

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 25**

**Catalog No. NR-19621**

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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-19621 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 25, NR-19621.”

**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](http://www.cdc.gov/biosafety/publications/bmb15/index.htm).

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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 25 (UYPVY)**

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37978	A02	NTL02YP3091	30S ribosomal subunit protein S2	810	AAM86687.1	2
38084	A03	NTL02YP3101	hypothetical protein	846	AAM86697.1	3.638826
38093	A04	NTL02YP3083	CDP-diglyceride synthetase	849	AAM86679.1	3.320585
38122	A05	NTL02YP3089	protein chain elongation factor EF-Ts	858	AAM86686.1	3.591314
38152	A06	NTL02YP3094	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	870	AAM8690.1	2.668132
38163	A07	NTL02YP3126	phosphatidylglycerol-prolipoprotein diacylglyceryl transferase	873	AAM86722.1	2.786418
38283	A08	NTL02YP3108	positive regulator of gcv operon	918	AAM86704.1	6.289144
38298	A09	NTL02YP0008	ribokinase	927	AAM83604.1	5.462254
38305	A10	NTL02YP0013	homoserine transsuccinylase	930	AAM83609.1	5.224742
35942	A11	NTL02YP3771	hypothetical protein	114	AAM87367.1	1.974026
35974	A12	NTL02YP0018	hypothetical protein	138	AAM83614.1	3.949438
35986	B01	NTL02YP0014	hypothetical protein	150	AAM83610.1	3.947368
36125	B02	NTL02YP3109	hypothetical protein	183	AAM86705.1	3.955157
36169	B03	NTL02YP3086	hypothetical protein	201	AAM86682.1	4.585062
36174	B04	NTL02YP0009	hypothetical protein	204	AAM83605.1	5.807377
36364	B05	NTL02YP3763	hypothetical protein	270	AAM87359.1	5.9
36464	B06	NTL02YP2676	putative transposase	306	AAM86273.1	6.254335
36659	B07	NTL02YP3098	hypothetical protein	378	AAM86694.1	5.638756
38363	B08	NTL02YP3775	dipeptide transport system inner membrane permease	948	AAM87371.1	6.100202
38466	B09	NTL02YP3139	positive regulator for lys	987	AAM86735.1	6.115871
38468	B10	NTL02YP3762	hypothetical protein	987	AAM87358.1	5.762415
38486	B11	NTL02YP0003	asparagine synthetase A	933	AAM83599.1	3.50242
38578	C01	NTL02YP3079	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase	1023	AAM86675.1	3.575729
38625	C03	NTL02YP3131	hypothetical protein	1041	AAM86727.1	2.888992
38711	C04	NTL02YP3090	hypothetical protein	1080	AAM86685.1	1.801786
38747	C05	NTL02YP3137	repressor of galETK operon	1092	AAM86733.1	3.469081
38775	C06	NTL02YP3106	hypothetical protein	1107	AAM86702.1	3.450741
38886	C07	NTL02YP3140	MFS transporter	1161	AAM86736.1	3.412989
36750	C08	NTL02YP0024	hypothetical protein	408	AAM83620.1	5.962054
36749	C09	NTL02YP0012	hypothetical protein	408	AAM83608.1	5.979911
36787	C10	NTL02YP0007	D-ribose high-affinity transport system membrane-associated protein	420	AAM83603.1	2

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36795	C11	NTL02YP3107	hypothetical protein	420	AAM86703.1	6.578261
36852	C12	NTL02YP0001	initiation of chromosome replication	441	AAM83597.1	2
36865	D01	NTL02YP3111	hypothetical protein	444	AAM86707.1	5.644628
36891	D02	NTL02YP3096	hypothetical protein	450	AAM86692.1	5.967347
36922	D03	NTL02YP0002	regulator for asnA, asnC and gidA	462	AAM83598.1	2
36964	D04	NTL02YP3122	hypothetical protein	471	AAM86718.1	2
38905	D05	NTL02YP3113	membrane-bound lytic murein transglycosylase A	1173	AAM86709.1	3.392415
38953	D06	NTL02YP3085	putative ATP-binding component of a transport system	1197	AAM86681.1	5.41633
38980	D07	NTL02YP3766	putative transposase	1209	AAM87362.1	3.329063
38993	D08	NTL02YP3134	putative resistance protein	1221	AAM86730.1	3.324346
39056	D09	NTL02YP3138	diaminopimelate decarboxylase	1263	AAM86734.1	4.025326
39062	D10	NTL02YP3115	putative amidase	1269	AAM86711.1	3.274255
39132	D11	NTL02YP0016	isocitrate lyase	1308	AAM83612.1	3.942878
39172	D12	NTL02YP3116	N-acetylglutamate synthase	1326	AAM86712.1	3.84041
39217	E01	NTL02YP3082	hypothetical protein	1356	AAM86678.1	1.281519
39225	E02	NTL02YP3770	regulator of uhpT	1362	AAM87366.1	6.651213
39229	E03	NTL02YP3102	hypothetical protein	1365	AAM86698.1	6.730249
37134	E05	NTL02YP3128	putative invasion protein	528	AAM86724.1	2.834507
37211	E06	NTL02YP3100	syd protein	552	AAM86696.1	6.194257
37227	E07	NTL02YP3087	ribosome releasing factor	558	AAM86683.1	1.994983
37228	E08	NTL02YP3765	molybdopterin-guanine dinucleotide biosynthesis protein B	558	AAM87361.1	2.82107
37266	E09	NTL02YP3124	hypothetical protein	570	AAM86720.1	6.790164
37337	E10	NTL02YP3080	automembrane protein H	591	AAM86676.1	3.087163
37383	E11	NTL02YP3123	hypothetical protein	609	AAM86719.1	2
37436	E12	NTL02YP3761	protein disulfide isomerase I	624	AAM87357.1	2.805723
37482	F01	NTL02YP3764	molybdopterin-guanine dinucleotide synthase	642	AAM87360.1	2
39271	F02	NTL02YP0022	aspartokinase III, lysine sensitive	1386	AAM83618.1	3.791024
39284	F03	NTL02YP3772	hypothetical protein	1392	AAM87368.1	3.898743
39319	F04	NTL02YP0010	putative permease	1425	AAM83606.1	3.734471
39462	F05	NTL02YP0005	putative 2-component regulator	1554	AAM83601.1	3.428482
39504	F06	NTL02YP0015	malate synthase A	1632	AAM83611.1	3.025718
39519	F07	NTL02YP0023	glucosephosphate isomerase	1647	AAM83619.1	3.413159
39576	F08	NTL02YP0017	isocitrate dehydrogenase kinase/phosphatase	1728	AAM83613.1	3.375566
39605	F09	NTL02YP3773	hemolysin activator protein precursor	1788	AAM87369.1	4.492888
39679	F10	NTL02YP3117	DNA helicase, ATP-dependent dsDNA/ssDNA exonuclease V subunit	1959	AAM86713.1	10.63982
37620	F11	NTL02YP3129	methyl-directed mismatch repair protein	687	AAM86725.1	6.151307
37622	F12	NTL02YP0011	hypothetical protein	690	AAM83607.1	2
37731	G01	NTL02YP3088	uridylyate kinase	726	AAM86684.1	2.792428
37770	G02	NTL02YP3769	sensor protein	738	AAM87365.1	2.775064
37825	G03	NTL02YP3084	hypothetical protein	759	AAM86680.1	5.305382
37869	G04	NTL02YP3097	hypothetical protein	774	AAM86693.1	3.627764
37913	G08	NTL02YP2666	putative 3-oxoacyl-acyl carrier protein reductase	792	AAM86266.1	5.412545
37920	G09	NTL02YP2670	putative 3-ketoacyl-acyl carrier protein reductase	832	AAM85802.1	5.677885

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37967	G10	NTL02YP1560	putative structural protein	807	AAM85156.1	3.316411
38092	G11	NTL02YP2664	putative acyl transferase	849	AAM86260.1	3.073116
38149	G12	NTL02YP1559	murein DD-endopeptidase	870	AAM85155.1	3.564835
36510	H01	NTL02YP3728	PTS system fructose-like IIB component 1	321	AAM87324.1	4.290859
38542	H02	NTL02YP1571	putative enzyme	1011	AAM85167.1	3.414843
38665	H03	NTL02YP2643	hypothetical protein	1059	AAM86239.1	6.993631
38714	H04	NTL02YP3754	histidine protein kinase sensor for GlnG regulator	1080	AAM87350.1	3.161607
36632	H05	NTL02YP0476	50S ribosomal subunit protein L7/L12	369	AAM84072.1	2
36819	H06	NTL02YP0473	50S ribosomal subunit protein L11	429	AAM84069.1	5.974414
36962	H07	NTL02YP2642	hypothetical protein	471	AAM86238.1	5.972603
38735	H08	NTL02YP1558	chorismate synthase	1089	AAM85154.1	3.441984
38877	H09	NTL02YP3734	hypothetical protein	1155	AAM87330.1	2.521339
38927	H10	NTL02YP0470	protein chain elongation factor EF-Tu	1185	AAM84066.1	3.318367
38939	H11	NTL02YP1570	erythronate-4-phosphate dehydrogenase	1188	AAM85166.1	3.164495
38954	H12	NTL02YP3732	hypothetical protein	1197	AAM87328.1	3.280517

<sup>1</sup>The 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://jcvicmr.org) webpage using the locus search option and inputting the above locus IDs.