

***Yersinia pestis*, Strain KIM, Gateway®
Clone Set, Recombinant in *Escherichia coli*, Plate 20****Catalog No. NR-19616**

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Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

Manufacturer:

BEI Resources

Product Description:

Clone plates are replicated using a BioMek® FX robot. 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 only confirms the clone plate orientation and viability of randomly picked clones. BEI Resources does not confirm or validate individual clone identities provided by the contributor.

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.

Plate orientation and viability were confirmed for NR-19616.

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.

Packaging/Storage:

NR-19616 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 20, NR-19616."

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:

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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.

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Table 1: *Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 20 (UYPVT)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36925	A01	NTL02YP0605	suppresses groEL, may be chaperone	462	AAM84201.1	3.98406
36956	A02	NTL02YP0618	hypothetical protein	471	AAM84214.1	3.98434
37120	A03	NTL02YP3881	shikimate kinase I	522	AAM87477.1	5.65836
38816	A04	NTL02YP3880	putative transport portein	1125	AAM87476.1	3.29099
38839	A05	NTL02YP2796	hypothetical	1137	AAM86392.1	3.33985
39048	A07	NTL02YP0625	putative protease specific for phage lambda cII	1260	AAM84221.1	3.50923
39070	A08	NTL02YP1690	hypothetical protein	1275	AAM85286.1	6.44106
39089	A09	NTL02YP0623	putative GTP binding subunit for protease of lambda cII repressor	1287	AAM84219.1	5.69706
39120	A10	NTL02YP0597	anaerobic C-4-dicarboxylate symporter	1302	AAM84193.1	4.0462
39137	A11	NTL02YP0627	adenylosuccinate synthetase	1311	AAM84223.1	2.8416
37186	A12	NTL02YP0599	hypothetical protein	546	AAM84195.1	5.21502
37217	B01	NTL02YP1699	hypothetical protein	555	AAM85295.1	5.63529
37234	B02	NTL02YP2783	putative chorismate mutase	561	AAM86379.1	5.62063
37284	B03	NTL02YP2781	putative enzyme	576	AAM86377.1	2.79221
37476	B04	NTL02YP1713	hypothetical protein	642	AAM85309.1	6.1129
37625	B05	NTL02YP3886	D-ribulose-5-phosphate 3-epimerase	690	AAM87482.1	6.48493
37627	B06	NTL02YP0615	hypothetical protein	693	AAM84211.1	6.2442
39203	B07	NTL02YP1696	hypothetical protein	1347	AAM85292.1	3.61788
39301	B08	NTL02YP2790	hypothetical protein	1401	AAM86386.1	3.71409
39338	B09	NTL02YP0598	aspartate ammonia-lyase (aspartase)	1437	AAM84194.1	3.5369
39393	B10	NTL02YP2779	putative dTDP-glucose enzyme	1491	AAM86375.1	5.42325
39419	B11	NTL02YP0617	hypothetical protein	1515	AAM84213.1	1.9254
39521	B12	NTL02YP0601	GroEL protein	1647	AAM84197.1	3.51097
39623	C01	NTL02YP0609	fumarate reductase, anaerobic, flavoprotein subunit	1824	AAM84205.1	3.36749
37753	C02	NTL02YP3887	phosphoglycolate phosphatase	732	AAM87483.1	6.00518
37755	C03	NTL02YP0608	fumarate reductase, anaerobic, iron-sulfur protein subunit	735	AAM84204.1	5.93677
37763	C04	NTL02YP1704	putative transcriptional activator protein	738	AAM85300.1	6.28663
37883	C05	NTL02YP2784	ATP-binding component of 3rd arginine transport system	780	AAM86380.1	2.7878
37944	C06	NTL02YP2791	putative ABC transport protein	798	AAM86387.1	6.27446

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38021	C07	NTL02YP1686	putative inner membrane permease of ABC transporter	825	AAM85282.1	3.02428
37563	C09	NTL02YP3276	hypothetical protein	666	AAM86872.1	5.66997
37660	C10	NTL02YP3239	putative oxidoreductase	702	AAM86835.1	4.58491
37659	C11	NTL02YP3234	catabolic regulation response regulator	702	AAM86830.1	5.93396
37677	C12	NTL02YP3270	DNA-specific endonuclease I	708	AAM86866.1	5.47193
37683	D01	NTL02YP2159	putative phage tail protein	711	AAM85755.1	5.98136
37736	D02	NTL02YP2174	hypothetical protein	729	AAM85770.1	4.82055
37886	D03	NTL02YP3265	hypothetical protein	780	AAM86861.1	4.79756
38009	D04	NTL02YP0582	positive regulator for rhaBAD operon	822	AAM84178.1	5.17285
35963	D05	NTL02YP3244	hypothetical protein	126	AAM86840.1	1.96988
35969	D06	NTL02YP1680	hypothetical protein	132	AAM85276.1	1.97674
38078	D07	NTL02YP3258	putative actin	843	AAM86854.1	1.66478
38153	D08	NTL02YP3260	putative transport protein	870	AAM86856.1	1.61429
38158	D09	NTL02YP0583	positive regulator for rhaRS operon	873	AAM84179.1	1.62432
38288	D10	NTL02YP2164	hypothetical protein	921	AAM85760.1	4.25598
38393	D11	NTL02YP3257	replication initiation inhibitor	957	AAM86853.1	4.94483
38562	D12	NTL02YP3263	D-erythrose 4-phosphate dehydrogenase	1017	AAM86859.1	2.81835
36282	E01	NTL02YP0595	hypothetical protein	243	AAM84191.1	3.85866
36310	E02	NTL02YP2168	hypothetical protein	255	AAM85764.1	3.98305
36347	E03	NTL02YP0586	hypothetical protein	267	AAM84182.1	4.40391
36349	E04	NTL02YP3236	hypothetical protein	267	AAM86832.1	3.97394
36448	E05	NTL02YP0587	putative transposase	303	AAM84183.1	3.77843
36480	E06	NTL02YP2163	hypothetical protein	312	AAM85759.1	4.52557
36565	E07	NTL02YP2161	putative phage tail protein	342	AAM85757.1	4.17801
36607	E08	NTL02YP0596	divalent cation tolerance protein	360	AAM84192.1	3.9875
36660	E09	NTL02YP3253	hypothetical protein	378	AAM86849.1	5.16986
38758	E10	NTL02YP3248	aminomethyltransferase of glycine cleavage system	1098	AAM86844.1	2.78998
38770	E11	NTL02YP3240	hypothetical protein	1104	AAM86836.1	2.30944
38789	E12	NTL02YP2172	hypothetical protein	1113	AAM85768.1	1.57676
38904	F01	NTL02YP2148	hypothetical protein	1173	AAM85744.1	3.12366
38914	F02	NTL02YP3250	2-octaprenyl-6-methoxyphynol hydroxylase	1179	AAM86846.1	3.01723
38971	F03	NTL02YP2170	hypothetical protein	1206	AAM85766.1	3.12279
36755	F05	NTL02YP2165	hypothetical protein	408	AAM85761.1	1.93973
36793	F06	NTL02YP2150	putative phage tail protein	420	AAM85746.1	5.30217
36801	F07	NTL02YP3277	hypothetical protein	423	AAM86873.1	4.91145
36808	F08	NTL02YP0588	hypothetical protein	426	AAM84184.1	2.99142
36813	F09	NTL02YP3235	hypothetical protein	426	AAM86831.1	4.85622
36830	F10	NTL02YP2157	hypothetical protein	432	AAM85753.1	5.11441
36848	F11	NTL02YP3245	hypothetical protein	438	AAM86841.1	2
36890	F12	NTL02YP2176	hypothetical protein	450	AAM85772.1	1.99388
37143	G01	NTL02YP3238	hypothetical protein	531	AAM86834.1	3.13485
37208	G02	NTL02YP2155	hypothetical protein	552	AAM85751.1	2.82264
37224	G03	NTL02YP0592	electron transport protein	558	AAM84188.1	6.4097
37226	G04	NTL02YP2169	hypothetical protein	558	AAM85765.1	2.83779
39053	G06	NTL02YP0578	L-rhamnose isomerase	1263	AAM84174.1	3.95165
39147	G07	NTL02YP3251	proline aminopeptidase P II	1314	AAM86847.1	3.88109
39198	G08	NTL02YP3255	D-3-phosphoglycerate dehydrogenase	1344	AAM86851.1	3.05058
39316	G09	NTL02YP3233	catabolite repression sensor kinase for PhoB	1419	AAM86829.1	3.52776

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39341	G10	NTL02YP3249	hypothetical protein	1437	AAM86845.1	5.09072
39604	G11	NTL02YP0594	thiol:disulfide interchange protein	1788	AAM84190.1	3.96444
39690	G12	NTL02YP3267	biosynthetic arginine decarboxylase	1980	AAM86863.1	3.62376
39693	H01	NTL02YP3264	transketolase 1 isozyme	1995	AAM86860.1	3.70319
37246	H02	NTL02YP3269	hypothetical protein	564	AAM86865.1	2
37293	H03	NTL02YP3252	hypothetical protein	579	AAM86848.1	2.81906
37313	H04	NTL02YP2166	hypothetical protein	585	AAM85762.1	2.7904
37332	H05	NTL02YP0590	hypothetical protein	591	AAM84186.1	2.80983
37350	H06	NTL02YP3254	putative ligase	597	AAM86850.1	2.79906
37405	H07	NTL02YP3259	hypothetical protein	618	AAM86855.1	2.81155
37417	H08	NTL02YP2154	putative phage tail protein	621	AAM85750.1	2.77458
37455	H09	NTL02YP2158	hypothetical protein	633	AAM85754.1	2
37478	H10	NTL02YP2173	hypothetical protein	642	AAM85769.1	2.40762
37536	H11	NTL02YP3256	ribosephosphate isomerase	657	AAM86852.1	2.7977
38106	H12	NTL02YP3183	tagatose-bisphosphate aldolase 2	855	AAM86779.1	3.58659

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.