

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 13**

Catalog No. NR-19609

This reagent is the tangible property of the U.S. Government.

For research use only. Not for human use.

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-19609 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 13, NR-19609.”

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:

You are authorized to use this product for research use only. It is not intended for human use.

Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at www.beiresources.org.

While BEI Resources uses reasonable efforts to include accurate and up-to-date information on this product sheet, neither ATCC® nor the U.S. Government makes any warranties or representations as to its accuracy. Citations from scientific literature and patents are provided for informational purposes only. Neither ATCC® nor the U.S. Government warrants that such information has been confirmed to be accurate.

This product is sent with the condition that you are responsible for its safe storage, handling, use and disposal. ATCC® and the U.S. Government are not liable for any damages or injuries arising from receipt and/or use of this product. While reasonable effort is made to ensure authenticity and reliability of materials on deposit, the U.S. Government, ATCC®, their suppliers and contributors to BEI Resources are not liable for damages arising from the

misidentification or misrepresentation of products.

Use Restrictions:

This material is distributed for internal research, non-commercial purposes only. This material, its product or its derivatives may not be distributed to third parties. Except as performed under a U.S. Government contract, individuals contemplating commercial use of the material, its products or its derivatives must contact the contributor to determine if a license is required. U.S. Government contractors may need a license before first commercial sale.

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.

ATCC® is a trademark of the American Type Culture Collection.



Table 1: *Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 13 (UYPVM)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38984	A01	NTL02YP0104	sodium/glutamate symporter	1215	AAM83700.1	2.364143426
39114	A02	NTL02YP2303	putative imidazolonepropionase	1296	AAM85899.1	3.035928144
39153	A03	NTL02YP1201	ATP-binding component of high affinity transport system	1317	AAM84797.1	3.020633751
39195	A04	NTL02YP3384	hypothetical protein	1341	AAM86980.1	5.769732078
36887	A05	NTL02YP1207	hypothetical protein	450	AAM84803.1	5
36938	A06	NTL02YP2288	hypothetical protein	465	AAM85884.1	5.516831683
36989	A07	NTL02YP1217	urease (urea amidohydrolase) beta subunit	477	AAM84813.1	5.061895551
37003	A08	NTL02YP1195	hypothetical protein	483	AAM84791.1	5.244741874
37132	A09	NTL02YP1189	flavodoxin 1	528	AAM84785.1	6.424295775
37166	A10	NTL02YP2297	hypothetical protein	540	AAM85893.1	2.655172414
37272	A11	NTL02YP2300	hypothetical protein	573	AAM85896.1	2
37315	A12	NTL02YP2290	hypothetical protein	585	AAM85886.1	2
37330	B01	NTL02YP0120	hypothetical protein	591	AAM83716.1	6.171156894
39315	B04	NTL02YP0127	glutamate synthase, small subunit	1419	AAM83723.1	5.602467443
39318	B05	NTL02YP1187	hypothetical protein	1422	AAM84783.1	3.55745554
39321	B06	NTL02YP2301	putative chlorohydrolase	1425	AAM85897.1	3.509897611
39337	B07	NTL02YP0105	putative transport protein, symporter	1437	AAM83701.1	3.055517942
39478	B08	NTL02YP1210	putative substrate-binding periplasmic protein of ABC transporter	1578	AAM84806.1	3.725587145
39530	B09	NTL02YP3380	hypothetical protein	1659	AAM86976.1	3.416715715
39564	B10	NTL02YP0098	putative enzyme	1704	AAM83694.1	2.844036697
37471	B11	NTL02YP2282	hypothetical protein	639	AAM85878.1	2.787923417
37515	B12	NTL02YP0123	sigma cross-reacting protein 27A (SCR-27A)	654	AAM83719.1	2
37514	C01	NTL02YP0108	putative transposase	654	AAM83704.1	4.220461095
37540	C02	NTL02YP2281	hypothetical protein	660	AAM85877.1	2.717142857
37600	C03	NTL02YP2280	putative oxidoreductase	681	AAM85876.1	4
37626	C04	NTL02YP0102	putative RNA methylase	693	AAM83698.1	1.993178718
37668	C05	NTL02YP1214	putative ATP-binding protein of ABC transport system	705	AAM84810.1	6.201342282
37664	C06	NTL02YP0113	hypothetical protein	705	AAM83709.1	5.684563758
37724	C07	NTL02YP0122	putative peptidoglycan enzyme	726	AAM83718.1	6.451697128
37844	C08	NTL02YP2302	putative repressor	768	AAM85898.1	5.870049505

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37893	C09	NTL02YP0085	lipopolysaccharide core biosynthesis glycosyl transferase	783	AAM83681.1	5.365735115
37979	C11	NTL02YP4069	putative amino acid ABC transport system permease	810	AAM87665.1	4.843529412
37971	C12	NTL02YP0088	formamidopyrimidine DNA glycosylase	810	AAM83683.1	1.778823529
38109	D01	NTL02YP4071	putative solute-binding periplasmic protein precursor for ABC	855	AAM87667.1	3.596648045
38130	D02	NTL02YP2960	putative inner membrane permease of ABC transporter	861	AAM86556.1	1.728079911
38132	D03	NTL02YP0096	putative alpha helix protein	864	AAM83692.1	1.717920354
38216	D04	NTL02YP4075	inner membrane permease	888	AAM87671.1	5.297413793
36206	D05	NTL02YP4041	hypothetical protein	210	AAM87637.1	4.884
38314	D07	NTL02YP2971	hypothetical protein	930	AAM86567.1	5.534020619
38313	D08	NTL02YP2961	putative solute-binding protein of ABC transporter	930	AAM86557.1	5.522680412
38334	D09	NTL02YP2968	penicillin-binding protein 7	936	AAM86564.1	5.295081967
38355	D10	NTL02YP2970	putative regulator protein	945	AAM86566.1	8.76751269
38383	D11	NTL02YP4052	putative ornithine cyclodeaminase	954	AAM87648.1	4.875251509
38433	D12	NTL02YP4076	inner membrane permease	972	AAM87672.1	5.306324111
38443	E01	NTL02YP0080	ADP-L-glycero-D-mannoheptose-6-epimerase	978	AAM83676.1	4.44302554
38472	E02	NTL02YP0083	heptosyl transferase I	990	AAM83679.1	4.75631068
38582	E03	NTL02YP0078	threonine dehydrogenase	1026	AAM83674.1	3.074108818
36534	E04	NTL02YP1871	hypothetical protein	333	AAM85467.1	6.597855228
36560	E05	NTL02YP4050	hypothetical protein	339	AAM87646.1	2.683377309
36596	E06	NTL02YP2965	hypothetical protein	354	AAM86561.1	4.799492386
36601	E07	NTL02YP1876	50S ribosomal subunit protein L20	357	AAM85472.1	2.906801008
36613	E08	NTL02YP4061	RNase P	360	AAM87657.1	5.3625
36777	E09	NTL02YP4049	heat shock protein	414	AAM87645.1	5.610132159
36919	E10	NTL02YP2974	molybdopterin converting factor, subunit 2	459	AAM86570.1	5.573146293
36953	E11	NTL02YP0092	deoxyuridinetriphosphatase	471	AAM83688.1	2
36975	E12	NTL02YP2958	hypothetical protein	474	AAM86554.1	4.871595331
36996	F01	NTL02YP0086	putative enzyme of lipopolysaccharide synthesis	480	AAM83682.1	1.986538462
38589	F02	NTL02YP2977	molybdopterin biosynthesis protein A	1026	AAM86573.1	4.110694184
38620	F03	NTL02YP4051	threonine dehydratase	1038	AAM87647.1	3.977736549
38628	F04	NTL02YP4077	periplasmic phosphate-binding protein	1041	AAM87673.1	3.0453284
38701	F05	NTL02YP0082	ADP-heptose--lps heptosyltransferase II	1077	AAM83678.1	1.552372426
38764	F06	NTL02YP4058	DNA polymerase III, beta-subunit	1101	AAM87654.1	5.752848379
38769	F07	NTL02YP2963	hypothetical protein	1104	AAM86559.1	2.753496504
38853	F08	NTL02YP1182	N-acetylglucosamine-6-phosphate deacetylase	1146	AAM84778.1	2.783305228
38960	F09	NTL02YP4065	hypothetical protein	1200	AAM87661.1	2.508064516
39026	F10	NTL02YP0079	2-amino-3-ketobutyrate CoA ligase (glycine acetyltransferase)	1242	AAM83675.1	4.610764431
39059	F11	NTL02YP1181	transcriptional repressor of nag (N-acetylglucosamine) operon	1266	AAM84777.1	2.539050536
39118	F12	NTL02YP2957	putative Leu/Ile/Val/Thr binding protein of ABC transporter	1299	AAM86553.1	1.289768484
37007	G01	NTL02YP2976	molybdopterin biosynthesis protein C	483	AAM86572.1	4.739961759
37079	G02	NTL02YP4048	heat shock protein	507	AAM87644.1	6.906764168
37168	G03	NTL02YP2966	putative adenylate cyclase	540	AAM86562.1	2

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37344	G04	NTL02YP0093	putative transcriptional regulator	597	AAM83689.1	6.481946625
37423	G05	NTL02YP4066	hypothetical protein	621	AAM87662.1	2.80484115
37425	G06	NTL02YP0097	hypothetical protein	624	AAM83693.1	2.484939759
37495	G07	NTL02YP4042	hypothetical protein	645	AAM87638.1	2.776642336
37497	G08	NTL02YP0094	orotate phosphoribosyltransferase	648	AAM83690.1	2.646802326
37542	G09	NTL02YP4040	putative outer membrane protein	660	AAM87636.1	4.517142857
37554	G10	NTL02YP1869	murein transglycosylase E	663	AAM85465.1	6.674253201
39176	G11	NTL02YP0091	flavoprotein affecting synthesis of DNA and pantothenate	1332	AAM83687.1	6.358600583
39230	G12	NTL02YP4064	GTP-binding protein	1365	AAM87660.1	2.527402135
39242	H01	NTL02YP4046	alanine-alpha-ketoisovalerate	1371	AAM87642.1	3.66335932
39272	H02	NTL02YP0084	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)	1386	AAM83680.1	5.726507714
39302	H03	NTL02YP4059	DNA biosynthesis protein	1401	AAM87655.1	3.595419847
39497	H04	NTL02YP2956	putative branched chain inner membrane permease of	1617	AAM86552.1	3.736873868
39516	H05	NTL02YP4063	60 kDa inner-membrane protein	1641	AAM87658.1	3.668649613
39531	H06	NTL02YP4047	putative membrane/transport protein	1659	AAM87643.1	2.928193055
39534	H07	NTL02YP1179	asparagine synthetase B	1665	AAM84775.1	3.426392962
39571	H08	NTL02YP2967	D-lactate dehydrogenase, FAD protein	1716	AAM86563.1	2.648063781
37566	H09	NTL02YP0090	DNA repair protein	669	AAM83686.1	6.094499295
37574	H10	NTL02YP4068	putative phosphatase	669	AAM87664.1	6.088857546
37573	H11	NTL02YP4053	putative transposase	669	AAM87649.1	4.007052186
37580	H12	NTL02YP4072	hypothetical protein	672	AAM87668.1	1.903089888

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.