

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 3**

Catalog No. NR-19599

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-19599 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 3, NR-19599.”

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 3 (UYPVC)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37892	A01	NTL02YP0041	putative transposase	783	AAM83637.1	4.63791009
38232	A02	NTL02YP2052	hypothetical protein	894	AAM85648.1	3.91755889
38295	A03	NTL02YP2076	putative transcriptional regulator LYSR-type	924	AAM85672.1	5.44190871
37778	A04	NTL02YP2559	putative oxidoreductase	741	AAM86155.1	5.73751601
37798	A05	NTL02YP0373	uroporphyrinogen III synthase	750	AAM83969.1	3.97974684
37813	A06	NTL02YP0345	chaperone	756	AAM83941.1	4.78894472
37917	A07	NTL02YP0348	glutamine cyclotransferase	792	AAM83944.1	5.09254808
37953	A08	NTL02YP3642	putative structural protein	801	AAM87238.1	4.10107015
38007	A09	NTL02YP3635	S-adenosylmethionine-6-N,N-adenosyl (rRNA) dimethyltransferase	819	AAM87231.1	5.61233993
38001	A10	NTL02YP0342	putative pilus chaperone, PapD family	819	AAM83938.1	3.98719441
38016	A11	NTL02YP3646	dihydrodipicolinate reductase	822	AAM87242.1	5.64617169
38048	A12	NTL02YP3631	putative DNA binding protein	834	AAM87227.1	4.61098398
38074	B01	NTL02YP2558	putative isomerase	843	AAM86154.1	5.60588901
36049	B02	NTL02YP1470	hypothetical protein	162	AAM85066.1	1.98514851
36059	B03	NTL02YP0351	hypothetical protein	165	AAM83947.1	4.88780488
36082	B04	NTL02YP2556	hypothetical protein	171	AAM86152.1	1.98578199
36135	B05	NTL02YP0377	hypothetical protein	189	AAM83973.1	7.72925764
36151	B06	NTL02YP1469	hypothetical protein	195	AAM85065.1	3.97446809
36259	B07	NTL02YP2527	hypothetical protein	234	AAM86123.1	2
36284	B08	NTL02YP1468	conserved protein	243	AAM85064.1	2.98233216
36386	B09	NTL02YP2519	hypothetical protein	279	AAM86115.1	3.85893417
36396	B10	NTL02YP2526	hypothetical protein	282	AAM86122.1	3.85403727
36434	B11	NTL02YP0349	peptidyl-prolyl cis-trans isomerase C	297	AAM83945.1	3.95252226
38154	B12	NTL02YP3637	diadenosine tetraphosphatase	870	AAM87233.1	4.64725275
38159	C01	NTL02YP1436	putative NAGC-like transcriptional regulator	873	AAM85032.1	8.52135816
38191	C02	NTL02YP2550	hypothetical protein	882	AAM86146.1	3.9197397
38244	C03	NTL02YP1433	putative acetylneuraminate lyase	900	AAM85029.1	8.22978723
38273	C04	NTL02YP1432	hypothetical protein	915	AAM85028.1	8.29528796
38422	C05	NTL02YP1464	cysteine synthase A, O-acetylserine sulfhydrylase A	969	AAM85060.1	7.83448959
38479	C06	NTL02YP1477	putative reductase	990	AAM85073.1	5.31456311
38540	C07	NTL02YP3634	pyridoxine biosynthesis protein	1008	AAM87230.1	5.2471374
38583	C08	NTL02YP1466	cell division protein	1026	AAM85062.1	3.82551595

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38771	C09	NTL02YP3616	hypothetical protein	1104	AAM87212.1	5.02272727
38819	C10	NTL02YP1435	putative membrane protein	1128	AAM85031.1	4.32106164
36442	C11	NTL02YP2525	hypothetical protein	300	AAM86121.1	3.87352941
36481	C12	NTL02YP2524	hypothetical protein	312	AAM86120.1	6.82954545
36586	D01	NTL02YP1476	hypothetical protein	351	AAM85072.1	3.99232737
36612	D02	NTL02YP3609	hypothetical protein	360	AAM87205.1	3.9675
36627	D03	NTL02YP3614	hypothetical protein	366	AAM87210.1	3.99507389
36653	D04	NTL02YP3613	hypothetical protein	375	AAM87209.1	3.98554217
36661	D05	NTL02YP3636	hypothetical protein	378	AAM87232.1	3.98564593
36769	D06	NTL02YP1430	hypothetical protein	414	AAM85026.1	5.5
36780	D07	NTL02YP1428	hypothetical protein	417	AAM85024.1	3.97374179
36942	D08	NTL02YP3638	hypothetical protein	465	AAM87234.1	3.99405941
36959	D09	NTL02YP1437	hypothetical protein	471	AAM85033.1	3.99021526
38830	D10	NTL02YP0372	uroporphyrinogen III methylase	1134	AAM83968.1	4.93867121
38854	D11	NTL02YP2555	L-lactate dehydrogenase	1146	AAM86151.1	4.7529511
38902	D12	NTL02YP0343	conserved hypothetical protein	1173	AAM83939.1	5.48227535
38968	E01	NTL02YP3645	carbamoyl-phosphate synthetase, glutamine (small) subunit	1203	AAM87241.1	4.84231698
38990	E02	NTL02YP0371	hemY protein	1221	AAM83967.1	4.53291039
39005	E03	NTL02YP1475	putative manganese transport system permease	1230	AAM85071.1	3.98031496
39074	E04	NTL02YP2557	hypothetical protein	1278	AAM86153.1	2.50227618
39086	E05	NTL02YP0352	putative ATP-dependent RNA helicase	1287	AAM83948.1	5.39939714
39104	E06	NTL02YP2546	putative membrane permease of ABC transporter	1293	AAM86142.1	5.20780195
36993	E07	NTL02YP3641	hypothetical protein	477	AAM87237.1	3.9787234
37010	E08	NTL02YP3640	dihydrofolate reductase type I	483	AAM87236.1	3.82600382
37026	E09	NTL02YP2560	hypothetical protein	489	AAM86156.1	4.95463138
37022	E10	NTL02YP0369	hypothetical protein	489	AAM83965.1	3.97920605
37082	E11	NTL02YP0136	putative transposase	510	AAM83732.1	4.79272727
37088	F01	NTL02YP1461	PTS system, glucose-specific IIA component	510	AAM85057.1	4
37084	F02	NTL02YP0223	putative transposase	510	AAM83819.1	3.98909091
37136	F03	NTL02YP0346	fimbrial protein (precursor)	531	AAM83942.1	4.79334501
37167	F04	NTL02YP2548	nucleoprotein/polynucleotide-associated enzyme	540	AAM86144.1	4.82758621
39194	F05	NTL02YP2551	putative inner membrane permease	1341	AAM86147.1	5.23171615
39207	F06	NTL02YP1458	putative kinase sensor protein	1350	AAM85054.1	5.09856115
39216	F07	NTL02YP2518	hypothetical protein	1356	AAM86114.1	4.91475645
39241	F08	NTL02YP2554	argininosuccinate synthetase	1371	AAM86150.1	4.41034727
39248	F09	NTL02YP3612	hypothetical protein	1374	AAM87208.1	5.2241867
39278	F10	NTL02YP0368	putative amino acid/amine symporter	1392	AAM83964.1	
39299	F11	NTL02YP2561	putative transport protein	1401	AAM86157.1	4.37890354
39313	F12	NTL02YP1473	glutamate tRNA synthetase, catalytic subunit	1416	AAM85069.1	4.88667582
39328	G01	NTL02YP2552	hypothetical protein	1431	AAM86148.1	5.00747791
39513	G02	NTL02YP3611	hypothetical protein	1638	AAM87207.1	4.70441001
39577	G03	NTL02YP1462	PEP-protein phosphotransferase system enzyme I	1728	AAM85058.1	4.45588235
37280	G04	NTL02YP1460	hypothetical protein	576	AAM85056.1	3.97727273
37387	G05	NTL02YP1471	hypothetical protein	612	AAM85067.1	4.80521472

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37406	G06	NTL02YP3615	hypothetical protein	618	AAM87211.1	4.79331307
37449	G07	NTL02YP2547	response regulator	630	AAM86143.1	4.79701493
37518	G08	NTL02YP2522	hypothetical protein	654	AAM86118.1	3.83285303
37595	G09	NTL02YP3643	hypothetical protein	678	AAM87239.1	4.81615599
37638	G10	NTL02YP2549	hypothetical protein	696	AAM86145.1	3.99320652
37655	G11	NTL02YP1434	putative enzyme	702	AAM85030.1	4
37756	G12	NTL02YP1465	cysZ protein	735	AAM85061.1	4.37935484
37766	H01	NTL02YP2521	hypothetical protein	738	AAM86117.1	4
38179	H02	NTL02YP1439	putative transcriptional regulator	879	AAM85035.1	4.8759521
38197	H03	NTL02YP0338	positive regulator for ilvC	885	AAM83934.1	5.9675676
38214	H04	NTL02YP2538	putative transcriptional regulator	888	AAM86134.1	4.5948276
38213	H05	NTL02YP2512	PTS enzyme IID, mannose-specific	888	AAM86108.1	4.5765086
38427	H06	NTL02YP1452	hypothetical protein	972	AAM85048.1	4.1758893
38555	H07	NTL02YP3628	hypothetical protein	1014	AAM87224.1	4.1185958
36000	H08	NTL02YP2516	hypothetical protein	150	AAM86112.1	3.9157895
36064	H09	NTL02YP2530	hypothetical protein	165	AAM86126.1	2.795122
36108	H10	NTL02YP2509	hypothetical protein	180	AAM86105.1	3.9681818
36189	H11	NTL02YP1451	hypothetical protein	207	AAM85047.1	1.8825911

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.