

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7**

**Catalog No. NR-19603**

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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-19603 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 7, NR-19603.”

**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 7 (UYPVG)**

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38135	A01	NTL02YP1369	putative permease of ABC transporter	864	AAM84965.1	3.571902655
38156	A02	NTL02YP0277	hypothetical protein	873	AAM83873.1	4.589266156
38401	A03	NTL02YP2452	hypothetical protein	960	AAM86048.1	5.389
36066	A04	NTL02YP3526	hypothetical protein	165	AAM87122.1	4.643902439
36277	A05	NTL02YP1354	hypothetical protein	240	AAM84950.1	4.857142857
38494	A06	NTL02YP2438	flagellar motor switch protein	993	AAM86034.1	3.315585673
38524	A07	NTL02YP2444	flagellar motor switch protein	1002	AAM86040.1	3.182341651
38577	A08	NTL02YP2453	putative permease of ABC transporter	1023	AAM86049.1	5.066792098
38602	A09	NTL02YP3546	hypothetical protein	1029	AAM86517.1	3.543498597
38793	A10	NTL02YP1363	ATP hydrolase of ABC transporter	1116	AAM84959.1	3.37283737
38804	A11	NTL02YP3521	ATP-binding component of sn-glycerol 3-phosphate transport system	1119	AAM87117.1	6.33649698
38945	A12	NTL02YP3542	putative enzyme	1191	AAM87138.1	3.170593014
36494	B01	NTL02YP2436	basal-body component	318	AAM86032.1	4.717877095
36517	B02	NTL02YP3535	hypothetical protein	324	AAM87131.1	4.799450549
36617	B03	NTL02YP0267	hypothetical protein	363	AAM83863.1	4
36672	B04	NTL02YP1357	hypothetical protein	384	AAM84953.1	5.125
36783	B05	NTL02YP2445	flagellar motor switch protein	417	AAM86041.1	6.407002188
36832	B06	NTL02YP3528	hypothetical protein	432	AAM87124.1	2.987288136
36877	B07	NTL02YP2441	flagellar fliJ protein	447	AAM86037.1	5.706365503
36883	B08	NTL02YP3523	hypothetical protein	447	AAM87119.1	6.739219713
39033	B09	NTL02YP3518	putative solute-binding periplasmic protein of ABC transporter	1245	AAM87114.1	2.577431907
39185	B10	NTL02YP1362	putative membrane protein	1335	AAM84958.1	6.52
39201	B11	NTL02YP0273	hypothetical protein	1347	AAM83869.1	5.085075703
39212	B12	NTL02YP2442	flagellar hook-length control protein	1353	AAM86038.1	3.91959799
36911	C01	NTL02YP0265	hypothetical protein	459	AAM83861.1	4.488977956
36990	C02	NTL02YP2435	hypothetical protein	477	AAM86031.1	
36999	C03	NTL02YP1349	hypothetical protein	480	AAM84945.1	4.646153846
37021	C04	NTL02YP0258	transcriptional repressor	489	AAM83854.1	5.958412098
37094	C05	NTL02YP3544	hypothetical protein	510	AAM87140.1	5.747272727
37087	C06	NTL02YP1353	hypothetical protein	510	AAM84949.1	6.850909091
37158	C07	NTL02YP2446	flagellar biosynthesis protein	537	AAM86042.1	5.341421144
37161	C08	NTL02YP3524	hypothetical protein	537	AAM87120.1	5.294627383
37183	C09	NTL02YP0274	hypothetical protein	546	AAM83870.1	2.389078498

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37267	C10	NTL02YP3540	hypothetical protein	570	AAM87136.1	2.770491803
37264	C11	NTL02YP2443	flagellar biosynthesis	570	AAM86039.1	3.118032787
39285	C12	NTL02YP1356	hypothetical protein	1395	AAM84952.1	3.083623693
39290	D01	NTL02YP1359	putative permease, major facilitator superfamily	1398	AAM84955.1	4.0472879
39404	D02	NTL02YP3539	hypothetical protein	1500	AAM87135.1	3.388961039
39518	D03	NTL02YP2454	ATP binding protein of ABC transporter for	1644	AAM86050.1	3.400831354
39555	D04	NTL02YP3532	putative hemolysin activator protein	1689	AAM87128.1	4.893001735
39581	D05	NTL02YP3538	hypothetical protein	1734	AAM87134.1	3.182638106
39658	D06	NTL02YP2432	hypothetical protein	1914	AAM86028.1	5.579836233
39379	D07	NTL02YP1371	putative divalent cation transporter	1476	AAM84967.1	3.700527704
37389	D08	NTL02YP2434	putative DNA repair enzyme	612	AAM86030.1	5.559815951
37420	D09	NTL02YP3527	hypothetical protein	621	AAM87123.1	5.881996974
37472	D10	NTL02YP3533	hypothetical protein	639	AAM87129.1	6.539027982
37481	D11	NTL02YP3534	putative tellurite resistance protein	642	AAM87130.1	6.486803519
37633	D12	NTL02YP0269	hypothetical protein	696	AAM83865.1	5.248641304
37661	E01	NTL02YP3536	hypothetical protein	702	AAM87132.1	2.772237197
37705	E02	NTL02YP1358	transcriptional response regulatory protein (sensor BaeS)	720	AAM84954.1	3.786842105
37714	E03	NTL02YP1347	hypothetical protein	723	AAM84943.1	7.374836173
37840	E04	NTL02YP0272	putative membrane protein	768	AAM83868.1	3.082920792
37950	E05	NTL02YP2421	putative periplasmic cysteine-binding ABC transport protein	801	AAM86017.1	3.084423306
38006	E06	NTL02YP3516	putative inner membrane permease protein of ABC	819	AAM87112.1	3.61233993
38100	E07	NTL02YP0240	putative ATP-binding component of a transport system	855	AAM83836.1	3.475977654
38118	E08	NTL02YP2413	putative cytochrome	858	AAM86009.1	3.638084633
38346	E09	NTL02YP0248	putative AraC-like regulator	942	AAM83844.1	6.387983707
35976	E10	NTL02YP3504	hypothetical protein	138	AAM87100.1	2.971910112
36043	E11	NTL02YP3496	hypothetical protein	159	AAM87092.1	4.969849246
36320	E12	NTL02YP1324	hypothetical protein	258	AAM84920.1	5.953020134
38474	F01	NTL02YP0231	putative permease of ABC transporter	990	AAM83827.1	3.177669903
38568	F02	NTL02YP2423	putative 1-aminocyclopropane-1-carboxylate deaminase	1020	AAM86019.1	3.413207547
38652	F03	NTL02YP3510	conserved hypothetical protein	1050	AAM87106.1	3.110091743
38783	F04	NTL02YP2426	putative flagellin	1110	AAM86022.1	6.477391304
38817	F05	NTL02YP1330	hypothetical protein	1128	AAM84926.1	3.48630137
38824	F06	NTL02YP0249	putative oxidoreductase	1131	AAM83845.1	3.230572161
38855	F07	NTL02YP0242	hypothetical protein	1149	AAM83838.1	3.419680404
36400	F08	NTL02YP3498	hypothetical protein	282	AAM87094.1	4
36425	F09	NTL02YP3492	hypothetical protein	291	AAM87088.1	5.864048338
36441	F10	NTL02YP1321	hypothetical protein	300	AAM84917.1	4
36458	F11	NTL02YP3501	hypothetical protein	303	AAM87097.1	3.982507289
36483	F12	NTL02YP3497	hypothetical protein	312	AAM87093.1	3.980113636
36550	G01	NTL02YP3509	hypothetical protein	336	AAM87105.1	4
36547	G02	NTL02YP2417	hypothetical protein	336	AAM86013.1	4
36670	G03	NTL02YP3503	hypothetical protein	381	AAM87099.1	4.990498812
36722	G04	NTL02YP2428	repressor of class 3a and 3b operons	399	AAM86024.1	4
36746	G05	NTL02YP3502	hypothetical protein	405	AAM87098.1	5.973033708
38872	G06	NTL02YP2412	hypothetical protein	1155	AAM86008.1	2.538912134

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38913	G07	NTL02YP2409	conserved hypothetical protein	1179	AAM86005.1	3.404429861
38918	G08	NTL02YP1333	putative dehydrogenase	1182	AAM84929.1	3.076923077
38952	G09	NTL02YP1327	hypothetical protein	1197	AAM84923.1	5.895715441
39108	G10	NTL02YP0235	hypothetical protein	1296	AAM83831.1	3.105538922
39213	G11	NTL02YP0237	putative transporter	1356	AAM83833.1	6.399713467
36773	G12	NTL02YP2429	repressor of class 3a and 3b operons	414	AAM86025.1	6.136563877
36797	H01	NTL02YP0254	hypothetical protein	423	AAM83850.1	5.622030238
36822	H02	NTL02YP1326	nucleoside diphosphate kinase	429	AAM84922.1	4.914712154
36882	H03	NTL02YP3505	hypothetical protein	447	AAM87101.1	5.921971253
36930	H04	NTL02YP3493	hypothetical protein	462	AAM87089.1	6.902390438
36998	H05	NTL02YP1342	hypothetical protein	480	AAM84938.1	5.926923077
37061	H06	NTL02YP0247	putative inner membrane permease	504	AAM83843.1	6.564338235
37100	H08	NTL02YP3494	hypothetical protein	513	AAM87090.1	6.963833635
37107	H09	NTL02YP3515	hypothetical protein	516	AAM87111.1	2.82733813
39298	H10	NTL02YP2427	filament capping protein	1401	AAM86023.1	3.731436502
39322	H11	NTL02YP2408	symporter of D-alanine, D-serine, and glycine	1425	AAM86004.1	2.965870307

<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://www.jcvi-cmr.org) webpage using the locus search option and inputting the above locus IDs.