	cell division protein	706	NP_207541.1	2
26695	57814	F02	HP0982	hypothetical protein	730	NP_207773.1	2
26695	57818	F03	HP1463	hypothetical protein	712	NP_208254.1	2
26695	57823	F04	HP0864	hypothetical protein	691	NP_207658.1	2
26695	57827	F05	HP1580	hypothetical protein	697	NP_208371.1	1.813
26695	57830	F06	HP1178	purine-nucleoside phosphorylase	736	NP_207969.1	1.958
26695	57834	F07	HP1577	probable nickel ABC transporter, permease protein	682	NP_208368.1	2

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26695	57842	F08	HP1386	D-ribulose-5-phosphate 3 epimerase	688	NP_208177.1	2
26695	57846	F09	HP1043	response regulator	706	NP_207833.1	2
26695	57850	F10	HP0819	osmoprotection protein	685	NP_207612.1	1.917
26695	57854	F11	HP1290	nicotinamide mononucleotide transporter	697	NP_208082.1	1.994
26695	57858	F12	HP0828	ATP synthase F0, subunit a	715	NP_207621.1	2
26695	57862	G01	HP1313	ribosomal protein S3	739	NP_208105.1	2
26695	57867	G02	HP0005	orotidine 5'-phosphate decarboxylase	718	NP_206807.1	1.71
26695	57870	G03	HP0194	triosephosphate isomerase	739	NP_206993.1	2
26695	57875	G04	HP1170	glutamine ABC transporter, permease protein	706	NP_207961.1	2.935
26695	57880	G05	HP1107	outer membrane protein	727	NP_207898.1	1.585
26695	57883	G06	HP0952	conserved hypothetical integral membrane protein	691	NP_207744.1	2
26695	57886	G07	HP1287	transcriptional regulator	688	NP_208079.1	2
26695	57891	G08	HP0181	hypothetical protein	709	NP_206980.1	2
26695	57894	G09	HP0613	ABC transporter, ATP-binding protein	736	NP_207408.1	1.995
26695	57898	G10	HP0628	hypothetical protein	712	NP_207422.1	2
26695	57902	G11	HP0257	conserved hypothetical secreted protein	694	NP_207055.1	2
26695	57907	G12	HP0639	conserved hypothetical protein	715	NP_207433.1	1.994
26695	57910	H01	HP1078	hypothetical protein	721	NP_207869.1	-
26695	57918	H02	HP0691	3-oxoadipate coA-transferase subunit A	733	NP_207485.1	2
26695	57923	H03	HP0862	hypothetical protein	706	NP_207656.1	1.694
26695	57933	H04	HP0474	molybdenum ABC transporter, permease protein	709	NP_207272.1	1.114
26695	57934	H05	HP1207	hypothetical protein	703	NP_207999.1	2
26695	57938	H06	HP1224	uroporphyrinogen III cosynthase	715	NP_208016.1	2
26695	57943	H07	HP0454	hypothetical protein	733	NP_207252.1	-
26695	57947	H08	HP0990	hypothetical protein	703	NP_207781.1	1.947
26695	57950	H09	HP1086	hemolysin	742	NP_207877.1	1.995
26695	57954	H10	HP0389	superoxide dismutase	676	NP_207187.1	2
26695	57958	H11	HP0050	adenine specific DNA methyltransferase	733	NP_206851.1	3.271
26695	57963	H12	HP0481	adenine specific DNA methyltransferase	670	NP_207279.1	1.869

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

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