Product Information Sheet for NR-19479

Helicobacter pylori Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 3

Catalog No. NR-19479

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For research use only. Not for human use.

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 *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.

Plate orientation and viability were confirmed for NR-19479.

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-19479 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: 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 3, NR-19479."

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 3 (ZHPAC)[1]

Strain	Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number[2]	Average Depth of Coverage
26695	56706	A01	HP0002	6,7-dimethyl-8-ribityllumazine synthase	505	NP_206804.1	2
26695	56711	A02	HP0105	conserved hypothetical protein	502	NP_206905.2	2
26695	56714	A03	HP1160	conserved hypothetical protein	457	NP_207951.1	2
26695	56718	A04	HP1196	ribosomal protein S7	502	NP_207987.1	1.97012
26695	56722	A05	HP0031	hypothetical protein	448	NP_206833.1	2
26695	56727	A06	HP0998	IS605 transposase	463	NP_207789.1	2
26695	56731	A07	HP1338	nickel responsive regulator NikR	481	NP_208130.1	2
26695	56735	A08	HP1246	ribosomal protein S6	463	NP_208038.1	2
26695	56739	A09	HP0737	conserved hypothetical integral membrane protein	511	NP_207531.1	2
26695	56742	A10	HP0877	Holliday junction endodeoxyribonuclease	508	NP_207671.1	1.992126
26695	56751	A11	HP0433	hypothetical protein	478	NP_207231.1	2
26695	56755	A12	HP0084	ribosomal protein L13	460	NP_206884.1	2
26695	56759	B01	HP0334	conserved hypothetical protein	439	NP_207132.1	2
26695	56766	B02	HP1502	hypothetical protein	472	NP_208293.1	1.991525
26695	56771	B03	HP0880	hypothetical protein	457	NP_207674.1	2
26695	56775	B04	HP0721	hypothetical protein	493	NP_207515.1	2
26695	56782	B05	HP0685	flagellar biosynthetic protein	493	NP_207479.1	2
26695	56786	B06	HP0375	hypothetical protein	466	NP_207173.1	1.987124
26695	56791	B07	HP1046	conserved hypothetical protein	475	NP_207836.1	2
26695	56799	B08	HP1228	invasion protein	502	NP_208020.1	2
26695	56803	B09	HP0661	ribonuclease H	466	NP_207455.1	2
26695	56806	B10	HP0556	hypothetical protein	472	NP_207351.1	2
26695	56811	B11	HP0420	hypothetical protein	463	NP_207218.1	2
26695	56814	B12	HP0798	molybdenum cofactor biosynthesis protein C	511	NP_207591.1	1.992172
26695	56823	C01	HP0371	biotin carboxyl carrier protein	505	NP_207169.1	2
26695	56831	C02	HP0344	hypothetical protein	499	NP_207142.1	2
26695	56835	C03	HP1197	ribosomal protein S12	442	NP_207988.1	2
26695	56838	C04	HP1579	hypothetical protein	463	NP_208370.1	2
26695	56843	C05	HP0868	hypothetical protein	496	NP_207662.1	2
26695	56846	C06	HP0129	hypothetical protein	460	NP_206929.1	2

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Strain	Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number[2]	Average Depth of Coverage
26695	56851	C07	HP0136	bacterioferritin comigratory protein	493	NP_206936.1	2
26695	56859	C08	HP1559	flagellar basal-body rod protein	457	NP_208350.1	2
26695	56866	C09	HP1413	conserved hypothetical protein	481	NP_208204.1	2
26695	56870	C10	HP1060	hypothetical protein	517	NP_207851.1	2
26695	56874	C11	HP1120	hypothetical protein	469	NP_207911.1	2
26695	56879	C12	HP1260	NADH-ubiquinone oxidoreductase, NQO7 subunit	436	NP_208052.1	2
26695	56882	D01	HP0219	hypothetical protein	514	NP_207017.1	2
26695	56887	D02	HP0437	IS605 transposase	463	NP_207235.1	2
26695	56891	D03	HP0542	cag pathogenicity island protein	463	NP_207338.1	2
26695	56895	D04	HP0962	acyl carrier protein	496	NP_207754.1	2
26695	56903	D05	HP1445	biopolymer transport protein	487	NP_208236.1	2
26695	56907	D06	HP0817	hypothetical protein	481	NP_207610.1	2
26695	56919	D07	HP1376	(3R)-hydroxymyristoyl-(acyl carrier protein) dehydratase	514	NP_208167.1	-
26695	56922	D08	HP0001	hypothetical protein	451	NP_206803.1	2
26695	56927	D09	HP0735	xanthine guanine phosphoribosyl transferase	496	NP_207529.1	2
26695	56930	D10	HP0308	hypothetical protein	439	NP_207106.1	1.940774
26695	56935	D11	HP0064	hypothetical protein	454	NP_206864.1	2
26695	56938	D12	HP0637	lipoprotein, putative	487	NP_207431.1	1.854209
26695	56943	E01	HP1312	ribosomal protein L16	460	NP_208104.1	2
26695	56951	E02	HP1568	hypothetical protein	586	NP_208359.1	2
26695	56954	E03	HP1006	conjugal transfer protein	568	NP_207797.1	2
26695	56959	E04	HP1245	single-strand DNA-binding protein	574	NP_208037.1	2
26695	56967	E05	HP0741	conserved hypothetical protein	520	NP_207535.1	2
26695	56970	E06	HP0572	adenine phosphoribosyltransferase	574	NP_207367.1	2
26695	56975	E07	HP1230	hypothetical protein	577	NP_208022.1	2
26695	56979	E08	HP1441	peptidyl-prolyl cis-trans isomerase B, cyclosporin-type rotamase	526	NP_208232.1	2
26695	56982	E09	HP1426	conserved hypothetical protein	577	NP_208217.1	2
26695	56986	E10	HP0935	hypothetical protein	520	NP_207727.1	2
26695	56990	E11	HP0323	membrane bound endonuclease	577	NP_207121.1	1.993068
26695	56994	E12	HP0157	shikimic acid kinase I	523	NP_206956.1	1.567878
26695	56998	F01	HP0287	hypothetical protein	553	NP_207085.1	2
26695	57002	F02	HP1038	3-dehydroquinase type II	538	NP_207828.1	1.927509
26695	57007	F03	HP1304	ribosomal protein L6	571	NP_208096.1	2
26695	57011	F04	HP0189	conserved hypothetical integral membrane protein	568	NP_206988.1	2
26695	57014	F05	HP1558	flagellar basal-body rod protein (proximal rod protein)	520	NP_208349.1	1.942308
26695	57019	F06	HP0272	hypothetical protein	568	NP_207070.1	2
26695	57022	F07	HP0390	adhesin-thiol peroxidase	535	NP_207188.1	2
26695	57026	F08	HP1136	ATP synthase F0, subunit b	550	NP_207927.1	2
26695	57030	F09	HP0273	hypothetical protein	574	NP_207071.1	2
26695	57035	F10	HP1462	secreted protein involved in flagellar motility	553	NP_208253.1	2
26695	57038	F11	HP0891	conserved hypothetical protein	559	NP_207684.1	2
26695	57043	F12	HP0809	hypothetical protein	586	NP_207602.1	2
26695	57047	G01	HP0883	Holliday junction DNA helicase	586	NP_207676.1	2
26695	57051	G02	HP1289	hypothetical protein	520	NP_208081.1	2

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26695	57054	G03	HP0305	hypothetical protein	589	NP_207103.1	2
26695	57058	G04	HP0460	hypothetical protein	523	NP_207258.1	2
26695	57062	G05	HP0860	conserved hypothetical protein	556	NP_207654.1	2
26695	57067	G06	HP1540	ubiquinol cytochrome c oxidoreductase, Rieske 2Fe-2S subunit	538	NP_208331.1	2
26695	57070	G07	HP1530	purine nucleoside phosphorylase	577	NP_208320.1	2
26695	57075	G08	HP1570	conserved hypothetical protein	529	NP_208361.1	2
26695	57079	G09	HP1236	hypothetical protein	586	NP_208028.1	2
26695	57082	G10	HP1456	membrane-associated lipoprotein	562	NP_208247.1	2
26695	57088	G11	HP0391	purine-binding chemotaxis protein	532	NP_207189.1	1.093985
26695	57090	G12	HP0793	polypeptide deformylase	559	NP_207586.1	1.864043
26695	57095	H01	HP1383	restriction modification system S subunit	517	NP_208174.1	2
26695	57098	H02	HP0634	quinone-reactive Ni/Fe hydrogenase	571	NP_207428.1	2
26695	57102	H03	HP0234	conserved hypothetical integral membrane protein	565	NP_207032.1	2
26695	57107	H04	HP0664	hypothetical protein	550	NP_207458.1	2
26695	57111	H05	HP1286	conserved hypothetical secreted protein	583	NP_208078.1	2
26695	57115	H06	HP1063	glucose-inhibited division protein	571	NP_207854.1	2
26695	57119	H07	HP0398	hypothetical protein	583	NP_207196.1	2
26695	57123	H08	HP0270	hypothetical protein	523	NP_207068.1	2
26695	57127	H09	HP0058	hypothetical protein	541	-	2
26695	57130	H10	HP1359	hypothetical protein	586	NP_208151.1	1.991468
26695	57134	H11	HP1269	NADH-ubiquinone oxidoreductase, NQO10 subunit	583	NP_208061.1	2
26695	57138	H12	HP1029	hypothetical protein	571	NP_207819.1	1.992995

[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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