

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 14**

Catalog No. NR-19610

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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-19610 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 14, NR-19610.”

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.

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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 14 (UYPVN)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37684	A01	NTL02YP2973	hypothetical protein	711	AAM86569.1	1.853529
37690	A02	NTL02YP1870	hypothetical protein	714	AAM85466.1	4.795756
37692	A03	NTL02YP0095	RNase PH	717	AAM83691.1	5.577279
37722	A04	NTL02YP4073	negative regulator for pho regulon	723	AAM87669.1	5.178244
37772	A05	NTL02YP4070	putative glutamate/aspartate ABC transport system permease protein	738	AAM87666.1	2.750643
37804	A06	NTL02YP1180	N-acetylglucosamine metabolism protein	753	AAM84776.1	6.423707
38102	A07	NTL02YP0776	pantothenate synthetase	855	AAM84372.1	1.796648
38121	A08	NTL02YP2952	hypothetical protein	858	AAM86027.1	3.351893
38125	A09	NTL02YP4026	formate dehydrogenase formation protein	858	AAM87622.1	1.760579
38133	A10	NTL02YP0777	3-methyl-2-oxobutanoate hydroxymethyltransferase	864	AAM84373.1	6.410398
38168	A11	NTL02YP1863	hypothetical protein	876	AAM85459.1	6.131004
38190	A12	NTL02YP1839	heat shock protein, integral membrane protein	882	AAM85435.1	4.842733
38200	B01	NTL02YP1866	permease for iron and manganese ABC transporter	885	AAM85462.1	6.201081
38220	B02	NTL02YP1855	putative inner membrane permease of oligogalacturonide ABC	891	AAM85451.1	4.831364
38231	B03	NTL02YP1865	permease for iron and manganese ABC transporter	894	AAM85461.1	6.024625
36212	B04	NTL02YP1864	hypothetical protein	213	AAM85460.1	3.956522
36324	B05	NTL02YP2931	hypothetical protein	258	AAM86527.1	2.969799
36348	B06	NTL02YP2944	hypothetical protein	267	AAM86540.1	5.680782
36541	B07	NTL02YP4029	hypothetical protein	333	AAM87625.1	4.884718
36540	B08	NTL02YP4018	hypothetical protein	333	AAM87614.1	4.86059
36555	B09	NTL02YP0773	hypothetical protein	339	AAM84369.1	3.98153
36574	B10	NTL02YP0767	hypothetical protein	348	AAM84363.1	5.719072
36587	B11	NTL02YP1859	putative pectin degradation protein	351	AAM85455.1	4.974425
38260	B12	NTL02YP0764	hypothetical protein	909	AAM84360.1	5.926238
38277	C01	NTL02YP4037	glycine tRNA synthetase, alpha subunit	915	AAM87633.1	5.608377
38301	C02	NTL02YP0771	putative ATP-binding component of ABC transport system	927	AAM84367.1	5.672182
38316	C03	NTL02YP4023	formate dehydrogenase formation protein	930	AAM87619.1	5.362887
38319	C04	NTL02YP0770	putative carbonic anhydrase	933	AAM84366.1	3.475848
38432	C05	NTL02YP4025	formate dehydrogenase-O, iron-sulfur subunit	972	AAM87621.1	4.784585

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38437	C06	NTL02YP0766	spermidine synthase putrescine aminopropyltransferase	975	AAM84362.1	4.717241
38463	C07	NTL02YP1854	putative inner membrane permease of oligogalacturonide ABC	987	AAM85450.1	4.098345
38553	C08	NTL02YP2955	putative inner membrane permease of ABC transporter	1014	AAM86551.1	2.431689
36606	C09	NTL02YP4031	hypothetical protein	357	AAM87627.1	5.433249
36663	C10	NTL02YP0775	aspartate 1-decarboxylase	381	AAM84371.1	3.95962
36943	C11	NTL02YP4019	putative transposase	465	AAM87615.1	5.889109
36950	C12	NTL02YP2949	hypothetical protein	468	AAM86545.1	4.785433
36994	D01	NTL02YP4030	hypothetical protein	477	AAM87626.1	5.93617
37180	D03	NTL02YP2935	hypothetical protein	543	AAM86531.1	2.653516
37177	D04	NTL02YP1840	putative fimbrial protein	543	AAM85436.1	5.614065
37187	D05	NTL02YP0769	hypoxanthine phosphoribosyltransferase	546	AAM84365.1	2.726962
37200	D06	NTL02YP1850	hypothetical protein	549	AAM5446.1	2.689304
38821	D07	NTL02YP1853	ABC transporter, ATP-binding protein	1128	AAM85449.1	2.873288
38892	D08	NTL02YP1846	putative oligogalacturonide lyase	1167	AAM85442.1	2.146645
38899	D09	NTL02YP1843	putative fimbrial component	1170	AAM85439.1	5.736364
38911	D10	NTL02YP2930	ribonucleoside-diphosphate reductase 1, beta subunit, B2	1176	AAM86526.1	2.797697
38948	D11	NTL02YP2933	hypothetical protein	1194	AAM86529.1	2.777958
38979	D12	NTL02YP2934	tyrosine-specific transport system protein	1209	AAM86530.1	2.760608
39064	E01	NTL02YP4033	mannitol-1-phosphate dehydrogenase	1269	AAM87629.1	2.811306
39102	E02	NTL02YP1852	putative solute-binding periplasmic protein of oligogalacturonide ABC	1293	AAM85448.1	3.540885
39186	E03	NTL02YP2943	putative symporter	1335	AAM86539.1	3.490909
39232	E04	NTL02YP1845	putative transport protein	1368	AAM85441.1	2.46875
37219	E05	NTL02YP1862	putative regulator of yfeABCD	555	AAM85458.1	2
37223	E06	NTL02YP4032	repressor for mtl	555	AAM87628.1	2.647059
37235	E07	NTL02YP2932	ecotin, serine protease inhibitor	561	AAM86528.1	2.663894
37276	E08	NTL02YP4038	3-methyl-adenine DNA glycosylase I	573	AAM87634.1	3.502447
37561	E09	NTL02YP1861	putative phosphatase	666	AAM85457.1	5.784703
37589	E10	NTL02YP4024	formate dehydrogenase, cytochrome B556 (FDO) subunit	675	AAM87620.1	6.896503
37733	E11	NTL02YP4035	hypothetical protein	726	AAM87631.1	6.241514
37737	E12	NTL02YP2928	3-demethylubiquinone-9 3-methyltransferase	729	AAM86524.1	6.016905
37833	F01	NTL02YP2953	ATP-binding component of ABC transporter	762	AAM86549.1	6.512469
39291	F02	NTL02YP1849	putative symporter	1398	AAM85445.1	3.133519
39297	F03	NTL02YP0756	aromatic amino acid transport protein	1401	AAM84352.1	5.244969
39314	F04	NTL02YP2951	putative aromatic-L-amino-acid decarboxylase	1416	AAM86547.1	3.415522
39325	F05	NTL02YP0760	lipoamide dehydrogenase (NADH) component of 2-oxodehydrogenase and	1428	AAM84356.1	3.387602
39538	F06	NTL02YP1856	putative pectate lyase	1668	AAM85452.1	2.890515
39667	F07	NTL02YP4034	PTS system mannitol-specific enzyme IIABC components	1932	AAM87630.1	5.509128
39674	F08	NTL02YP4028	methyl-accepting chemotaxis protein II	1950	AAM87624.1	3.305025
37881	F09	NTL02YP1841	probable pilin chaperone	780	AAM85437.1	3.281707
37919	F10	NTL02YP1847	putative regulator	792	AAM85443.1	4.260817
37927	F11	NTL02YP0765	S-adenosylmethionine decarboxylase	795	AAM84361.1	5.833533
37957	F12	NTL02YP1844	putative pilin chaperone	804	AAM85440.1	3.208531

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37969	G01	NTL02YP1857	2-deoxy-D-gluconate 3-dehydrogenase	807	AAM85453.1	6.067296
38057	G02	NTL02YP2954	hypothetical ABC transporter ATP-binding protein	837	AAM86550.1	3.200684
38051	G03	NTL02YP0757	transcriptional regulator for pyruvate dehydrogenase complex	837	AAM84353.1	5.881414
38094	G04	NTL02YP1848	putative regulator	852	AAM85444.1	3.232063
38105	G05	NTL02YP2950	putative thiosulfate sulfurtransferase	855	AAM86546.1	3.231285
38034	G06	NTL02YP4008	putative chaperone	828	AAM87604.1	3.28341
38359	G07	NTL02YP3993	ferric anguibactin transport system permease protein	945	AAM87589.1	3.126904
38381	G08	NTL02YP1819	hypothetical protein	954	AAM85415.1	5.696177
38480	G09	NTL02YP1828	hypothetical protein	990	AAM85424.1	3.147573
36298	G10	NTL02YP1822	hypothetical protein	249	AAM85418.1	3
38507	G11	NTL02YP4004	xylose binding periplasmic protein of ABC transport	996	AAM87600.1	5.920849
38538	G12	NTL02YP0731	ornithine carbamoyltransferase 1	1008	AAM84327.1	6.105916
38598	H03	NTL02YP2915	hypothetical protein	1029	AAM86510.1	3.08232
38749	H04	NTL02YP0738	hypothetical protein	1095	AAM84334.1	2.899559
36623	H05	NTL02YP3997	hypothetical protein	363	AAM87593.1	2
36827	H06	NTL02YP0732	hypothetical protein	432	AAM84328.1	4.279661
36837	H07	NTL02YP1818	hypothetical protein	435	AAM85414.1	4.974737
36912	H08	NTL02YP0730	hypothetical protein	459	AAM84326.1	4.977956
37001	H09	NTL02YP2908	hypothetical protein	480	AAM86504.1	2.75
37078	H11	NTL02YP3998	putative transposase	507	AAM87594.1	4.694698
38951	H12	NTL02YP4002	inner membrane permease of D-xylose ABC transporter	1194	AAM87598.1	2.928687

¹The 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.