

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 12**

Catalog No. NR-19608

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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-19608 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 12, NR-19608.”

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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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 12 (UYPVL)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37710	A01	NTL02YP3431	putative chaperone	720	AAM87027.1	5.125
37777	A02	NTL02YP2354	putative pilin chaperone	741	AAM85950.1	5.717029449
37793	A03	NTL02YP1250	hypothetical protein	747	AAM84846.1	6.08386277
37750	A04	NTL02YP3404	putative flagellar rod protein	732	AAM87000.1	5.961139896
37788	A05	NTL02YP3415	hypothetical protein	744	AAM87011.1	5.257653061
37895	A06	NTL02YP0143	hypothetical protein	783	AAM83739.1	6.267314702
38000	A07	NTL02YP0144	putative ATP-binding component of ABC transport system	819	AAM83740.1	6.806752037
36085	A08	NTL02YP0154	probable sigma-54 modulation protein	174	AAM83750.1	3.943925234
36106	A09	NTL02YP1228	hypothetical protein	180	AAM84824.1	4.968181818
36336	A10	NTL02YP0139	hypothetical protein	264	AAM83735.1	4.963815789
36350	A11	NTL02YP3411	hypothetical protein	267	AAM87007.1	4.605863192
36403	A12	NTL02YP2316	hypothetical protein	285	AAM85912.1	1.969230769
36430	B01	NTL02YP3400	hypothetical protein	294	AAM86996.1	3.526946108
36446	B02	NTL02YP0140	hypothetical protein	303	AAM83736.1	5.551020408
36486	B03	NTL02YP2324	putative cytochrome precursor	315	AAM85920.1	-
38435	B04	NTL02YP0145	hypothetical protein	975	AAM83741.1	4.673891626
38696	B05	NTL02YP0146	putative isomerase	1074	AAM83742.1	2.999102334
36577	B06	NTL02YP1231	PEP-dependent phosphotransferase IIA component for cellobiose, arbutin	348	AAM84827.1	-
36576	B07	NTL02YP1229	PEP-dependent phosphotransferase enzyme IV for cellobiose, arbutin	348	AAM84825.1	5.961340206
36716	B08	NTL02YP0131	30S ribosomal subunit protein S9	399	AAM83727.1	6.047835991
36739	B09	NTL02YP0134	hypothetical protein	405	AAM83730.1	4.959550562
36762	B10	NTL02YP1226	hypothetical protein	411	AAM84822.1	4.024390244
36815	B11	NTL02YP3412	hypothetical protein	426	AAM87008.1	5.510729614
36814	B12	NTL02YP3408	flagellar biosynthesis protein, cell-proximal portion of basal-body	426	AAM87004.1	2.993562232
36821	C01	NTL02YP1238	conserved hypothetical protein	429	AAM84834.1	3.987206823
38731	C02	NTL02YP0137	protease	1089	AAM83733.1	3.270150576
38762	C03	NTL02YP2314	sodium-calcium/proton antiporter	1101	AAM85910.1	2.439088519
38842	C04	NTL02YP0133	hypothetical protein	1140	AAM83729.1	2.754237288
38912	C05	NTL02YP3401	putative flagella basal body protein	1176	AAM86997.1	2.246710526
38908	C06	NTL02YP1225	putative potassium channel	1176	AAM84821.1	2.446546053
38975	C07	NTL02YP3394	lateral flagellin	1206	AAM86990.1	2.439004815
38989	C08	NTL02YP2322	outer membrane protein	1218	AAM85918.1	4.76073132

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39051	C09	NTL02YP0138	UDP-N-glucosamine 1-carboxyvinyltransferase	1263	AAM83734.1	4.047582502
36880	C10	NTL02YP3396	hypothetical protein	447	AAM86992.1	5.821355236
36949	C11	NTL02YP2318	inner membrane protein	468	AAM85914.1	4.147637795
37012	C12	NTL02YP0128	hypothetical protein	486	AAM83724.1	4.595057034
37036	D01	NTL02YP0155	phosphotransferase system enzyme IIA	495	AAM83751.1	4.510280374
37141	D03	NTL02YP2325	putative thioredoxin-family protein	531	AAM85921.1	5.234676007
37154	D04	NTL02YP0684	putative transposase	537	AAM84280.1	6.244367418
37171	D05	NTL02YP1235	negative modulator of initiation of replication	543	AAM84831.1	6.173241852
37239	D06	NTL02YP0149	hypothetical protein	564	AAM83745.1	4.162251656
39223	D07	NTL02YP1230	PEP-dependent phosphotransferase enzyme II for cellobiose, arbutin	1362	AAM84826.1	3.165477889
39224	D08	NTL02YP3399	putative flagellar hook-associated protein	1362	AAM86995.1	3.14764622
39240	D09	NTL02YP2308	hypothetical protein	1371	AAM85904.1	5.432317505
39247	D10	NTL02YP2319	hypothetical protein	1374	AAM85915.1	5.622347949
39277	D11	NTL02YP0135	serine endoprotease	1392	AAM83731.1	3.696927374
39330	D12	NTL02YP0152	RNA polymerase, sigma(54 or 60) factor	1434	AAM83748.1	3.421302578
39352	E01	NTL02YP2312	multi modular putative transcriptional regulator; also putative	1449	AAM85908.1	3.001343183
39424	E02	NTL02YP2309	putative aldehyde dehydrogenase	1518	AAM85905.1	3.103979461
39515	E03	NTL02YP3417	putative flagellar M ring protein	1641	AAM87013.1	2.95240928
39550	E04	NTL02YP1236	phosphoglucosmutase	1686	AAM84832.1	3.211471611
37238	E05	NTL02YP0148	hypothetical protein	564	AAM83744.1	6.105960265
37248	E06	NTL02YP0150	hypothetical protein	567	AAM83746.1	1.815485997
37269	E07	NTL02YP0142	hypothetical protein	573	AAM83738.1	2.804241436
37446	E08	NTL02YP1239	regulator of kdp operon (transcriptional effector)	630	AAM84835.1	2.785074627
37473	E09	NTL02YP0130	regulator of transcription stringent starvation protein A	642	AAM83726.1	1.804985337
37537	E10	NTL02YP3406	putative flagellar assembly protein	657	AAM87002.1	2.738880918
37550	E11	NTL02YP1221	urease accessory protein	663	AAM84817.1	4.780938834
37613	E12	NTL02YP1220	urease accessory protein	687	AAM84816.1	4.635488308
37842	F01	NTL02YP1192	hypothetical protein	768	AAM84788.1	2
37900	F04	NTL02YP0685	putative transposase	786	AAM84281.1	5.468523002
37965	F05	NTL02YP1213	putative ATP-binding protein of ABC transport system	807	AAM84809.1	2
37964	F06	NTL02YP1212	putative permease of ABC transporter	807	AAM84808.1	2.598583235
38095	F07	NTL02YP2295	hypothetical protein	852	AAM85891.1	3.507847534
38233	F08	NTL02YP2304	putative histidine degradation enzyme	894	AAM85900.1	3.358672377
38227	F09	NTL02YP0111	putative transcriptional regulator LYSR-type	894	AAM83707.1	3.950749465
35987	F10	NTL02YP0112	hypothetical protein	150	AAM83708.1	2.973684211
36130	F11	NTL02YP1193	hypothetical protein	186	AAM84789.1	2
36267	F12	NTL02YP1204	glutaredoxin-like protein	237	AAM84800.1	3.981949458
36287	G01	NTL02YP3386	hypothetical protein	243	AAM86982.1	3.96819788
38292	G03	NTL02YP0107	putative acetyltransferase	924	AAM83703.1	4.760373444
38371	G04	NTL02YP2279	hypothetical protein	951	AAM85875.1	5.16851665
38409	G05	NTL02YP2292	putative oxidoreductase	963	AAM85888.1	2
38426	G06	NTL02YP1202	ribonucleoside-diphosphate reductase 2, beta chain, frag	972	AAM84798.1	4.869565217

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38454	G07	NTL02YP1211	putative permease of ABC transporter	984	AAM84807.1	4.614257813
38502	G08	NTL02YP2307	hypothetical protein	996	AAM85903.1	2.448841699
38531	G09	NTL02YP1199	solute-binding periplasmic protein of high-affinity glycine betaine/proline	1005	AAM84795.1	2.733971292
38560	G10	NTL02YP2296	putative nucleotide di-P-sugar epimerase or dehydratase	1017	AAM85892.1	3.122043519
38571	G11	NTL02YP3389	putative transcription repressor	1020	AAM86985.1	3.198113208
36378	G12	NTL02YP0100	RNA polymerase, omega subunit	276	AAM83696.1	-
36545	H01	NTL02YP1206	hypothetical protein	336	AAM84802.1	3.835106383
36592	H02	NTL02YP0117	hypothetical protein	354	AAM83713.1	4.223350254
36641	H03	NTL02YP1205	acid shock protein	372	AAM84801.1	5.405339806
36662	H04	NTL02YP0118	hypothetical protein	381	AAM83714.1	2.833729216
36726	H05	NTL02YP3378	hypothetical protein	399	AAM86974.1	2
36740	H06	NTL02YP1208	hypothetical protein	405	AAM84804.1	2.997752809
38599	H08	NTL02YP3391	hypothetical protein	1029	AAM86987.1	4.036482694
38782	H09	NTL02YP2293	hypothetical protein	1110	AAM85889.1	4.008695652
38891	H10	NTL02YP1200	permease of high-affinity ABC transport system for	1167	AAM84796.1	3.072908036
38940	H11	NTL02YP2289	hypothetical protein	1188	AAM85885.1	3.147394137

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.