

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 27**

Catalog No. NR-19623

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-19623 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 27, NR-19623.”

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 27 (UYPWA)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36850	A01	NTL02YP3701	DNA polymerase III, psi subunit	438	AAM87297.1	5
36924	A02	NTL02YP0420	hypothetical protein	462	AAM84016.1	5.591633
38587	A04	NTL02YP2617	inner membrane permease of galactoside ABC transporter	1026	AAM86213.1	3.572233
38603	A05	NTL02YP1508	hypothetical protein	1032	AAM85104.1	3.558769
38624	A06	NTL02YP2593	putative inner membrane permease of ABC transporter	1041	AAM86189.1	3.53469
38635	A07	NTL02YP3702	putative enzyme	1044	AAM87298.1	3.458487
38669	A08	NTL02YP1511	hypothetical protein	1062	AAM85106.1	2.553539
38691	A09	NTL02YP1509	hypothetical protein	1071	AAM85105.1	3.420342
38745	A10	NTL02YP2608	putative ABC transporter binding protein	1092	AAM86204.1	3.469965
38773	A11	NTL02YP0421	hypothetical protein	1107	AAM84017.1	3.4551
38790	A12	NTL02YP2604	putative ATPase	1113	AAM86200.1	3.450997
37029	B01	NTL02YP0426	hypothetical protein	492	AAM84022.1	3.983083
37075	B02	NTL02YP3683	putative outer membrane protein	507	AAM87279.1	1.985375
37110	B04	NTL02YP0422	hypothetical protein	519	AAM84018.1	2.813953
37191	B05	NTL02YP1519	hypothetical protein	546	AAM85115.1	2.8157
37260	B06	NTL02YP1521	hypothetical protein	570	AAM85117.1	2
37301	B07	NTL02YP2596	putative siderophore biosynthetic protein	582	AAM86192.1	2.811897
37354	B08	NTL02YP1522	hypothetical protein	600	AAM85118.1	2.814063
37366	B09	NTL02YP1503	hypothetical protein	603	AAM85099.1	2.793157
38920	B11	NTL02YP2610	putative transport protein	1182	AAM86206.1	3.310147
39043	C01	NTL02YP2609	hypothetical protein	1257	AAM86205.1	4.046261
39068	C02	NTL02YP3695	hypothetical protein	1272	AAM87291.1	3.395579
39076	C03	NTL02YP3682	hypothetical protein	1278	AAM87278.1	3.820182
39116	C04	NTL02YP2597	putative siderophore biosynthetic protein	1299	AAM86193.1	3.342793
39135	C05	NTL02YP3693	putative transport system permease protein	1308	AAM87289.1	3.96365
39159	C06	NTL02YP0427	periplasmic binding protein	1320	AAM84023.1	3.458824
37381	C07	NTL02YP2602	2-deoxycytidine 5-triphosphate deaminase	609	AAM86198.1	2.802773
37396	C08	NTL02YP3697	hyperosmotically inducible periplasmic protein	615	AAM87293.1	2.789313
37435	C09	NTL02YP3681	hypothetical protein	624	AAM87277.1	2.793675
37556	C10	NTL02YP2607	hypothetical protein	663	AAM86203.1	2.853485
37545	C11	NTL02YP0423	hypothetical protein	663	AAM84019.1	2.802276

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37601	C12	NTL02YP2603	uridine/cytidine kinase	681	AAM86199.1	2.790569
37639	D01	NTL02YP2612	putative membrane protein	696	AAM86208.1	7.153533
37662	D02	NTL02YP3689	hypothetical protein	702	AAM87285.1	4.101078
37732	D03	NTL02YP3690	purine-nucleoside phosphorylase	726	AAM87286.1	2.250653
37741	D04	NTL02YP0419	ATP-binding component of leucine transport	732	AAM84015.1	7.160622
39431	D05	NTL02YP1520	conserved hypothetical protein	1524	AAM85116.1	3.658568
39482	D07	NTL02YP3698	peptide chain release factor RF-3	1590	AAM87294.1	3.704908
39560	D08	NTL02YP2615	NAD-linked malate dehydrogenase (malic enzyme)	1698	AAM86211.1	3.310702
39643	D09	NTL02YP1512	hypothetical protein	1881	AAM85108.1	3.695992
39646	D10	NTL02YP2595	putative siderophore biosynthetic protein	1890	AAM86191.1	3.633161
37805	D11	NTL02YP1506	hypothetical protein	753	AAM85102.1	6.167718
37841	D12	NTL02YP0418	ATP-binding component of high-affinity branched-chain amino acid	768	AAM84014.1	2
37880	E01	NTL02YP1516	probable pilin chaperone	780	AAM85112.1	3.632927
37963	E03	NTL02YP0437	uridine phosphorylase	807	AAM84033.1	4.035419
37988	E04	NTL02YP3694	hypothetical protein	813	AAM87290.1	6.811254
37987	E05	NTL02YP3692	2-deoxyribose-5-phosphate aldolase	813	AAM87288.1	6.574443
38081	E06	NTL02YP0429	inner membrane permease	846	AAM84025.1	2
38087	E07	NTL02YP1496	hypothetical protein	849	AAM85092.1	3.24072
38110	E08	NTL02YP0412	RNA polymerase, sigma(32) factor	858	AAM84008.1	6.14588
38114	E09	NTL02YP1056	putative CDP-paratose synthetase	858	AAM84652.1	2
38177	E10	NTL02YP0389	outer membrane phospholipase A	879	AAM83985.1	6.394995
35965	E11	NTL02YP1483	hypothetical protein	129	AAM85080.1	2
36013	E12	NTL02YP1484	hypothetical protein	153	AAM85081.1	2.917098
36401	F01	NTL02YP1071	hypothetical protein	285	AAM84667.1	4.852308
36498	F02	NTL02YP0405	hypothetical protein	321	AAM84001.1	5.34903
36704	F03	NTL02YP0402	hypothetical protein	396	AAM83998.1	2
36735	F04	NTL02YP1488	hypothetical protein	402	AAM85084.1	5.753394
36788	F05	NTL02YP0406	hypothetical protein	420	AAM84002.1	4.293478
36789	F06	NTL02YP1076	putative transcriptional regulator	420	AAM84512.1	5.521739
36845	F07	NTL02YP0414	hypothetical protein	438	AAM84010.1	6.307531
38438	F08	NTL02YP1480	glucokinase	975	AAM85076.1	5.854187
38509	F09	NTL02YP0386	magnesium and cobalt permease	999	AAM83982.1	4.662175
38648	F10	NTL02YP1499	ATP-binding protein of iron ABC transporter	1050	AAM85095.1	3.182569
38686	F11	NTL02YP2581	imidazoglycerolphosphate dehydratase histidinol-phosphate phosphatase	1068	AAM86177.1	2.778881
36855	F12	NTL02YP1486	hypothetical protein	441	AAM85082.1	2
36886	G01	NTL02YP1077	hypothetical protein	450	AAM84673.1	1.987755
36955	G02	NTL02YP0388	hypothetical protein	471	AAM83984.1	1.927593
37025	G03	NTL02YP1072	hypothetical protein	489	AAM84668.1	1.994329
37125	G05	NTL02YP1498	hypothetical protein	525	AAM85094.1	2
37130	G06	NTL02YP0400	hypothetical protein	528	AAM83996.1	2.797535
37133	G07	NTL02YP1479	hypothetical protein	528	AAM85075.1	2
37353	G08	NTL02YP1485	putative cytochrome	600	AAM85079.1	2
38847	G09	NTL02YP1061	putative mannosyltransferase protein	1143	AAM84500.1	3.393068
38862	G11	NTL02YP1067	putative O-antigen chain length determinant	1152	AAM84663.1	3.390101
38982	G12	NTL02YP0395	hypothetical protein	1212	AAM83991.1	3.126997

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38985	H01	NTL02YP1070	putative drug efflux protein	1215	AAM84666.1	1.633466
38987	H02	NTL02YP0384	hypothetical protein	1218	AAM83980.1	3.251987
39034	H03	NTL02YP1481	hypothetical protein	1248	AAM85077.1	3.195652
39082	H04	NTL02YP1057	putative O-antigen synthesis protein, WbyH	1284	AAM84653.1	3.889728
39087	H05	NTL02YP0417	inner membrane permease of high-affinity branched-chain amino	1287	AAM84013.1	6.182366
39100	H06	NTL02YP0398	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit	1293	AAM83994.1	3.770443
39122	H07	NTL02YP1068	inosine-guanosine kinase	1305	AAM84664.1	3.976208
37394	H08	NTL02YP2586	phosphoribosyl-amp cyclohydrolase	615	AAM86182.1	2.79542
37404	H09	NTL02YP2582	hypothetical protein	618	AAM86178.1	2.574468
37411	H10	NTL02YP0392	putative homoserine/homoserine lactone efflux protein	621	AAM83988.1	2.783661
37410	H11	NTL02YP0391	threonine efflux protein	621	AAM83987.1	2.789713
37438	H12	NTL02YP0404	putative enzyme	627	AAM84000.1	2.794603

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.