

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 1**

Catalog No. NR-19597

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Contributor:

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

Manufacturer:

BEI Resources

Product Description:

The *Yersinia pestis* (*Y. pestis*), strain KIM, Gateway® clone set consists of 43 plates (plate 2 of this clone set has been discontinued) which contain more than 3600 sequence validated clones from *Y. pestis*, strain KIM 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 a TAG 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.

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-19597 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 18 to 24 hours.

Citation:

Acknowledgment for publications should read “The following reagent was obtained through BEI Resources, NIAID, NIH: *Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 1, NR-19597.”

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/bmb15/index.htm.

Disclaimers:

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References:

1. Deng, W., et al. "Genome Sequence of *Yersinia pestis* KIM." *J. Bacteriol.* 184 (2002): 4601-4611. PubMed: 12142430.
2. Lindler, L. E., et al. "Complete DNA Sequence and Detailed Analysis of the *Yersinia pestis* KIM5 Plasmid Encoding Murine Toxin and Capsular Antigen." *Infect. Immun.* 66 (1998): 5731-5742. PubMed: 9826348.

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Table 1: *Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 1 (UYPVA)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38250	A01	NTL02YP3655	transcriptional activator of nhaA	900	AAM87251.1	3.90531915
38268	A02	NTL02YP0999	apbA protein	912	AAM84595.1	6.01785714
38344	A03	NTL02YP3653	putative regulator	939	AAM87249.1	5.6680286
38375	A04	NTL02YP3668	homoserine kinase	951	AAM87264.1	5.57214934
38386	A05	NTL02YP1006	cytochrome o ubiquinol oxidase subunit II	957	AAM84602.1	5.45937813
38408	A06	NTL02YP2211	suppressor of htrB, heat shock protein	963	AAM85807.1	5.40877368
38447	A07	NTL02YP3649	penicillin tolerance protein	978	AAM87245.1	5.34086444
38477	A08	NTL02YP0988	thiamin-monophosphate kinase	990	AAM84584.1	6.8223301
36045	A09	NTL02YP3670	hypothetical protein	159	AAM87266.1	4.53266332
36094	A10	NTL02YP3672	hypothetical protein	174	AAM87268.1	4.72429907
36136	A11	NTL02YP1000	hypothetical protein	189	AAM84596.1	5.25327511
36241	A12	NTL02YP2577	hypothetical protein	225	AAM86173.1	3.88301887
36280	B01	NTL02YP4086	membrane-bound ATP synthase, F0 sector, subunit c	240	AAM87682.1	4.79285714
36342	B02	NTL02YP3654	30S ribosomal subunit protein S20	264	AAM87250.1	3.86513158
36362	B03	NTL02YP2570	hypothetical protein	270	AAM86166.1	5.40322581
38504	B04	NTL02YP2573	putative ABC transporter permease	996	AAM86169.1	6.65444015
38516	B05	NTL02YP0234	putative heat shock protein	1002	AAM83830.1	2.08445298
38780	B06	NTL02YP0985	bifunctional pyrimidine deaminase/reductase	1110	AAM84581.1	6.64173913
38843	B07	NTL02YP2567	putative hemolysin	1140	AAM86163.1	6.50169492
38933	B08	NTL02YP3656	Na ⁺ /H antiporter, pH dependent	1185	AAM87252.1	6.04244898
36435	B10	NTL02YP0995	exonuclease VII, small subunit	297	AAM84591.1	3.96142433
36474	B11	NTL02YP2568	hypothetical protein	309	AAM86165.1	4.90830946
36516	B12	NTL02YP2566	putative alpha helix protein	324	AAM86162.1	6.35714286
36671	C01	NTL02YP3648	hypothetical protein	381	AAM87244.1	5.58194774
36779	C02	NTL02YP0987	transcription termination L factor	417	AAM84583.1	5.97592998
36804	C03	NTL02YP4080	membrane-bound ATP synthase, F1 sector, epsilon-subunit	423	AAM87676.1	5.95464363
36893	C04	NTL02YP4088	membrane-bound ATP synthase	450	AAM87684.1	5.99387755
36885	C05	NTL02YP0984	hypothetical protein	450	AAM84580.1	5.97755102
36951	C06	NTL02YP3674	hypothetical protein	468	AAM87270.1	5.96456693
36966	C07	NTL02YP4085	membrane-bound ATP synthase, F0 sector, subunit b	471	AAM87681.1	5.98238748
37033	C08	NTL02YP2837	pH 6 Antigen fimbrial subunit	492	AAM86433.1	4.9943609

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39239	C09	NTL02YP1002	putative transport protein	1371	AAM84598.1	5.897236
39255	C10	NTL02YP4079	N-acetyl glucosamine-1-phosphate uridylyltransferase	1377	AAM87675.1	6.22582922
39275	C11	NTL02YP3661	putative proline/betaine transporter	1389	AAM87257.1	6.28551435
39356	C12	NTL02YP0997	putative oxidoreductase	1452	AAM84593.1	6.13739946
39397	D01	NTL02YP2569	exonuclease I	1494	AAM86164.1	5.74380704
39453	D02	NTL02YP4083	membrane-bound ATP synthase, F1 sector, alpha-subunit	1542	AAM87679.1	6.03539823
39637	D03	NTL02YP0993	1-deoxyxylulose-5-phosphate synthase	1860	AAM84589.1	5.79
37095	D04	NTL02YP3651	prolipoprotein signal peptidase (SPase II)	510	AAM87247.1	5.98363636
37137	D07	NTL02YP0986	riboflavin synthase, beta chain	531	AAM84582.1	7.13309982
37150	D08	NTL02YP3650	probable FKBP-type 16KD peptidyl-prolyl cis-trans isomerase	534	AAM87246.1	7.14111498
37153	D09	NTL02YP4084	membrane-bound ATP synthase, F1 sector, delta-subunit	534	AAM87680.1	5.81707317
37182	D10	NTL02YP3677	hypothetical protein	543	AAM87273.1	6.79588336
37326	D11	NTL02YP3662	putative molybdochetalase	588	AAM87258.1	4.11464968
37341	D12	NTL02YP0983	hypothetical protein	594	AAM84579.1	6.5
37346	E01	NTL02YP0998	4-methyl-5(beta-hydroxyethyl)-thiazole monophosphate synthesis enzyme	597	AAM84594.1	6.80376766
39687	E02	NTL02YP4090	hypothetical protein	1971	AAM87686.1	5.23421183
39692	E03	NTL02YP1005	cytochrome o ubiquinol oxidase subunit I	1992	AAM84601.1	5.41043307
39880	E04	NTL02YP3652	isoleucine tRNA synthetase	2817	AAM87248.1	5.18340917
37392	E05	NTL02YP1004	cytochrome o ubiquinol oxidase subunit III	615	AAM84600.1	6.79236641
37505	E06	NTL02YP3676	phosphoglyceromutase 2	648	AAM87272.1	6.71511628
37581	E07	NTL02YP4089	glucose-inhibited division protein	672	AAM87685.1	6.77668539
37634	E08	NTL02YP0982	hypothetical protein	696	AAM84578.1	6
38027	E10	NTL02YP4087	membrane-bound ATP synthase, F0 sector, subunit a	825	AAM87683.1	7.01040462
38031	E11	NTL02YP2575	putative enzyme of sugar metabolism	828	AAM86171.1	7.58410138
38136	E12	NTL02YP4082	membrane-bound ATP synthase, F1 sector, gamma-subunit	864	AAM87678.1	6.4170354
36859	F01	NTL02YPB0035	low calcium response protein R	441	NP_857749.1	4.97505198
36995	F02	NTL02YPD0056	unknown	477	NP_857841.1	4.98646035
37053	F04	NTL02YPB0010	secreted effector protein	498	NP_857725.1	4.98698885
37081	F05	NTL02YPB0038	secretion chaperone	507	NP_857752.1	5.96160878
37203	F06	NTL02YPB0047	yopK targeting protein	549	NP_857759.1	4.72665535
37213	F07	NTL02YPB0063	putative resolvase	552	NP_857768.1	4.79898649
37329	F08	NTL02YPA0007	hypothetical protein	588	NP_857644.2	4.79936306
37385	F09	NTL02YPA0003	tail fiber assembly protein G	609	NP_857640.2	4.38983051
36165	F10	NTL02YPB0049	hypothetical protein	198	NP_954879.1	3.94117647
36196	F11	NTL02YPE0007	hypothetical protein	207	NP_857909.1	4.80161943
36344	G01	NTL02YPB0012	needle complex major subunit	264	NP_857727.1	3.90131579
37458	G03	NTL02YPD0049	unknown	633	NP_857833.1	4.80089153
37523	G04	NTL02YPB0024	needle complex export protein	654	NP_857738.1	4.78530259
37543	G05	NTL02YPB0055	secreted effector protein	660	NP_857762.1	4.78857143
37565	G06	NTL02YPB0006	needle complex assembly protein	666	NP_857721.1	4.78328612
37761	G07	NTL02YPB0008	needle complex inner membrane lipoprotein	735	NP_857723.1	4.38193548
37909	G10	NTL02YPB0022	needle complex export protein	786	NP_857736.1	3.99031477
37932	G11	NTL02YPA0076	hypothetical protein	795	NP_857699.2	5.63353293
37998	H01	NTL02YPB0018	transcriptional regulator	816	NP_857733.1	5.62149533

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36391	H02	NTL02YPB0030	secretion and targeting control protein	279	NP_857744.1	3.80877743
36420	H03	NTL02YPB0036	low calcium response protein G	288	NP_857750.1	3.99085366
36440	H04	NTL02YPB0054	yKCD1p58 hypothetical protein	297	NP_954882.1	5.7537092
38040	H07	NTL02YPA0050	hypothetical protein	831	NP_857682.2	5.57520092
38195	H08	NTL02YPB0029	secretion control protein	882	NP_857743.1	4.23318872
38297	H09	NTL02YPB0025	needle complex export protein	924	NP_857739.1	2.93568465
38413	H10	NTL02YPB0051	plasmid-partitioning control protein	963	NP_857761.2	3.53938185
38424	H11	NTL02YPB0046	secreted effector protein	969	NP_857758.1	3.60951437

¹The locus ID numbers given in this table were obtained from JCVI at the time of deposition. Please note that the locus tags have since been updated by JCVI and the corrected locus ID numbers can be obtained from the [JCVI-CMR](http://www.jcvi-cmr.org) webpage using the locus search option and inputting the above locus IDs.