

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 16**

**Catalog No. NR-19612**

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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-19612 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 16, NR-19612.”

**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 16 (UYPVP)**

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36931	A01	NTL02YP0678	hypothetical protein	465	AAM84274.1	5.932673
36961	A02	NTL02YP2274	hypothetical protein	471	AAM85870.1	3
36969	A03	NTL02YP1174	hypothetical protein	474	AAM84770.1	2
37056	A04	NTL02YP1166	putative alpha helical protein	501	AAM84762.1	7.120148
37325	A06	NTL02YP3349	hypothetical protein	588	AAM86945.1	2.818471
37604	A07	NTL02YP3341	putative transposase	681	AAM86937.1	2
39308	A08	NTL02YP0696	putative outer membrane protein, efflux pump	1407	AAM84292.1	2.959917
39334	A09	NTL02YP3340	putative carbohydrate symporter permease	1434	AAM86936.1	2.717775
39387	A10	NTL02YP3356	hypothetical protein	1485	AAM86952.1	3.339672
39395	A11	NTL02YP3348	putative enterotoxin-like protein	1491	AAM86944.1	3.598955
39409	A12	NTL02YP0679	transcription pausing L factor	1506	AAM84275.1	2.980595
39449	B01	NTL02YP1176	hypothetical protein	1539	AAM84772.1	3.553515
39480	B02	NTL02YP1171	apolipoprotein N-acyltransferase	1587	AAM84582.1	2.808851
39598	B03	NTL02YP3375	ATP-binding cassette transporter A	1773	AAM86971.1	3.341975
39600	B04	NTL02YP3376	ATP-binding protein	1776	AAM86972.1	3.849119
39621	B05	NTL02YP3354	partial leucine-rich repeat protein	1818	AAM86950.1	3.827234
39644	B06	NTL02YP3351	partial leucine-rich repeat protein	1881	AAM86947.1	3.766268
37631	B07	NTL02YP2270	putative 2-component transcriptional regulator	693	AAM85866.1	2.695771
37637	B08	NTL02YP2267	hypothetical protein	696	AAM85863.1	2.798913
37734	B09	NTL02YP1167	ATP-binding protein of glutamate/aspartate transport system	729	AAM84763.1	6.386216
37847	B10	NTL02YP3373	thioesterase	768	AAM86969.1	5.153465
37918	C01	NTL02YP1169	glutamate/aspartate ABC transport system inner membrane permease	792	AAM84765.1	6.528846
37976	C02	NTL02YP2250	putative transcriptional regulator	810	AAM85846.1	3.603529
37787	C03	NTL02YP3329	putative transcriptional activator	744	AAM86925.1	7.118622
37815	C04	NTL02YP2219	hypothetical protein	756	AAM85815.1	6.052764
37846	C05	NTL02YP3306	hypothetical protein	768	AAM86902.1	5.950495
37959	C06	NTL02YP2225	hypothetical protein	804	AAM85821.1	3.593602
37983	C07	NTL02YP2227	putative copper homeostasis protein	813	AAM85823.1	5.550996
37992	C08	NTL02YP2223	hypothetical protein	816	AAM85819.1	4.398364
37989	C09	NTL02YP1136	putative myo-inositol catabolism protein iolB	816	AAM84732.1	3.635514
38037	C10	NTL02YP2241	putative phosphodiesterase	831	AAM85837.1	3.304248

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38045	C11	NTL02YP3331	hypothetical protein	834	AAM86927.1	3.613272
36010	C12	NTL02YP1150	hypothetical protein	153	AAM84746.1	2
36122	D01	NTL02YP2247	hypothetical protein	183	AAM85843.1	4.627803
36119	D02	NTL02YP1142	hypothetical protein	183	AAM84738.1	3.950673
36179	D03	NTL02YP1137	hypothetical protein	204	AAM84733.1	5.79918
36209	D04	NTL02YP1154	hypothetical protein	213	AAM84750.1	6.474308
36257	D05	NTL02YP1148	hypothetical protein	234	AAM84744.1	2.850365
38141	D06	NTL02YP2242	putative ABC transporter permease	867	AAM85838.1	3.246968
38171	D07	NTL02YP2246	hypothetical protein	876	AAM85842.1	6.046943
38309	D08	NTL02YP1130	putative periplasmic solute-binding protein of ABC transporter	930	AAM84726.1	5.023711
38416	D09	NTL02YP1152	lipote biosynthesis protein A	966	AAM84748.1	5.767396
38415	D10	NTL02YP1143	hypothetical protein	966	AAM84739.1	5.199801
38430	D11	NTL02YP2226	putative enzyme	972	AAM85822.1	5.41502
38593	D12	NTL02YP1132	D-ribose high-affinity transport system	1029	AAM84728.1	3.272217
38607	E01	NTL02YP1163	DNA polymerase III, delta subunit	1035	AAM84759.1	3.422326
38718	E02	NTL02YP2244	putative ABC transporter periplasmic binding protein	1083	AAM85840.1	3.089938
38694	E03	NTL02YP3335	aerobactin synthetase (subunit alpha)	1071	AAM86931.1	4.227723
36319	E04	NTL02YP1151	hypothetical protein	258	AAM84747.1	1.969799
36325	E05	NTL02YP3310	putative transposase	258	AAM86906.1	2.966443
36338	E06	NTL02YP1155	hypothetical protein	264	AAM84751.1	3.973684
36387	E07	NTL02YP3305	putative transposase	279	AAM86901.1	2.971787
36413	E08	NTL02YP1140	conserved hypothetical protein	288	AAM84736.1	5.579268
36549	E09	NTL02YP3309	putative transposase	336	AAM86905.1	3.930851
36645	E10	NTL02YP3324	hypothetical protein	372	AAM86920.1	2.07767
36683	E11	NTL02YP1149	hypothetical protein	390	AAM84745.1	2
36688	E12	NTL02YP3313	hypothetical protein	390	AAM86909.1	5.167442
38716	F01	NTL02YP1157	rlpA lipoprotein	1083	AAM84753.1	3.197685
38786	F02	NTL02YP1158	rod shape-determining membrane protein	1113	AAM84754.1	3.336513
38792	F03	NTL02YP3332	hypothetical protein	1113	AAM86928.1	3.277537
38837	F04	NTL02YP1133	conserved hypothetical protein	1137	AAM84729.1	3.114698
38871	F05	NTL02YP2240	putative transcriptional regulator	1155	AAM85836.1	1.521339
38961	F06	NTL02YP1156	D-alanyl-D-alanine carboxypeptidase, fraction A	1203	AAM84752.1	3.202735
38972	F07	NTL02YP2236	putative permease	1206	AAM85832.1	3.250401
39252	F08	NTL02YP3330	hypothetical protein	1377	AAM86926.1	3.701482
39434	F09	NTL02YP1128	putative aldehyde dehydrogenase	1527	AAM84724.1	3.749202
39448	F10	NTL02YP2233	putative virulence factor	1536	AAM85829.1	3.071066
39456	F11	NTL02YP2662	hypothetical protein	1545	AAM86258.1	3.685804
36711	F12	NTL02YP3325	hypothetical protein	396	AAM86921.1	5.974771
36708	G01	NTL02YP2224	hypothetical protein	396	AAM85820.1	5.931193
36958	G02	NTL02YP1160	hypothetical protein	471	AAM84756.1	4.309198
37030	G03	NTL02YP1146	putative cold-shock protein	492	AAM84742.1	2
37066	G04	NTL02YP2663	hypothetical protein	504	AAM86259.1	6.683824
37119	G05	NTL02YP2218	Holliday junction nuclease	522	AAM85814.1	4
37232	G06	NTL02YP2238	putative oxidoreductase component	561	AAM85834.1	2.810316
37283	G07	NTL02YP2228	hypothetical protein	576	AAM85824.1	2.795455
39508	G08	NTL02YP2232	putative hemolysin activator protein	1635	AAM85828.1	3.423284
39585	G09	NTL02YP3337	aerobactin synthetase (subunit beta)	1749	AAM86933.1	3.428731
39610	G10	NTL02YP2222	aspartate tRNA synthetase	1797	AAM85818.1	3.769733

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39648	G11	NTL02YP1159	peptidoglycan synthetase, penicillin-binding protein 2	1896	AAM84755.1	3.245351
37401	G12	NTL02YP1145	putative regulatory protein	618	AAM84741.1	2.50304
37429	H01	NTL02YP1164	rlpB lipoprotein	624	AAM84760.1	2.641566
37463	H02	NTL02YP3308	hypothetical protein	636	AAM86904.1	2.807692
37511	H03	NTL02YP3328	putative N-acylhomoserine lactone synthase	651	AAM86924.1	2.709117
37628	H04	NTL02YP1162	hypothetical protein	693	AAM84758.1	2.799454
37654	H05	NTL02YP1153	lipoate biosynthesis protein	702	AAM84749.1	2.397574
37616	H06	NTL02YP2196	cell division inhibitor	687	AAM85792.1	2.790922
37630	H07	NTL02YP2193	putative isomerase	693	AAM85789.1	6.687585
37709	H08	NTL02YP3292	hypothetical protein	720	AAM86888.1	3.897368
37739	H09	NTL02YP3281	hypothetical protein	729	AAM86877.1	2.621586
37810	H10	NTL02YP2202	hypothetical protein	753	AAM85798.1	2.754098

<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.