

Yersinia pestis, Strain KIM, Gateway® Clone Set, Recombinant in Escherichia coli, Plate 21

Catalog No. NR-19617

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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-19617 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 21, NR-19617."

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/bmbl5/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 21 (UYPVU)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38127	A01	NTL02YP2118	hypothetical protein	901	AAM85357.1	3.59267481
38326	A02	NTL02YP3227	hypothetical protein	973	AAM86251.1	3.47687564
38323	A03	NTL02YP2137	putative oxidoreductase	973	AAM85374.1	5.95272354
38390	A04	NTL02YP2099	hypothetical protein	997	AAM85695.1	5.96389168
38534	A05	NTL02YP2131	hypothetical protein	1045	AAM85369.1	3.5492823
35997	A06	NTL02YP2124	hypothetical protein	190	AAM85363.1	3.95263158
36181	A07	NTL02YP3217	hypothetical protein	244	AAM86813.1	3.70081967
36398	A08	NTL02YP3224	hypothetical protein	322	AAM86248.1	5.77950311
36466	A09	NTL02YP3211	hypothetical protein	346	AAM86239.1	2.9017341
38546	A10	NTL02YP3198	molybdopterin biosynthesis protein	1051	AAM86226.1	4.04852521
38559	A11	NTL02YP2127	hypothetical protein	1057	AAM85366.1	3.52034059
38558	A12	NTL02YP2114	hypothetical protein	1057	AAM85353.1	3.0756859
38579	B01	NTL02YP3199	molybdopterin biosynthesis protein	1063	AAM86227.1	5.75634995
38640	B03	NTL02YP2123	transcriptional regulatory protein	1087	AAM85362.1	3.06071757
38721	B04	NTL02YP3185	putative transport protein	1123	AAM86218.1	2.79252004
38776	B05	NTL02YP3196	putative arylsulfatase activating enzyme	1147	AAM86225.1	3.26503923
38849	B06	NTL02YP3210	hypothetical protein	1183	AAM86238.1	2.772612
38861	B07	NTL02YP3188	putative esterase	1189	AAM86221.1	3.47182506
38965	B08	NTL02YP2139	hypothetical protein	1243	AAM85376.1	3.21962993
36465	B09	NTL02YP3205	hypothetical protein	346	AAM86233.1	4.63872832
36482	B10	NTL02YP3190	hypothetical protein	352	AAM86786.1	7.13352273
36536	B11	NTL02YP3213	hypothetical protein	373	AAM86241.1	2
36603	B12	NTL02YP2145	hypothetical protein	397	AAM85380.1	3.78589421
36644	C01	NTL02YP3221	hypothetical protein	412	AAM86817.1	4.97572816
36658	C02	NTL02YP2129	hypothetical protein	418	AAM85725.1	5.61961722
36677	C03	NTL02YP2120	putative peptidase T	427	AAM85359.1	2
36725	C04	NTL02YP3220	hypothetical protein	439	AAM86816.1	1.9977221
36754	C05	NTL02YP2112	hypothetical protein	448	AAM85351.1	2.97767857
36782	C06	NTL02YP2104	hypothetical protein	457	AAM85700.1	2
36823	C07	NTL02YP2108	hypothetical protein	469	AAM85347.1	2
38966	C08	NTL02YP3192	hypothetical protein	1243	AAM86788.1	3.20675784
39057	C09	NTL02YP3195	putative ATP-binding ABC transporter protein	1303	AAM86224.1	3.92018419
39134	C10	NTL02YP3194	hypothetical protein	1348	AAM86223.1	3.74035608

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39133	C11	NTL02YP3186	putative transcriptional regulator LYSR-type	1348	AAM86219.1	3.86424332
39162	C12	NTL02YP2135	aerotaxis sensor receptor, flavoprotein	1360	AAM85373.1	3.81911765
39181	D01	NTL02YP3189	putative outer membrane protein	1372	AAM86785.1	3.7638484
39246	D02	NTL02YP2113	transcription-repair coupling factor	1414	AAM85352.1	3.76520509
39281	D03	NTL02YP2103	hypothetical protein	1432	AAM85344.1	3.72346369
36960	D04	NTL02YP2130	putative phosphohydrolase	511	AAM85368.1	2
37115	D05	NTL02YP3200	putative transposase	559	AAM86228.1	2.81753131
37207	D06	NTL02YP2125	hypothetical protein	592	AAM85364.1	2
37292	D07	NTL02YP3184	GTP cyclohydrolase I	619	AAM86217.1	2.80129241
37303	D08	NTL02YP3231	hypothetical protein	622	AAM86253.1	2.84565916
37335	D09	NTL02YP2111	hypothetical protein	631	AAM85350.1	2.8177496
37502	D10	NTL02YP2128	hypothetical protein	688	AAM85367.1	2.79215116
37603	D11	NTL02YP3203	hypothetical protein	721	AAM86231.1	2.79750347
37699	D12	NTL02YP3229	protein disulfide isomerase II	757	AAM86825.1	2.65785997
39286	E01	NTL02YP2100	hypothetical protein	1435	AAM85340.1	5.76445993
39389	E02	NTL02YP3182	hypothetical protein	1528	AAM86778.1	3.3841623
39401	E03	NTL02YP2107	putative carboxypeptidase	1540	AAM85703.1	3.5987013
39435	E04	NTL02YP2101	hypothetical protein	1567	AAM85341.1	3.71346522
39447	E05	NTL02YP2141	hypothetical protein	1576	AAM85377.1	3.70685279
39451	E06	NTL02YP3197	ATP-binding component of D-ribose high-affinity transport system	1579	AAM86793.1	3.709943
39670	E07	NTL02YP2134	hypothetical protein	1975	AAM85372.1	3.65316456
37707	E08	NTL02YP2143	negative regulator for Fad regulon, and positive activator of fabA	760	AAM85739.1	2.78421053
37808	E09	NTL02YP2116	putative kinase	793	AAM85355.1	3.64943253
37807	E10	NTL02YP2098	hypothetical protein	793	AAM85339.1	5.73518285
37845	E11	NTL02YP3207	hypothetical protein	808	AAM86235.1	6.65717822
37856	E12	NTL02YP2133	putative sucrose specific transcriptional regulator	811	AAM85371.1	3.6350185
37885	F01	NTL02YP3206	hypothetical protein	820	AAM86234.1	2.64756098
37904	F03	NTL02YP2146	putative regulator	826	AAM85381.1	5.78571429
37940	F04	NTL02YP2138	hypothetical protein	838	AAM85375.1	3.57398568
37949	F05	NTL02YP2105	respiratory NADH dehydrogenase	841	AAM85345.1	6.2508918
37759	F06	NTL02YP2761	putative oxidoreductase	775	AAM85876.1	1.99354839
37929	F08	NTL02YP2090	putative thymidylate kinase	835	AAM85331.1	6.56886228
38003	F09	NTL02YP2084	3-oxoacyl-[acyl-carrier-protein] reductase	859	AAM85326.1	3.57974389
38012	F10	NTL02YP2083	malonyl-CoA-[acyl-carrier-protein] transacylase	862	AAM85325.1	3.62180974
38060	F11	NTL02YP3847	protein of Glp regulon	877	AAM87443.1	6.78563284
38194	F12	NTL02YP3867	hypothetical protein	922	AAM86797.1	6.26898048
36133	G01	NTL02YP3854	hypothetical protein	226	AAM87450.1	2
36159	G02	NTL02YP1674	putative oxidoreductase	238	AAM84983.1	5.74369748
36191	G03	NTL02YP2766	hypothetical protein	247	AAM85881.1	2.9757085
36202	G04	NTL02YP2777	putative nucleotide diphosphate-sugar epimerase or dehydratase	250	AAM85892.1	5.352
38237	G05	NTL02YP2773	putative oxidoreductase	937	AAM85888.1	6.08537887
38351	G06	NTL02YP3873	hypothetical protein	982	AAM86802.1	6.15580448
38348	G07	NTL02YP1664	hypothetical protein	982	AAM84974.1	6.09775967
38362	G08	NTL02YP2771	hypothetical protein	988	AAM85886.1	5.34311741
38492	G09	NTL02YP1662	putative inner membrane permease of high-affinity phosphate-specific	1033	AAM84972.1	9.67086157

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38532	G10	NTL02YP1663	phosphate-specific transport component	1045	AAM84973.1	3.54545455
38557	G11	NTL02YP2080	50S ribosomal subunit protein L32	1057	AAM85321.1	3.16461684
38604	H01	NTL02YP2082	3-oxoacyl-[acyl-carrier-protein] synthase III	1072	AAM85324.1	2.55317164
38666	H02	NTL02YP3179	inner membrane permease of galactoside ABC transporter	1099	AAM86213.1	3.36214741
36227	H03	NTL02YP2762	hypothetical protein	259	AAM85877.1	5.78764479
36272	H04	NTL02YP2754	hypothetical protein	277	AAM86351.1	3.03249097
36305	H05	NTL02YP1672	putative transposase	292	AAM84981.1	4.08219178
36389	H06	NTL02YP3857	possible beta-D-galactosidase	319	AAM86787.1	1.99059561
36493	H07	NTL02YP2093	hypothetical protein	358	AAM85334.1	5.61173184
36698	H08	NTL02YP1676	putative permease	433	AAM84985.1	7.14318707
36741	H09	NTL02YP1675	hypothetical protein	445	AAM84984.1	2
36758	H10	NTL02YP3868	hypothetical protein	448	AAM87464.1	1.91517857
38693	H11	NTL02YP2775	hypothetical protein	1111	AAM85889.1	3.20342034
38756	H12	NTL02YP1665	hypothetical protein	1138	AAM84975.1	3.35413005