

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 8**

Catalog No. NR-19604

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-19604 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 8, NR-19604.”

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 8 (UYPVH)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39436	A01	NTL02YP3512	putative membrane protein	1527	AAM87108.1	3.733886407
39459	A02	NTL02YP1339	IMP dehydrogenase	1548	AAM84935.1	3.558564232
39652	A04	NTL02YP3511	hypothetical protein	1902	AAM87107.1	3.779608651
37296	A05	NTL02YP0244	hypothetical protein	582	AAM83840.1	7.45659164
37555	A06	NTL02YP2420	putative ABC transporter permease for cystine	663	AAM86016.1	2.806543385
37649	A07	NTL02YP0245	putative deoxyribose-phosphate aldolase	702	AAM83841.1	2.684636119
37700	A08	NTL02YP3500	hypothetical protein	717	AAM87096.1	5.739762219
37717	A09	NTL02YP2425	alternative sigma factor 28	723	AAM86021.1	6.52948886
37801	A10	NTL02YP1328	putative fimbrial biogenesis protein	750	AAM84924.1	5.373417722
37832	A11	NTL02YP2419	putative ATP-binding component of ABC transport system	762	AAM86015.1	5.347880299
37924	A12	NTL02YP0252	hypothetical protein	795	AAM83848.1	3.102994012
37263	B01	NTL02YP2385	hypothetical protein	570	AAM85981.1	2.793442623
37309	B02	NTL02YP1301	outer membrane protein X	585	AAM84897.1	2.8224
37434	B03	NTL02YP3480	hypothetical protein	624	AAM87076.1	2.796686747
37534	B04	NTL02YP2404	putative 2-component transcriptional regulator	657	AAM86000.1	2.797704448
37584	B05	NTL02YP1306	hypothetical protein	675	AAM84902.1	2.808391608
37726	B06	NTL02YP0214	putative transcriptional regulator	726	AAM83810.1	2.808093995
37780	B07	NTL02YP3484	hypothetical protein	741	AAM87080.1	6.882202305
37865	B08	NTL02YP1309	putative ATP synthase beta subunit	774	AAM84905.1	3.633906634
36088	B10	NTL02YP1304	hypothetical protein	174	AAM84900.1	4
37956	B11	NTL02YP1308	suppressor protein	804	AAM84904.1	3.645734597
38005	B12	NTL02YP3482	bacitracin resistance protein	819	AAM87078.1	3.076833527
38028	C01	NTL02YP0218	hypothetical protein	828	AAM83814.1	3.632488479
38099	C02	NTL02YP0227	hypothetical protein	855	AAM83823.1	3.079329609
38285	C03	NTL02YP0210	methylase for 50S ribosomal subunit protein L11	921	AAM83806.1	3.825182102
38400	C04	NTL02YP2398	putative transposase	960	AAM85994.1	4.722
38551	C05	NTL02YP2380	putative periplasmic solute-binding protein of ABC transporter	1014	AAM85976.1	4.95540797
38575	C06	NTL02YP1307	hypothetical protein	1023	AAM84903.1	3.335841957
36247	C08	NTL02YP2401	hypothetical protein	228	AAM85997.1	3.981343284
36281	C09	NTL02YP0208	hypothetical protein	243	AAM83804.1	3.96819788

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36311	C10	NTL02YP2406	hypothetical protein	255	AAM86002.1	4.949152542
36383	C11	NTL02YP2393	putative phage protein	276	AAM85989.1	3.537974684
36410	C12	NTL02YP0222	cold shock-like protein	288	AAM83818.1	5.93597561
36416	D01	NTL02YP2394	hypothetical protein	288	AAM85990.1	4
36433	D02	NTL02YP0212	site-specific DNA inversion stimulation factor	297	AAM83808.1	3.985163205
36463	D03	NTL02YP2395	hypothetical protein	306	AAM85991.1	6.176300578
36470	D04	NTL02YP0221	cold shock-like protein	309	AAM83817.1	3.558739255
38601	D05	NTL02YP3486	putative O-sialoglycoprotein endopeptidase	1029	AAM87082.1	3.64546305
38685	D06	NTL02YP1292	hypothetical protein	1068	AAM84888.1	3.084837545
38705	D07	NTL02YP2388	hypothetical protein	1077	AAM85984.1	5.397493286
38878	D08	NTL02YP1302	MFS (major facilitator superfamily) transporter	1158	AAM84898.1	3.316360601
38907	D09	NTL02YP0225	hypothetical protein	1176	AAM83821.1	3.394736842
38922	D10	NTL02YP3479	hypothetical protein	1182	AAM87075.1	4.023731588
38942	D11	NTL02YP1298	dihydropteridine reductase	1191	AAM84894.1	3.34037368
39061	D12	NTL02YP2379	putative periplasmic solute-binding protein of ABC transporter	1269	AAM85975.1	3.057295646
36512	E01	NTL02YP1313	putative regulator	324	AAM84909.1	4.266483516
36546	E02	NTL02YP1317	[2FE-2S] ferredoxin, electron carrier protein	336	AAM84913.1	3.861702128
36557	E03	NTL02YP1295	regulatory protein P-II for glutamine synthetase	339	AAM84891.1	4.82585752
36568	E04	NTL02YP3491	hypothetical protein	342	AAM87087.1	5.12565445
36571	E05	NTL02YP2405	hypothetical protein	345	AAM86001.1	3.836363636
36611	E06	NTL02YP2391	putative phage protein	360	AAM85987.1	5.315
36616	E07	NTL02YP0224	hypothetical protein	363	AAM83820.1	4.163771712
36621	E08	NTL02YP3483	putative kinase	363	AAM87079.1	3.533498759
36709	E09	NTL02YP2392	hypothetical protein	396	AAM85988.1	4.327981651
36838	E10	NTL02YP2383	hypothetical protein	435	AAM85979.1	4.877894737
39200	E11	NTL02YP0226	hypothetical protein	1347	AAM83822.1	4.330209084
39226	E12	NTL02YP0215	putative metabolite transport protein, permease	1365	AAM83811.1	3.834163701
39280	F01	NTL02YP1303	hypothetical protein	1392	AAM84899.1	3.802374302
39364	F02	NTL02YP0209	sodium/pantothenate symporter	1461	AAM83805.1	5.00799467
39501	F03	NTL02YP1294	putative NH ₃ -dependent NAD(+) synthetase	1623	AAM84890.1	2.992182802
39586	F04	NTL02YP3488	DNA primase	1749	AAM87084.1	2.885969816
39668	F05	NTL02YP1316	heat shock protein	1935	AAM84912.1	3.351392405
36844	F06	NTL02YP0216	putative decarboxylase	438	AAM83812.1	6.441422594
36876	F07	NTL02YP2397	putative transposase	447	AAM85993.1	4.784394251
36968	F08	NTL02YP0219	putative outer membrane receptor	474	AAM83815.1	4.501945525
36983	F09	NTL02YP0213	hypothetical protein	477	AAM83809.1	1.992263056
37083	F10	NTL02YP0206	acetyl CoA carboxylase, BCCP subunit	510	AAM83802.1	2
37124	F11	NTL02YP1315	hypothetical protein	525	AAM84911.1	5.111504425
37201	F12	NTL02YP2402	phosphatidylglycerophosphate synthetase	549	AAM85593.1	4.23089983
37209	G01	NTL02YP2407	putative outer membrane protein	552	AAM86003.1	2.817567568
37521	G02	NTL02YP3059	putative transport system permease protein	654	AAM86655.1	4.716138329
37539	G03	NTL02YP1971	putative transport ATPase	660	AAM85567.1	2.771428571

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37635	G04	NTL02YP1284	hypothetical protein	696	AAM84880.1	3.495923913
37676	G05	NTL02YP3062	hypothetical protein	708	AAM86658.1	2.779411765
37708	G06	NTL02YP3050	hypothetical protein	720	AAM86646.1	2.773684211
37746	G07	NTL02YP1278	pyridoxine biosynthesis	732	AAM84874.1	5.752590674
37838	G08	NTL02YP3048	DNA polymerase III, epsilon subunit	765	AAM86644.1	5.624844721
37854	G09	NTL02YP1962	putative carboxypeptidase	771	AAM85558.1	6.371146732
37897	G10	NTL02YP3053	hypothetical protein	783	AAM86649.1	2.582017011
36168	G12	NTL02YP3067	hypothetical protein	201	AAM86663.1	4.975103734
36279	H01	NTL02YP3046	hypothetical protein	240	AAM86642.1	2.95
36447	H02	NTL02YP0184	hypothetical phage protein	303	AAM83780.1	5.259475219
37915	H03	NTL02YP3077	UDP-N-acetylglucosamine acetyltransferase	789	AAM86673.1	1.998793727
37962	H04	NTL02YP3055	putative aldose reductase	804	AAM86651.1	3.097156398
37996	H05	NTL02YP3060	putative lipoprotein	816	AAM86656.1	3.324766355
38063	H06	NTL02YP1282	hypothetical protein	840	AAM84878.1	3.640909091
38077	H07	NTL02YP3051	probable hydroxyacylglutathione hydrolase	843	AAM86647.1	4.988674972
38164	H08	NTL02YP0179	putative transcriptional regulator	876	AAM83775.1	3.177947598
38207	H09	NTL02YP1283	putative regulator	888	AAM84879.1	4.581896552
38265	H10	NTL02YP0178	putative transcriptional regulator LYSR-type	912	AAM83774.1	4.961134454
38331	H11	NTL02YP1966	hypothetical protein	936	AAM85562.1	5.095286885

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.