

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 18**

Catalog No. NR-19614

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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-19614 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 18, NR-19614."

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 18 (UYPVR)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38597	A01	NTL02YP2867	hypothetical protein	1069	AAM85965.1	1.517306
38676	A02	NTL02YP1084	putative transposase	1105	AAM84519.1	1.743891
38763	A03	NTL02YP2866	putative transport system permease protein	1141	AAM86462.1	2.658195
38795	A04	NTL02YP1771	hypothetical protein	1156	AAM85367.1	2.50173
38848	A05	NTL02YP2850	putative prophage integrase	1183	AAM85951.1	2.262891
38947	A06	NTL02YP2857	HMWP2 nonribosomal peptide synthetase	1234	AAM85957.1	7.576985
38958	A07	NTL02YP2871	putative transposase	1240	AAM85968.1	2.98629
36702	A08	NTL02YP3951	biosynthetic arginine decarboxylase	433	AAM86863.1	2.979215
36767	A09	NTL02YP3944	50S ribosomal subunit protein L16	451	AAM87540.1	3.43459
36786	A10	NTL02YP3945	hypothetical protein	457	AAM87541.1	3.503282
36803	A11	NTL02YP3967	hypothetical protein	463	AAM86877.1	2
36842	A12	NTL02YP3965	hypothetical protein	475	AAM86875.1	3.981053
36841	B01	NTL02YP3957	DNA-specific endonuclease I	475	AAM86866.1	4.684211
36871	B02	NTL02YP1772	hypothetical protein	487	AAM85065.1	2
36978	B03	NTL02YP3973	hypothetical protein	514	AAM86883.1	6.136187
37037	B04	NTL02YP1088	peptidyl-prolyl cis-trans isomerase B	535	AAM84684.1	2
39125	B07	NTL02YP1774	hypothetical protein	1345	AAM85067.1	3.577695
39182	B08	NTL02YP3958	hypothetical protein	1372	AAM86867.1	3.338192
39254	B09	NTL02YP3968	putative pyrroline-5-carboxylate reductase	1417	AAM86878.1	3.804517
39258	B10	NTL02YP1769	DNA ligase	1420	AAM85063.1	3.714789
39327	B11	NTL02YP1089	cysteine tRNA synthetase	1471	AAM84685.1	3.662814
39360	B12	NTL02YP1765	cysteine synthase A, O-acetylserine sulfhydrylase A	1495	AAM85060.1	3.664883
39375	C01	NTL02YP2858	HMWP1 nonribosomal peptide/polyketide synthase	1513	AAM85958.1	3.658295
39502	C02	NTL02YP2868	hypothetical protein	1666	AAM85966.1	3.342737
39511	C03	NTL02YP1777	permease of transport system for 3 nucleosides	1678	AAM85070.1	2.800954
39587	C04	NTL02YP2873	putative ATP-dependent helicase	1798	AAM86469.1	3.354283
37123	C05	NTL02YP1085	phosphoribosylaminoimidazole carboxylase, catalytic subunit	565	AAM84681.1	2.817699
37169	C06	NTL02YP3949	50S ribosomal subunit protein L5	580	AAM87545.1	2.817241
37237	C07	NTL02YP3974	hypothetical protein	601	AAM86884.1	2.815308
37320	C08	NTL02YP3975	hypothetical protein	625	AAM86885.1	2.8128

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37375	C09	NTL02YP3939	putative transport protein	646	AAM86856.1	2
37422	C10	NTL02YP3962	hypothetical protein	661	AAM86872.1	6.155825
37760	C11	NTL02YP3926	hypothetical protein	775	AAM86845.1	5.180645
37911	C12	NTL02YP1760	hypothetical protein	829	AAM85056.1	5.501809
37914	D01	NTL02YP2828	putative LysR-type transcriptional regulator	829	AAM85935.1	5.47889
38013	D02	NTL02YP2836	putative transcriptional regulator	862	AAM85942.1	2.585847
38067	D03	NTL02YP3925	aminomethyltransferase of glycine cleavage system	880	AAM86844.1	2
38160	D04	NTL02YP2832	hypothetical protein	913	AAM85938.1	1.874042
38182	D05	NTL02YP1741	cysteine synthase B, O-acetylserine sulfhydrylase B	919	AAM85041.1	5.274211
36072	D06	NTL02YP1761	PTS system, glucose-specific IIA component	208	AAM85057.1	2.947115
36144	D07	NTL02YP0652	hypothetical protein	232	AAM84155.1	3.887931
36152	D08	NTL02YP1750	hypothetical protein	235	AAM85048.1	3.961702
36235	D09	NTL02YP3921	hypothetical protein	262	AAM87517.1	4.118321
36251	D10	NTL02YP3922	hypothetical protein	268	AAM87518.1	4.958955
36380	D11	NTL02YP0661	quinone oxidoreductase	316	AAM84164.1	4.702532
38203	D12	NTL02YP2834	putative transcriptional regulator LYSR-type	925	AAM85940.1	2.03027
38341	E01	NTL02YP2841	putative histidine protein kinase sensor	979	AAM85945.1	5.346272
38337	E02	NTL02YP0660	hypothetical protein	979	AAM84163.1	5.319714
38461	E03	NTL02YP0666	excision nuclease subunit A	1027	AAM84168.1	5.024343
38514	E04	NTL02YP2844	putative fimbrial precursor	1039	AAM85946.1	1.599615
38684	E05	NTL02YP0668	hypothetical protein	1108	AAM84171.1	3.437726
38774	E06	NTL02YP2833	hypothetical protein	1147	AAM85939.1	3.027899
36419	E07	NTL02YP3929	hypothetical protein	328	AAM86848.1	3.771341
36428	E08	NTL02YP0672	rhamnulokinase	334	AAM84175.1	2.979042
36484	E09	NTL02YP3937	putative actin	352	AAM86854.1	2.977273
36543	E10	NTL02YP0677	positive regulator for rhaRS operon	376	AAM84179.1	3.601064
36594	E11	NTL02YP1742	hypothetical protein	394	AAM85042.1	3.893401
36600	E12	NTL02YP0654	4-hydroxybenzoate-octaprenyltransferase	397	AAM84157.1	4.093199
36608	F01	NTL02YP0664	tyrosine aminotransferase	400	AAM84167.1	5.57
36629	F02	NTL02YP3928	proline aminopeptidase P II	406	AAM86847.1	3.975369
36657	F03	NTL02YP3931	hypothetical protein	415	AAM86849.1	5.828916
36681	F04	NTL02YP3930	hypothetical protein	427	AAM87526.1	2
36713	F05	NTL02YP3927	2-octaprenyl-6-methoxyphynol hydroxylase	436	AAM86846.1	3.720183
36730	F06	NTL02YP0662	replicative DNA helicase	442	AAM84165.1	3.988688
38800	F07	NTL02YP0656	diacylglycerol kinase	1159	AAM84159.1	5.289905
38832	F08	NTL02YP2842	PTS system, fructose-specific IIA/fpr component	1174	AAM86438.1	3.042589
38901	F09	NTL02YP2830	putative major facilitator superfamily (MFS) transport protein	1210	AAM85937.1	4.541322
38903	F10	NTL02YP0667	ssDNA-binding protein	1213	AAM84170.1	2.483924
38909	F11	NTL02YP1764	hypothetical protein	1216	AAM85360.1	2.448191
38935	F12	NTL02YP3934	D-3-phosphoglycerate dehydrogenase	1225	AAM86851.1	5.213061
38963	G01	NTL02YP1757	transcriptional regulator in 2-component system	1243	AAM85053.1	5.671762
36770	G03	NTL02YP1752	putative permease	454	AAM85049.1	3.471366
36906	G04	NTL02YP1743	hypothetical protein	496	AAM85339.1	4.15121

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36965	G05	NTL02YP3932	putative ligase	511	AAM86850.1	2.982387
36957	G06	NTL02YP0659	hypothetical protein	511	AAM84162.1	2.984344
36977	G07	NTL02YP3936	replication initiation inhibitor	514	AAM86853.1	3.515564
36986	G08	NTL02YP0671	L-rhamnose isomerase	517	AAM84174.1	4.709865
37059	G09	NTL02YP2838	putative membrane protein	541	AAM86434.1	2
37159	G10	NTL02YP2843	hypothetical protein	577	AAM86439.1	5.214905
37175	G11	NTL02YP1748	putative aminotransferase	583	AAM85046.1	2
39191	G12	NTL02YP0676	mrsA protein	1381	AAM84272.1	1.724837
39262	H01	NTL02YP0657	regulator for SOS (lexA) regulon	1423	AAM84160.1	5.189037
39332	H02	NTL02YP1739	sulfate/thiosulfate permease	1474	AAM85039.1	4.037992
39351	H03	NTL02YP0670	rhamnulose-phosphate aldolase	1489	AAM84173.1	5.696441
39416	H04	NTL02YP2831	lysine specific permease	1552	AAM86427.1	3.701031
39477	H05	NTL02YP2845	putative pilin chaperone	1615	AAM85947.1	4.814241
39582	H06	NTL02YP0651	hypothetical protein	1777	AAM84248.1	5.185706
39618	H07	NTL02YP3920	hypothetical protein	1849	AAM86841.1	3.905895
39671	H08	NTL02YP0674	hypothetical protein	1984	AAM84177.1	3.25504
37212	H09	NTL02YP3919	putative NAD(P)H oxidoreductase	592	AAM87515.1	6.445946
37253	H10	NTL02YP1754	hypothetical protein	607	AAM85350.1	4.672158
37261	H11	NTL02YP1751	hypothetical protein	610	AAM85347.1	2
37275	H12	NTL02YP3918	hypothetical protein	613	AAM86840.1	2.980424