

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 6**

Catalog No. NR-19602

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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-19602 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 6, NR-19602.”

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.

Disclaimers:

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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 6 (UYPVF)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37445	A01	NTL02YP0939	Na ⁺ -translocating NADH ubiquinone oxidoreductase	630	AAM84535.1	2
37501	A02	NTL02YP2013	putative outer membrane protein	648	AAM85609.1	3.80232558
37516	A03	NTL02YP0920	putative permease of ABC transporter	654	AAM84516.1	3.38040346
37549	A04	NTL02YP0934	hypothetical protein	663	AAM84530.1	3.42247511
37568	A05	NTL02YP0919	putative inner membrane permease of ABC transporter	669	AAM84515.1	2
37764	A06	NTL02YP2037	orotidine-5-phosphate decarboxylase	738	AAM85633.1	3.76478149
37792	A07	NTL02YP0930	hypothetical protein	747	AAM84526.1	6.12579416
37791	A08	NTL02YP0921	glutamine transport ATP-binding protein	747	AAM84517.1	2
37821	A09	NTL02YP0953	hypothetical protein	759	AAM84549.1	7.61827284
37823	A10	NTL02YP2007	energy transducer	759	AAM85603.1	5.40801001
37830	A11	NTL02YP2033	membrane bound non-essential phosphatidylglycerophosphate phosphatase	762	AAM85629.1	7.1084788
37645	A12	NTL02YP2466	cell-distal portion of basal-body rod	699	AAM86062.1	5.69012179
37743	B01	NTL02YP0899	hypothetical protein	732	AAM84495.1	1.99870466
37742	B02	NTL02YP0897	hypothetical protein	732	AAM84493.1	2.9857513
37748	B03	NTL02YP2465	basal-body outer-membrane L (lipopolysaccharide layer) ring protein	732	AAM86061.1	6.75
37800	B04	NTL02YP0904	hypothetical protein	750	AAM84500.1	4.15949367
37836	B05	NTL02YP2472	putative flagella basal body P-ring formation protein	765	AAM86068.1	3.79627329
37862	B06	NTL02YP0889	hypothetical protein	774	AAM84485.1	4.16953317
35984	B10	NTL02YP3560	hypothetical protein	147	AAM87156.1	1.98395722
36023	B11	NTL02YP1987	hypothetical protein	156	AAM85583.1	2.82653061
36028	B12	NTL02YP3556	hypothetical protein	156	AAM87152.1	3.85714286
36081	C01	NTL02YP2473	hypothetical protein	171	AAM86069.1	1.98578199
36090	C02	NTL02YP2476	hypothetical protein	174	AAM86072.1	5.89252336
36112	C03	NTL02YP3565	hypothetical protein	180	AAM87161.1	3.84090909
36210	C04	NTL02YP1372	hypothetical protein	213	AAM84968.1	6.43873518
36240	C05	NTL02YP2458	hypothetical protein	225	AAM86054.1	2.66037736
37980	C06	NTL02YP0887	hypothetical protein	813	AAM84483.1	4.64712778
37981	C07	NTL02YP1377	phosphate-specific transport component	813	AAM84973.1	4.59554513
38033	C08	NTL02YP3575	cell division protein	828	AAM87171.1	4.60023041
38054	C09	NTL02YP1983	hypothetical protein	837	AAM85579.1	6.63968073

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38184	C10	NTL02YP3554	negative regulator of exu regulon, exuT, uxaAC	879	AAM87150.1	1.99673558
38228	C11	NTL02YP0879	hypothetical protein	894	AAM84475.1	5.21199143
38289	C12	NTL02YP3576	D-alanine-D-alanine ligase B	921	AAM87172.1	6.16961498
38335	D01	NTL02YP3572	UDP-3-O-acyl N-acetylglucosamine deacetylase	936	AAM87168.1	6.48360656
38353	D02	NTL02YP2463	flagellar biosynthesis protein	945	AAM86059.1	5.49238579
38389	D03	NTL02YP1979	putative transcriptional regulator	957	AAM85575.1	6.13640923
38525	D04	NTL02YP2459	putative transcriptional regulator	1002	AAM86055.1	6.22072937
36296	D05	NTL02YP0882	30S ribosomal subunit protein S16	249	AAM84478.1	3.96193772
36408	D06	NTL02YP3563	hypothetical protein	285	AAM87159.1	3.8
36456	D07	NTL02YP2474	anti-FlhA factor	303	AAM86070.1	7.52186589
36467	D08	NTL02YP3561	hypothetical protein	306	AAM87157.1	6.04913295
36473	D09	NTL02YP1984	acid shock protein	309	AAM85580.1	7.42120344
36514	D10	NTL02YP1982	hypothetical protein	324	AAM85578.1	4.31043956
36562	D11	NTL02YP0901	hypothetical protein	342	AAM84497.1	4.14397906
36575	D12	NTL02YP0885	50S ribosomal subunit protein L19	348	AAM84481.1	3.98453608
36602	E01	NTL02YP1989	hypothetical protein	357	AAM85585.1	3.97732997
36680	E02	NTL02YP3568	7,8-dihydro-8-oxoguanine-triphosphatase	387	AAM87164.1	2
36689	E03	NTL02YP3558	hypothetical protein	390	AAM87154.1	5.87674419
38552	E04	NTL02YP2460	flagellar biosynthesis protein, hook-filament junction protein	1014	AAM86056.1	6.46110057
38703	E08	NTL02YP0890	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	1077	AAM84486.1	4.40107431
38784	E09	NTL02YP2464	homolog of Salmonella P-ring of flagella basal	1110	AAM86060.1	2.93478261
38806	E10	NTL02YP0891	chorismate mutase-T	1122	AAM84487.1	4.18932874
38867	E11	NTL02YP3573	tubulin-like GTP-binding protein and GTPase	1152	AAM87169.1	4.05536913
38916	E12	NTL02YP0906	hypothetical protein	1182	AAM84502.1	1.74549918
39045	F01	NTL02YP3574	ATP-binding cell division protein	1257	AAM87170.1	4.64687741
39081	F02	NTL02YP0878	conserved hypothetical protein	1284	AAM84474.1	4.71676737
39092	F03	NTL02YP2468	hook protein	1287	AAM86064.1	4.78824416
36743	F04	NTL02YP2470	cell-proximal portion of basal-body rod protein	405	AAM86066.1	5.83820225
36766	F05	NTL02YP3564	hypothetical protein	411	AAM87160.1	7.94235033
36774	F06	NTL02YP2471	cell-proximal portion of basal-body rod protein	414	AAM86067.1	6.30396476
36800	F07	NTL02YP2477	flagellar protein	423	AAM86073.1	6.61987041
36846	F08	NTL02YP0905	putative thioredoxin-like protein	438	AAM84501.1	5.79079498
36864	F09	NTL02YP2475	flagellar biosynthesis protein	444	AAM86071.1	2
36934	F10	NTL02YP0896	putative yhbH sigma 54 modulator	465	AAM84492.1	8.04554455
36972	F11	NTL02YP1986	putative cytochrome	474	AAM85582.1	1.8151751
37009	F12	NTL02YP3559	hypothetical protein	483	AAM87155.1	2
39130	G03	NTL02YP3553	transport of hexuronates	1305	AAM87149.1	6.57695167
39218	G04	NTL02YP0902	phosphatidylserine synthase	1359	AAM84498.1	4.62115797
39221	G05	NTL02YP0880	GTP-binding export factor	1362	AAM84476.1	7.04707561
39303	G06	NTL02YP1978	putative D-arabinitol dehydrogenase	1404	AAM85574.1	4.4432133
39359	G07	NTL02YP3551	altronate oxidoreductase	1452	AAM87147.1	3.31903485
39396	G08	NTL02YP3550	altronate hydrolase	1491	AAM87146.1	4.22403658
39432	G09	NTL02YP3577	UDP-N-acetyl-muramate:alanine ligase	1524	AAM87173.1	3.98976982
39446	G10	NTL02YP0907	putative membrane translocase	1536	AAM84503.1	3.70748731

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39470	G11	NTL02YP1373	putative membrane translocase	1536	AAM84503.1	4.356875
39536	G12	NTL02YP2462	flagellar biosynthesis protein, hook-filament junction protein 1	1665	AAM86058.1	4.10791789
37145	H01	NTL02YP3571	hypothetical protein	531	AAM87167.1	8.12259194
37144	H02	NTL02YP3549	hypothetical protein	531	AAM87145.1	1.92994746
37149	H03	NTL02YP3570	hypothetical protein	534	AAM87166.1	2.76132404
37230	H04	NTL02YP0883	hypothetical protein	561	AAM84479.1	4.80199667
37304	H05	NTL02YP3555	hypothetical protein	582	AAM87151.1	1.70418006
37371	H06	NTL02YP1980	acyl carrier protein phosphodiesterase	606	AAM85576.1	6.54489164
37488	H07	NTL02YP1995	putative channel protein	645	AAM85591.1	2.77080292
37594	H08	NTL02YP2469	basal-body rod modification protein	678	AAM86065.1	6.59610028
37596	H09	NTL02YP0888	putative anaerobic c4-dicarboxylate transport protein	681	AAM84484.1	3.7295423
37646	H10	NTL02YP3557	hypothetical protein	699	AAM87153.1	5.34912043
37896	H11	NTL02YP2449	flagellar biosynthesis protein	783	AAM86045.1	6.54556501
38023	H12	NTL02YP2447	flagellar biosynthesis protein	825	AAM86043.1	6.71676301

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://jcvicmr.org) webpage using the locus search option and inputting the above locus IDs.