

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4**

Catalog No. NR-19600

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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-19600 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 4, NR-19600.”

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 4 (UYPVD)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36443	A01	NTL02YP2534	hypothetical protein	300	AAM86130.1	3.2
38615	A03	NTL02YP1441	thiosulfate binding periplasmic protein of sulfate/thiosulfate ABC	1038	AAM85037.1	4.40445269
38697	A04	NTL02YP0359	dTDP-glucose 4,6-dehydratase	1074	AAM83955.1	4.43716338
38707	A05	NTL02YP0356	putative transport protein	1080	AAM83952.1	4.38035714
38725	A07	NTL02YP0364	TDP-Fuc4NAc:lipid II Fuc4NAc transferase	1086	AAM83960.1	4.28419183
38741	A08	NTL02YP0360	glucose-1-phosphate thymidyltransferase	1092	AAM83956.1	6.97173145
38754	A09	NTL02YP0355	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase	1098	AAM83951.1	6.46924429
38760	A10	NTL02YP3598	3-isopropylmalate dehydrogenase	1098	AAM87194.1	2.36906854
38801	A11	NTL02YP1444	ATP-binding component of sulfate permease A protein	1119	AAM85040.1	3.83951682
38923	A12	NTL02YP3601	putative efflux protein	1182	AAM87197.1	3.22094926
38926	B01	NTL02YP0357	UDP-N-acetyl glucosamine -2-epimerase	1185	AAM83953.1	2.29714286
36519	B02	NTL02YP0353	thioredoxin 1	327	AAM83949.1	4.9346049
36538	B03	NTL02YP3619	hypothetical protein	333	AAM87216.1	5.58713137
36678	B04	NTL02YP2529	putative regulator	387	AAM86125.1	3.99297424
36866	B05	NTL02YP3624	hypothetical protein	444	AAM87220.1	4.23760331
36904	B06	NTL02YP1421	cytochrome c-type protein	456	AAM85017.1	5.83669355
36915	B07	NTL02YP1425	hypothetical protein	459	AAM85021.1	3.44088176
36923	B08	NTL02YP0337	hypothetical protein	462	AAM83933.1	5.53984064
37002	B09	NTL02YP0336	hypothetical protein	483	AAM83932.1	2
38970	B10	NTL02YP1456	putative membrane protein, possible efflux component	1206	AAM85052.1	3.89486356
38969	B11	NTL02YP0362	putative regulator	1206	AAM83958.1	2.92857143
38999	C01	NTL02YP1450	putative aminotransferase	1227	AAM85046.1	3.78768745
39010	C02	NTL02YP1446	hypothetical protein	1233	AAM85042.1	4.0494894
39031	C03	NTL02YP2540	galactoside permease (M protein)	1245	AAM86136.1	4.10116732
39040	C04	NTL02YP0363	putative cytochrome	1257	AAM83959.1	4.52505783
39047	C05	NTL02YP0354	transcription termination factor Rho polarity suppressor	1260	AAM83950.1	5.24538462
39052	C06	NTL02YP0358	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase	1263	AAM83954.1	3.42747506
39227	C07	NTL02YP0365	TDP-Fuc4NAc:lipidIII transferase	1365	AAM83961.1	3.67544484

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39287	C08	NTL02YP2508	putative transport protein	1395	AAM86104.1	3.68850174
39344	C09	NTL02YP0341	hypothetical protein	1443	AAM83937.1	5.96358732
37072	C10	NTL02YP2545	hypothetical protein	507	AAM86141.1	7.4095064
37116	C11	NTL02YP3625	hypothetical protein	519	AAM87221.1	6.72271914
37114	C12	NTL02YP2517	hypothetical protein	519	AAM86113.1	6.5706619
37236	D01	NTL02YP3627	hypothetical protein	561	AAM87223.1	5.83361065
37265	D02	NTL02YP2514	hypothetical protein	570	AAM86110.1	2.72622951
37368	D03	NTL02YP3600	isopropylmalate isomerase subunit	603	AAM87196.1	4.79160187
37402	D04	NTL02YP1422	cytochrome c-type protein	618	AAM85018.1	5.80243161
37421	D05	NTL02YP3630	hypothetical protein	621	AAM87226.1	2
37430	D06	NTL02YP1423	hypothetical protein	624	AAM85019.1	2.80120482
37535	D07	NTL02YP2543	yersiniabactin biosynthesis component	657	AAM86139.1	5.13629842
37608	D08	NTL02YP1457	transcriptional regulator in 2-component system	684	AAM85053.1	2
39366	D09	NTL02YP1453	putative permease	1461	AAM85049.1	3.47368421
39381	D10	NTL02YP0339	ketol-acid reductoisomerase	1479	AAM83935.1	3.9526004
39405	D11	NTL02YP3599	3-isopropylmalate isomerase (dehydratase) subunit	1500	AAM87195.1	2.36168831
39418	D12	NTL02YP3626	hypothetical protein	1512	AAM87222.1	4.29381443
39438	E01	NTL02YP1449	hypothetical protein	1530	AAM85045.1	3.98917197
39455	E02	NTL02YP1448	putative sensor kinase	1545	AAM85044.1	5.56845426
39499	E03	NTL02YP3604	putative ABC transport system thiamine permease protein	1620	AAM87200.1	3.11385542
39572	E04	NTL02YP2532	putative ABC transporter	1719	AAM86127.1	3.15747584
39629	E05	NTL02YP3623	hypothetical protein	1845	AAM87219.1	5.76976127
37752	E06	NTL02YP3605	putative ATP-binding component of a transport system	732	AAM87201.1	5.27072539
37773	E07	NTL02YP0366	probable UDP-N-acetyl-D-mannosaminuronic acid transferase	741	AAM83962.1	3.76568502
37789	E08	NTL02YP3629	hypothetical protein	744	AAM87225.1	6.37372449
37848	E09	NTL02YP3606	hypothetical protein	768	AAM87202.1	6.24752475
37925	E10	NTL02YP0361	hypothetical protein	795	AAM83957.1	2.17964072
37984	E11	NTL02YP2535	hypothetical protein	813	AAM86131.1	4.56740914
38043	E12	NTL02YP1442	inner membrane permease T of sulfate/thiosulfate ABC	834	AAM85038.1	4.56750572
38065	F01	NTL02YP2511	PTS enzyme IIC, mannose-specific	840	AAM86107.1	2.33181818
38096	F02	NTL02YP2533	hypothetical protein	852	AAM86129.1	1.98654709
37960	F03	NTL02YP2502	putative 2-oxo-hept-3-ene-1,7-dioate hydratase	804	AAM86098.1	3.78672986
38042	F04	NTL02YP1379	hypothetical protein	834	AAM84975.1	4.37070938
38119	F05	NTL02YP2505	putative 3,4-dihydroxyphenylacetate 2,3-dioxygenase	858	AAM86101.1	4.63028953
38139	F06	NTL02YP1398	hypothetical protein	867	AAM84994.1	4.51157663
38185	F07	NTL02YP0327	hypothetical protein	882	AAM83923.1	6.59761388
38201	F08	NTL02YP2482	putative resistance protein, exporter	885	AAM86078.1	2
36061	F09	NTL02YP1412	hypothetical protein	165	AAM85008.1	-
36268	F10	NTL02YP1401	hypothetical protein	237	AAM84997.1	2.94945848
36361	F11	NTL02YP2485	DNA polymerase III, theta subunit	270	AAM86081.1	3.70645161
36385	F12	NTL02YP1416	hypothetical protein	279	AAM85012.1	3
36489	G01	NTL02YP0297	repressor of all met genes but metF	318	AAM83893.1	-
36604	G02	NTL02YP2481	hypothetical protein	357	AAM86077.1	3.79093199

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38278	G03	NTL02YP0315	activator, hydrogen peroxide-inducible genes	918	AAM83911.1	6.73695198
38307	G04	NTL02YP0289	1,4-dihydroxy-2-naphthoate octaprenyltransferase	930	AAM83885.1	6.80721649
38372	G05	NTL02YP2486	putative proline iminopeptidase	951	AAM86082.1	6.96367306
38423	G06	NTL02YP3594	probable transcriptional activator for leuABCD operon	969	AAM87190.1	5.81863231
38487	G07	NTL02YP0326	putative ABC transporter permease protein	993	AAM83922.1	4.51597289
38517	G08	NTL02YP0332	branched-chain amino-acid aminotransferase	1002	AAM83928.1	5.38387716
38547	G09	NTL02YP3589	transcriptional repressor of fru operon and others	1011	AAM87185.1	5.46146527
38631	G10	NTL02YP1383	phosphoribosylaminoimidazole synthetase	1044	AAM84979.1	4.12730627
38668	G11	NTL02YP1395	lipoprotein-34	1062	AAM84991.1	3.48366606
36792	G12	NTL02YP1392	hypothetical protein	420	AAM84988.1	6.56521739
36798	H01	NTL02YP0328	hypothetical protein	423	AAM83924.1	2.99352052
36908	H02	NTL02YP3588	hypothetical protein	456	AAM87184.1	2
36918	H03	NTL02YP2480	hypothetical protein	459	AAM86076.1	4.55310621
36914	H04	NTL02YP1387	putative oxidoreductase	459	AAM84983.1	4.77154309
36946	H05	NTL02YP0296	hypothetical protein	468	AAM83892.1	2
36971	H06	NTL02YP1399	hypothetical protein	474	AAM84995.1	4.89688716
36970	H07	NTL02YP1393	bacterioferritin comigratory protein	474	AAM84989.1	5.5
36991	H08	NTL02YP2507	putative regulator	477	AAM86103.1	2
38677	H09	NTL02YP1389	putative permease	1065	AAM84985.1	3.3520362
38818	H10	NTL02YP1403	N-succinyl-diaminopimelate deacylase	1128	AAM84999.1	3.38955479
38885	H11	NTL02YP2479	flagellar biosynthesis protein	1161	AAM86075.1	4.05578684
38898	H12	NTL02YP0304	acetylornithine deacetylase	1170	AAM83900.1	3.97355372

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