

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 24**

**Catalog No. NR-19620**

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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-19620 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 24, NR-19620.”

**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 24 (UYPVX)**

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36567	A01	NTL02YP2682	hypothetical protein	342	AAM86278.1	4.95026
36718	A02	NTL02YP0520	hypothetical protein	399	AAM84116.1	5.95216
36729	A03	NTL02YP0519	hypothetical protein	402	AAM84115.1	1.97738
36764	A04	NTL02YP2697	hypothetical protein	411	AAM86293.1	5.97118
36784	A05	NTL02YP2683	hypothetical protein	417	AAM86279.1	5.9628
36861	A06	NTL02YP1591	putative phosphotransferase system IIA component	444	AAM85187.1	5.76446
36879	A07	NTL02YP2687	hypothetical protein	447	AAM86283.1	2
36905	A08	NTL02YP1596	hypothetical protein	456	AAM85192.1	6.57661
38683	A09	NTL02YP0489	uroporphyrinogen decarboxylase	1068	AAM84085.1	2.61552
38746	A10	NTL02YP2691	outer membrane porin A	1092	AAM86287.1	3.447
38838	A11	NTL02YP1592	putative transcriptional regulator	1137	AAM85188.1	3.41886
38943	A12	NTL02YP2681	putative oxidoreductase	1191	AAM86277.1	3.26158
38962	B01	NTL02YP1595	acetate kinase	1203	AAM85191.1	3.19871
38998	B03	NTL02YP0508	putative type III secretion system component	1227	AAM84104.1	3.27624
39098	B04	NTL02YP3785	C4-dicarboxylic acids symporter	1290	AAM86729.1	7.06466
39101	B05	NTL02YP1601	putative aminotransferase	1293	AAM85197.1	3.22356
36939	B06	NTL02YP2685	methylglyoxal synthase	465	AAM86281.1	5.97228
37039	B07	NTL02YP2693	putative dehydrogenase	495	AAM86289.1	2
37046	B08	NTL02YP1597	hypothetical protein	498	AAM85193.1	2
37058	B09	NTL02YP1603	NADH dehydrogenase I chain A	501	AAM85199.1	2
37076	B10	NTL02YP3784	hypothetical protein	507	AAM87380.1	7.04022
37073	B11	NTL02YP2690	suppressor of lon	507	AAM86286.1	1.97989
37199	C01	NTL02YP1587	putative regulator	549	AAM85183.1	7.14771
37229	C02	NTL02YP0516	putative type III secretion system component	561	AAM84112.1	5.71381
37243	C03	NTL02YP1606	NADH dehydrogenase I chain E	564	AAM85202.1	2.83113
37324	C04	NTL02YP1586	hypothetical protein	588	AAM85182.1	2.77866
37323	C05	NTL02YP1579	3-octaprenyl-4-hydroxybenzoate carboxylase	588	AAM85175.1	4
39273	C06	NTL02YP1607	NADH dehydrogenase I chain F	1386	AAM85203.1	3.78191
39406	C07	NTL02YP3786	hypothetical protein	1500	AAM87382.1	3.64935
39423	C08	NTL02YP1578	amidophosphoribosyltransferase PRPP amidotransferase	1518	AAM85174.1	3.73556

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39476	C09	NTL02YP0507	putative secretin	1572	AAM84103.1	3.67928
39507	C10	NTL02YP0495	phosphoribosylaminoimidazolecarboxamide formyltransferase	1635	AAM84091.1	3.58806
39528	C11	NTL02YP0501	putative sodium/proline symporter	1656	AAM84097.1	3.5855
39574	C12	NTL02YP3783	pectate lyase	1719	AAM87379.1	8.12678
39609	D01	NTL02YP1605	NADH dehydrogenase I chain C, D	1797	AAM85201.1	5.15188
39647	D02	NTL02YP1599	putative ion transport protein	1893	AAM85195.1	3.7522
39681	D03	NTL02YP0503	acetyl CoA synthetase	1965	AAM84099.1	3.45686
37331	D04	NTL02YP0491	hypothetical protein	591	AAM84087.1	2.80349
37342	D05	NTL02YP1600	putative alpha helix protein	594	AAM85196.1	5.02839
37345	D06	NTL02YP0515	hypothetical protein	597	AAM84111.1	2.7551
37412	D07	NTL02YP0510	putative type III secretion system component	621	AAM84106.1	2.78971
37453	D08	NTL02YP0505	response regulator/transcription activator	633	AAM84101.1	2
37552	D09	NTL02YP1598	putative phosphatase	663	AAM85194.1	2.78947
37592	D10	NTL02YP1604	NADH dehydrogenase I chain B	678	AAM85200.1	2.77716
37602	D11	NTL02YP2684	hypothetical protein	681	AAM86280.1	6.2982
37615	D12	NTL02YP1581	histidine ABC transport system inner membrane permease	687	AAM85177.1	1.9945
37643	E01	NTL02YP1585	hypothetical protein	699	AAM85181.1	2
37916	E03	NTL02YP3174	putative permease protein	789	AAM86770.1	1.98914
36294	E04	NTL02YP0074	glutaredoxin 3	249	AAM83670.1	6.84429
36316	E05	NTL02YP0040	putative transposase	258	AAM83636.1	2
38276	E06	NTL02YP3149	putative type IV prepilin peptidase	915	AAM86745.1	3.66702
38306	E07	NTL02YP0032	periplasmic protein of mal regulon	930	AAM83628.1	5.5567
38373	E08	NTL02YP3163	hypothetical protein	951	AAM86759.1	6.27548
38392	E09	NTL02YP3152	hypothetical protein	957	AAM86748.1	5.71916
38394	E10	NTL02YP0061	hypothetical protein	960	AAM83657.1	6.222
38518	E11	NTL02YP0481	thiG protein	1002	AAM84077.1	3.3618
38564	E12	NTL02YP0072	glycerol-3-phosphate dehydrogenase (NAD+)	1020	AAM83668.1	3.61792
36847	F02	NTL02YP3155	putative general protein secretion protein	438	AAM86751.1	5.95816
36853	F03	NTL02YP0038	hypothetical protein	441	AAM83634.1	1.99376
36928	F04	NTL02YP3150	hypothetical protein	462	AAM86746.1	1.98008
36981	F05	NTL02YP0073	protein export molecular chaperone	477	AAM83669.1	5.96712
38642	F06	NTL02YP3156	putative general protein secretion protein	1047	AAM86752.1	3.35051
38674	F07	NTL02YP0069	O6-methylguanine-DNA methyltransferase transcription activator/repressor	1065	AAM83665.1	3.56742
38778	F08	NTL02YP0030	maltose ABC transporter ATP-binding protein	1110	AAM83626.1	3.50174
38798	F09	NTL02YP0047	hypothetical protein	1119	AAM83643.1	3.43917
38981	F11	NTL02YP0027	periplasmic maltose-binding protein	1212	AAM83623.1	3.27476
39107	F12	NTL02YP0052	putative transcriptional regulator	1296	AAM83643.1	6.3009
39119	G01	NTL02YP3171	putative tagatose 6-phosphate kinase 2	1299	AAM86767.1	4.04182
36992	G02	NTL02YP3145	hypothetical protein	477	AAM86741.1	4.53191
37019	G03	NTL02YP0065	putative solute-binding periplasmic protein of ABC transporter	489	AAM83661.1	5.96408
37051	G04	NTL02YP3173	PTS family enzyme IIB component 2 (EIIB-AGA)	498	AAM86209.1	3.99071
37054	G05	NTL02YP0036	conserved hypothetical protein	501	AAM83632.1	2
37085	G06	NTL02YP0485	putative transcriptional regulator	510	AAM84081.1	6.36727

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37109	G07	NTL02YP0035	hemolysin co-regulated protein	519	AAM83631.1	5.77818
37306	G08	NTL02YP0070	hypothetical protein	585	AAM83666.1	3.1152
37338	G09	NTL02YP3154	hypothetical protein	591	AAM86750.1	2.82092
37391	G10	NTL02YP0050	hypothetical protein	615	AAM83646.1	2.7771
39324	G11	NTL02YP0055	putative membrane pump protein	1428	AAM83651.1	3.75341
39343	G12	NTL02YP0031	maltose high-affinity receptor	1440	AAM83627.1	3.80203
39417	H01	NTL02YP3157	putative general secretion protein	1512	AAM86753.1	3.73582
39457	H02	NTL02YP0076	putative 2,3-bisphosphoglycerate-independent phosphoglycerate mutase	1548	AAM83672.1	3.78526
39466	H03	NTL02YP3169	hypothetical protein	1554	AAM86765.1	3.57842
39563	H05	NTL02YP3144	putative methyl-accepting chemotaxis protein	1701	AAM86740.1	3.00747
39662	H06	NTL02YP3158	putative general secretion protein	1923	AAM86754.1	3.63882
37461	H07	NTL02YP3143	hypothetical protein	636	AAM86739.1	2.54734
37671	H08	NTL02YP3146	hypothetical protein	705	AAM86742.1	2.78255
37686	H09	NTL02YP0054	hypothetical protein	714	AAM83650.1	2.40584
37790	H10	NTL02YP0048	ferredoxin-NADP reductase	747	AAM83644.1	6.64676
37839	H11	NTL02YP0051	triosephosphate isomerase	768	AAM83647.1	5.87252
37879	H12	NTL02YP3170	putative DEOR-type transcriptional regulator of aga operon	777	AAM86766.1	3.08568

<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.