

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 10**

**Catalog No. NR-19606**

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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-19606 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 10, NR-19606.”

**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 10 (UYPVJ)**

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36121	A01	NTL02YP1895	hypothetical protein	183	AAM85491.1	2
36187	A02	NTL02YP0835	hypothetical protein	207	AAM84431.1	3.700404858
36204	A03	NTL02YP2978	hypothetical protein	210	AAM86574.1	4.648
36290	A04	NTL02YP2980	hypothetical protein	246	AAM86576.1	2.982517483
36499	A05	NTL02YP0816	hypothetical protein	321	AAM84412.1	2.980609418
36548	A06	NTL02YP3001	putative starvation-inducible protein	336	AAM86597.1	3.643617021
36544	A07	NTL02YP0815	putative cytochrome oxidase subunit	336	AAM84411.1	4.14893617
36561	A08	NTL02YP0834	transcriptional repressor of chromosomal ars operon	342	AAM84430.1	2
38519	A09	NTL02YP0822	lipoprotein	1002	AAM84418.1	3.453934741
38537	A10	NTL02YP2988	putative isomerase	1005	AAM86584.1	3.133971292
38561	A11	NTL02YP2998	UDP-galactose-4-epimerase	1017	AAM86594.1	3.522232734
38556	A12	NTL02YP1897	lipoate-protein ligase A	1017	AAM85493.1	3.487228004
38585	B02	NTL02YP1920	transcriptional repressor for pur regulon, glyA, glnB	1026	AAM85516.1	3.422138837
38619	B03	NTL02YP2986	biotin synthetase	1038	AAM86582.1	2.833951763
38638	B04	NTL02YP1898	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase (DAHP synthetase, tryptophan repressible)	1047	AAM85494.1	4.890524379
38646	B05	NTL02YP0819	putative hydrogenase subunit	1050	AAM84415.1	3.503669725
38658	B06	NTL02YP3003	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	1053	AAM86599.1	3.464775846
38657	B07	NTL02YP2999	galactose-1-phosphate uridylyltransferase	1053	AAM86595.1	5.774931382
38671	B08	NTL02YP3006	quinolinate synthetase	1062	AAM86602.1	4.999092559
36619	B09	NTL02YP1893	hypothetical protein	363	AAM85489.1	3.17866005
36626	B10	NTL02YP1923	hypothetical protein	366	AAM85519.1	2
36721	B11	NTL02YP1904	hypothetical protein	399	AAM85500.1	2
36781	B12	NTL02YP1903	hypothetical protein	417	AAM85499.1	2
36935	C01	NTL02YP1896	lipoprotein	465	AAM85492.1	2
37097	C02	NTL02YP0811	hypothetical protein	513	AAM84407.1	6.640144665
38678	C03	NTL02YP1910	hypothetical protein	1065	AAM85506.1	5.352036199
38734	C04	NTL02YP0829	putative dihydroxyacetone kinase	1089	AAM84425.1	3.336581045
38857	C05	NTL02YP0827	putative dehydrogenase	1149	AAM84423.1	3.308662742
38858	C06	NTL02YP1901	hypothetical protein	1149	AAM85497.1	6.002523129
38863	C07	NTL02YP1917	cyclopropane fatty acyl phospholipid synthase	1152	AAM85513.1	3.341442953
38866	C08	NTL02YP3000	galactokinase	1152	AAM86596.1	3.291107383

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38865	C09	NTL02YP2985	8-amino-7-oxononanoate synthase	1152	AAM86581.1	3.323825503
38964	C10	NTL02YP1918	putative transport protein	1203	AAM85514.1	3.249396621
39011	C11	NTL02YP1908	hypothetical protein	1233	AAM85504.1	3.184603299
39079	C12	NTL02YP2987	7,8-diaminopelargonic acid synthetase	1281	AAM86583.1	3.358819076
37321	D01	NTL02YP0806	superoxide dismutase precursor (Cu-Zn)	588	AAM84402.1	4.839171975
37415	D02	NTL02YP1921	superoxide dismutase, iron	621	AAM85517.1	3.444780635
37440	D03	NTL02YP0821	L-isoaspartate protein carboxylmethyltransferase type II	627	AAM84417.1	2.796101949
37575	D04	NTL02YP0807	hypothetical protein	672	AAM84403.1	6.203651685
37582	D05	NTL02YP0830	hypothetical protein	675	AAM84426.1	4.548251748
37685	D06	NTL02YP2982	putative ATP-binding protein of ABC transporter	711	AAM86578.1	2.776298269
37730	D07	NTL02YP3005	nucleoside/purine/pyrimidine transporter	726	AAM86601.1	3.775456919
37769	D08	NTL02YP2983	dethiobiotin synthetase	738	AAM86579.1	3.228791774
39110	D09	NTL02YP0805	enolase	1296	AAM84401.1	2.574850299
39245	D10	NTL02YP1915	putative transport protein	1374	AAM85511.1	3.873408769
39256	D11	NTL02YP0837	cytochrome C peroxidase	1380	AAM84433.1	3.629577465
39312	D12	NTL02YP1914	pyruvate kinase I	1413	AAM85510.1	3.641431521
39414	E01	NTL02YP1905	hypothetical protein	1512	AAM85501.1	3.754510309
39422	E02	NTL02YP0813	ATP-sulfurylase, subunit 1	1518	AAM84409.1	5.122593068
39468	E03	NTL02YP2996	ATP-binding component of molybdate transport system	1557	AAM86592.1	2.987476518
39509	E04	NTL02YP0804	CTP synthetase	1638	AAM84400.1	3.161501788
39535	E05	NTL02YP1892	hypothetical protein	1665	AAM85488.1	3.651612903
39642	E06	NTL02YP0809	sulfite reductase (NADPH), flavoprotein beta subunit	1881	AAM84405.1	5.246746486
37834	E07	NTL02YP0820	survival protein	765	AAM84416.1	1.971428571
37852	E08	NTL02YP0836	hypothetical protein	771	AAM84432.1	3.622688039
37866	E09	NTL02YP1906	putative ATP-binding component of a transport system	774	AAM85502.1	4.506142506
37922	E11	NTL02YP2992	molybdate-binding periplasmic protein of molybdate ABC transporter	792	AAM86588.1	3.286057692
37961	E12	NTL02YP2984	biotin biosynthesis protein	804	AAM86580.1	5.648104265
37977	F01	NTL02YP3007	hypothetical protein	810	AAM86603.1	3.637647059
38014	F02	NTL02YP2989	putative phosphatase	822	AAM86585.1	3.792343387
37928	F04	NTL02YP0787	ATP-binding component of hydroxymate- dependent iron ABC transporter	795	AAM84383.1	5.508982036
38030	F05	NTL02YP2377	putative permease	828	AAM85973.1	5.918202765
38047	F06	NTL02YP3453	hypothetical protein	834	AAM87049.1	6.598398169
38070	F07	NTL02YP0803	hypothetical protein	843	AAM84399.1	6.966024915
38069	F08	NTL02YP0795	hypothetical protein	843	AAM84391.1	5.997734994
38124	F09	NTL02YP3465	regulator of lacZ	858	AAM87061.1	3.636971047
38165	F10	NTL02YP0783	probable regulator for maltose metabolism	876	AAM84379.1	2.77510917
36201	F11	NTL02YP2370	hypothetical protein	210	AAM85966.1	4.72
36437	F12	NTL02YP1883	hypothetical protein	297	AAM85479.1	3.913946588
38223	G01	NTL02YP2376	ATP-binding component of transport system for maltose	891	AAM85972.1	3.932330827
38218	G02	NTL02YP1272	hypothetical protein	891	AAM84868.1	1.992481203
38235	G03	NTL02YP3450	putative AraC-type regulatory protein	894	AAM87046.1	4.549250535
38269	G04	NTL02YP1276	GTP-binding protein	912	AAM84872.1	8.298319328
38399	G05	NTL02YP2360	AraC-type transcriptional regulator for yersiniabactin uptake and	960	AAM85956.1	4.992

Clone	Well Position	Locus ID <sup>1</sup>	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38513	G06	NTL02YP1274	leader peptidase (signal peptidase I)	999	AAM84870.1	3.327237729
38672	G07	NTL02YP3447	TonB complex protein	1062	AAM87043.1	3.316696915
38704	G08	NTL02YP1885	vitamin B12 transport permease protein	1077	AAM85481.1	3.111011638
36436	G09	NTL02YP1881	integration host factor (IHF), alpha subunit	297	AAM85478.1	3
36566	G10	NTL02YP2375	hypothetical protein	342	AAM85971.1	3.827225131
36609	G11	NTL02YP0792	hypothetical protein	360	AAM84388.1	3.895
36673	G12	NTL02YP1882	hypothetical protein	384	AAM85477.1	2
36816	H01	NTL02YP3466	putative enzyme	426	AAM87062.1	3
36831	H02	NTL02YP3446	TonB-complex protein	432	AAM87042.1	5.199152542
36903	H03	NTL02YP1271	sigma-E factor, negative regulatory protein	456	AAM84867.1	3.629032258
36916	H04	NTL02YP1884	hypothetical protein	459	AAM85480.1	5.661322645
36976	H05	NTL02YP3443	hypothetical protein	474	AAM87039.1	3
36997	H06	NTL02YP0778	7,8-dihydro-6-hydroxymethylpterin-pyrophosphokinase	480	AAM84374.1	5.580769231
37008	H07	NTL02YP3473	hypothetical protein	483	AAM87069.1	1.984703633
38733	H08	NTL02YP0788	solute-binding periplasmic protein of hydroxamate-dependent iron ABC	1089	AAM84384.1	5.141718335
38868	H09	NTL02YP0780	putative tRNA synthetase	1155	AAM84376.1	4.297071113
38880	H10	NTL02YP3451	putative oxidoreductase	1158	AAM87047.1	3.641068447
38887	H11	NTL02YP3470	putative synthetase/amidase	1161	AAM87066.1	1.716069942
38983	H12	NTL02YP3448	cystathionine beta-lyase (beta-cystathionase)	1212	AAM87044.1	2.694089457

<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.