

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 17**

**Catalog No. NR-19613**

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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-19613 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 17, NR-19613."

**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/bmbli5/index.htm](http://www.cdc.gov/biosafety/publications/bmbli5/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 17 (UYPVQ)**

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37905	A01	NTL02YP2215	putative fimbrial protein	826	AAM85436.1	4.204600484
37941	A02	NTL02YP2178	protein methylesterase	838	AAM85407.1	3.081145585
35960	A03	NTL02YP2183	putative regulator	166	AAM85412.1	2
36018	A05	NTL02YP3302	aspartate aminotransferase	193	AAM86312.1	3.968911917
36024	A06	NTL02YP2180	chemotaxis phosphatase	196	AAM85410.1	2.974489796
36200	A07	NTL02YP2181	hypothetical protein	250	AAM5777.1	5.872
36304	A08	NTL02YP1117	probable LysR-type transcriptional regulatory protein	292	AAM84542.1	2
36359	A09	NTL02YP2198	cell division topological specificity factor	310	AAM85794.1	3.738709677
38015	A10	NTL02YP3282	3-oxoacyl-[acyl-carrier-protein] synthase II	862	AAM86296.1	3.554524362
38103	A11	NTL02YP1127	gamma-glutamylphosphate reductase	895	AAM84548.1	6.54301676
38204	A12	NTL02YP3278	hypothetical protein	925	AAM86874.1	5.644324324
38229	B01	NTL02YP1105	Na <sup>+</sup> -translocating NADH ubiquinone oxidoreductase	934	AAM84535.1	5.880085653
38308	B02	NTL02YP1098	putative phosphatidate cytidyltransferase	970	AAM84694.1	4.884536082
38391	B03	NTL02YP2213	carboxy-terminal protease for penicillin-binding protein 3	997	AAM85434.1	5.311935807
38404	B04	NTL02YP3300	periplasmic binding protein for ABC transporter	1000	AAM86896.1	8.169
38489	B05	NTL02YP1106	hypothetical protein	1033	AAM84536.1	3.485963214
38535	B06	NTL02YP2216	probable pilin chaperone	1045	AAM85437.1	3.475598086
36375	B07	NTL02YP3294	hypothetical protein	313	AAM86890.1	3.808306709
36450	B08	NTL02YP1122	putative regulator	343	AAM84718.1	3.973760933
36457	B09	NTL02YP3284	hypothetical protein	343	AAM86298.1	5.959183673
36471	B10	NTL02YP1115	hypothetical protein	349	AAM84711.1	5.853868195
36523	B11	NTL02YP3291	dihydroorotate dehydrogenase	367	AAM86306.1	3.931880109
36570	B12	NTL02YP2204	putative pilus assembly chaperone	385	AAM85426.1	5.451948052
36579	C01	NTL02YP2205	hypothetical protein	388	AAM85427.1	6.399484536
36637	C02	NTL02YP3304	hypothetical protein	409	AAM86313.1	5.621026895
36685	C03	NTL02YP2184	hypothetical protein	430	AAM85413.1	3.802325581
36734	C04	NTL02YP1119	hypothetical protein	442	AAM84543.1	4.746606335
38570	C05	NTL02YP3298	asparagine tRNA synthetase	1060	AAM86310.1	2.923584906
38586	C07	NTL02YP2209	hypothetical protein	1066	AAM85431.1	5.237335835
38739	C08	NTL02YP3295	membrane-bound lytic murein transglycosylase C	1129	AAM86891.1	3.056687334

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38736	C09	NTL02YP2194	putative transglycosylase	1129	AAM85790.1	2.657218778
38759	C10	NTL02YP3279	hypothetical protein	1138	AAM86293.1	2.585237258
38785	C11	NTL02YP3296	putative solute-binding periplasmic protein of ABC transporter	1150	AAM86892.1	3.634782609
38850	C12	NTL02YP3286	paraquat-inducible protein A	1183	AAM86300.1	5.634826712
38883	D01	NTL02YP2199	hypothetical protein	1201	AAM85423.1	2.159034138
36854	D02	NTL02YP1120	hypothetical protein	481	AAM84716.1	5.553014553
36875	D03	NTL02YP2192	hypothetical protein	487	AAM85788.1	4.104722793
36874	D04	NTL02YP2187	hypothetical protein	487	AAM85415.1	4.425051335
37044	D05	NTL02YP1093	putative membrane protein	538	AAM84524.1	4.650557621
37138	D07	NTL02YP1111	hypothetical protein	571	AAM84707.1	4.65323993
37215	D08	NTL02YP1126	gamma-glutamate kinase	595	AAM84547.1	4.630252101
37222	D09	NTL02YP3283	putative transposase	595	AAM86297.1	4.638655462
37245	D10	NTL02YP2182	hypothetical protein	604	AAM85411.1	4.437086093
37270	D11	NTL02YP1118	hypothetical protein	613	AAM84714.1	4.644371941
39023	D12	NTL02YP2191	hypothetical protein	1279	AAM85419.1	1.738076622
39036	E01	NTL02YP3293	aminopeptidase N	1288	AAM86308.1	5.562111801
39161	E02	NTL02YP1101	hypothetical protein	1360	AAM84531.1	4.580147059
39346	E03	NTL02YP2210	hypothetical protein	1483	AAM85432.1	3.643964936
39403	E04	NTL02YP3299	putative ATP-binding component of ABC transport system	1540	AAM86895.1	3.026623377
39588	E06	NTL02YP1100	hypothetical protein	1804	AAM84530.1	3.033259424
39660	E07	NTL02YP1116	putative autotransporter	1957	AAM84712.1	3.0148186
39653	E08	NTL02YP2203	hypothetical protein	1945	AAM85425.1	2.743958869
37285	E09	NTL02YP3289	hypothetical protein	616	AAM86304.1	1.998376623
37363	E10	NTL02YP1097	phosphoheptose isomerase	643	AAM84528.1	5.085536547
37373	E11	NTL02YP2201	hypothetical protein	646	AAM85424.1	2
37372	E12	NTL02YP2186	putative phage ninG-like protein	646	AAM85782.1	4
37462	F01	NTL02YP3303	hypothetical protein	676	AAM86899.1	6.133136095
37479	F02	NTL02YP2207	hypothetical protein	682	AAM85429.1	4.384164223
37490	F03	NTL02YP2188	putative DNA methyltransferase	685	AAM85784.1	4.468613139
37579	F04	NTL02YP3285	paraquat-inducible protein B	712	AAM86299.1	4.262640449
37599	F05	NTL02YP2217	putative usher protein	721	AAM85438.1	3.79889043
37431	F06	NTL02YP1767	hypothetical protein	664	AAM85363.1	4.575301205
37441	F07	NTL02YP1773	hypothetical protein	667	AAM85066.1	5.257871064
37451	F08	NTL02YP3938	hypothetical protein	670	AAM86855.1	5.273134328
37454	F09	NTL02YP1770	conserved protein	673	AAM85064.1	5.23922734
37569	F10	NTL02YP1081	glutamine transport atp-binding protein	709	AAM84517.1	5.550070522
37576	F11	NTL02YP1766	etoposide-induced protein 2.4, cysZ protein	712	AAM85061.1	5.825842697
37612	F12	NTL02YP1082	putative ATP-binding component of a transport system	727	AAM84768.1	5.127922971
37647	G01	NTL02YP3943	D-erythrose 4-phosphate dehydrogenase	739	AAM86859.1	6.292286874
37658	G02	NTL02YP2862	hypothetical protein	742	AAM86458.1	5.588948787
37675	G03	NTL02YP2872	putative transposase	748	AAM85969.1	4.657754011
36148	G04	NTL02YP3946	50S ribosomal subunit protein L16	232	AAM87540.1	1.961206897
36208	G05	NTL02YP1091	putative membrane protein, C-terminal part of adhesion	253	AAM84522.1	3.936758893
36406	G06	NTL02YP2875	hypothetical protein	325	AAM85970.1	2.987692308
36459	G07	NTL02YP3940	50S ribosomal subunit protein L23	343	AAM87536.1	1.895043732
37713	G08	NTL02YP1087	hypothetical protein	763	AAM84683.1	3.770642202

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37872	G09	NTL02YP1080	putative permease of ABC transporter	817	AAM84516.1	2
38017	G10	NTL02YP3976	putative glutaminase	862	AAM86886.1	5.032482599
38026	G11	NTL02YP3941	fructose-bisphosphate aldolase, class II	865	AAM86857.1	2.537572254
38148	G12	NTL02YP1079	putative inner membrane permease of ABC transporter	910	AAM84515.1	1.824175824
38272	H01	NTL02YP1078	putative solute-binding protein of ABC transporter	955	AAM84514.1	5.719371728
38364	H02	NTL02YP3970	hypothetical protein	988	AAM86880.1	5.686234818
38421	H03	NTL02YP2851	anthranilate synthase	1006	AAM85952.1	4.137176938
38458	H04	NTL02YP2861	salicyl-AMP ligase	1024	AAM85961.1	5.391601563
38484	H05	NTL02YP3963	hypothetical protein	1030	AAM86873.1	2.82815534
36468	H06	NTL02YP3950	hypothetical protein	346	AAM86862.1	2.959537572
36488	H07	NTL02YP3948	hypothetical protein	355	AAM86861.1	2.977464789
36539	H08	NTL02YP3942	phosphoglycerate kinase	373	AAM86858.1	4.967828418
36572	H09	NTL02YP2869	hypothetical protein	385	AAM86465.1	3.571428571
36595	H10	NTL02YP2874	hypothetical protein	394	AAM86470.1	2.984771574
36597	H11	NTL02YP3954	methionine adenosyltransferase 1	394	AAM86864.1	2.987309645
36646	H12	NTL02YP3947	transketolase 1 isozyme	412	AAM86860.1	3.927184466