

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 26**

Catalog No. NR-19622

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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-19622 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 26, NR-19622.”

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 26 (UYPVZ)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39012	A01	NTL02YP2646	hypothetical protein	1233	AAM86242.1	3.26394
39157	A02	NTL02YP3745	hypothetical protein	1317	AAM87341.1	3.8703
37042	A03	NTL02YP0475	50S ribosomal subunit protein L10	498	AAM84071.1	5.80112
37089	A04	NTL02YP1577	membrane protein	510	AAM85173.1	6.11091
37139	A05	NTL02YP1566	fimbrial A protein precursor	531	AAM85162.1	2.7268
37162	A06	NTL02YP3731	hypothetical protein	537	AAM87327.1	2.79029
37302	A07	NTL02YP2639	hypothetical protein	582	AAM86235.1	3.10289
39263	A08	NTL02YP1575	dihydrofolate:folylpolyglutamate synthetase	1383	AAM85171.1	6.73928
39276	A09	NTL02YP3735	hypothetical protein	1389	AAM87331.1	3.6767
39336	A10	NTL02YP3753	glutamine synthetase	1434	AAM87349.1	3.60176
37339	B01	NTL02YP3751	putative phosphatase	591	AAM87347.1	2.79556
37388	B02	NTL02YP1556	hypothetical protein	612	AAM85152.1	2.7362
37624	B03	NTL02YP1573	hypothetical protein	690	AAM85169.1	7.55342
37795	B04	NTL02YP2674	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	747	AAM86270.1	2.38501
37858	B05	NTL02YP2668	putative enoyl-coa hydratase protein	771	AAM86264.1	5.59309
37951	B07	NTL02YP2631	molybdopterin biosynthesis protein	801	AAM86227.1	7.28181
37966	B08	NTL02YP1533	hypothetical protein	807	AAM85129.1	3.61983
38075	B09	NTL02YP2625	putative esterase	843	AAM86221.1	3.08267
38088	B10	NTL02YP1532	hypothetical protein	849	AAM85127.1	3.61192
38151	B11	NTL02YP2623	putative transcriptional regulator LYSR-type	870	AAM86219.1	2.83516
38174	B12	NTL02YP3722	hypothetical protein	876	AAM87318.1	6.57533
38365	C01	NTL02YP0466	pantothenate kinase	951	AAM84062.1	6.24117
38396	C02	NTL02YP0465	biotin-[acetyl CoA carboxylase] holoenzyme synthetase	960	AAM84061.1	5.27
36262	C03	NTL02YP3710	hypothetical protein	234	AAM87306.1	3.9708
36328	C04	NTL02YP1530	hypothetical protein	261	AAM85126.1	2
36426	C05	NTL02YP3723	hypothetical protein	291	AAM87319.1	5.49245
36453	C06	NTL02YP1551	hypothetical protein	303	AAM85147.1	1.97668
38515	C07	NTL02YP3709	putative multidrug resistance protein	999	AAM87305.1	3.77478
38574	C08	NTL02YP0452	5-aminolevulinatase dehydratase	1023	AAM84048.1	3.18438
38610	C10	NTL02YP0464	UDP-N-acetylenolpyruvoylglucosamine reductase	1038	AAM84059.1	3.33766

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38729	C11	NTL02YP3726	PTS system fructose-like enzyme 2IIC component	1086	AAM87322.1	3.42185
38728	C12	NTL02YP3706	putative pectinesterase	1086	AAM87302.1	3.19893
38768	D01	NTL02YP2619	periplasmic D-galactose-binding ABC transport protein	1104	AAM86215.1	3.45979
38815	D02	NTL02YP3721	putative LACI-type transcriptional regulator	1125	AAM87317.1	6.12532
38864	D03	NTL02YP2622	putative transport protein	1152	AAM86218.1	3.34983
36542	D04	NTL02YP0451	hypothetical protein	336	AAM84047.1	4.9734
36564	D05	NTL02YP1536	hypothetical protein	342	AAM85132.1	1.99476
36581	D06	NTL02YP3707	hypothetical protein	348	AAM87303.1	3.99742
36625	D07	NTL02YP1535	hypothetical protein	366	AAM85131.1	2
36727	D08	NTL02YP3727	hypothetical protein	399	AAM87323.1	5.67426
36984	D09	NTL02YP0460	hypothetical protein	477	AAM84056.1	2
37000	D10	NTL02YP1534	hypothetical protein	480	AAM85130.1	2
37023	D11	NTL02YP0453	transcriptional activator	489	AAM83991.1	2
37035	D12	NTL02YP3724	putative glycoprotein/receptor	492	AAM87320.1	5.96617
37038	E01	NTL02YP1544	possible subunit of a heme lyase	495	AAM85140.1	2
38906	E02	NTL02YP3705	hemin storage system protein	1173	AAM87301.1	3.06183
38910	E03	NTL02YP2620	hypothetical protein	1176	AAM86216.1	3.24507
38959	E04	NTL02YP3712	lipopolysaccharide biosynthesis protein	1200	AAM87308.1	3.28548
39000	E06	NTL02YP1548	putative cytochrome c-type biogenesis protein	1227	AAM85144.1	3.10024
39017	E07	NTL02YP3711	hypothetical protein	1233	AAM87307.1	3.22702
39055	E08	NTL02YP2627	hypothetical protein	1263	AAM86223.1	4.01151
39066	E09	NTL02YP1550	long-chain fatty acid transport protein	1272	AAM85146.1	3.24162
39071	E10	NTL02YP2630	molybdopterin biosynthesis protein	1275	AAM86226.1	4.03726
39138	E11	NTL02YP1552	putative acyltransferase	1311	AAM85148.1	3.99556
39140	E12	NTL02YP2629	putative arylsulfatase activating enzyme	1311	AAM86225.1	3.77646
37071	F01	NTL02YP1539	hypothetical protein	507	AAM85135.1	2
37099	F03	NTL02YP1547	putative cytochrome c-type biogenesis protein	513	AAM85143.1	2
37146	F04	NTL02YP0462	protoporphyrin oxidase	534	AAM84058.1	2.82404
37163	F05	NTL02YP0448	hypothetical protein	540	AAM84044.1	2.81552
37206	F06	NTL02YP1538	hypothetical protein	552	AAM85134.1	5.46284
37258	F07	NTL02YP0440	hypothetical protein	570	AAM84036.1	2.83934
37307	F08	NTL02YP0467	putative acetyltransferase	585	AAM84063.1	2
37433	F09	NTL02YP2635	hypothetical protein	624	AAM86231.1	2.78464
37519	F10	NTL02YP2633	hypothetical protein	654	AAM86229.1	2.81124
39184	F11	NTL02YP0458	proline dipeptidase	1335	AAM84054.1	3.93891
39234	F12	NTL02YP2636	hypothetical protein	1368	AAM86232.1	3.89063
39355	G01	NTL02YP0461	potassium uptake protein	1452	AAM84057.1	3.68097
39408	G02	NTL02YP0441	putative alpha helix chain	1506	AAM84037.1	3.55951
39426	G03	NTL02YP0454	putative oxidoreductase	1521	AAM84050.1	3.5663
39428	G04	NTL02YP2618	ATP-binding component of methyl-galactoside ABC transporter and	1521	AAM86214.1	3.5868
39506	G05	NTL02YP3713	putative kinase	1632	AAM87309.1	3.39773
39527	G06	NTL02YP3718	putative ATP-binding component of a transport system	1653	AAM87314.1	3.15535
39589	G07	NTL02YP2634	putative ATP-binding component of ABC transport system	1764	AAM86230.1	3.00554

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39620	G08	NTL02YP0439	carbon starvation protein	1818	AAM84035.1	3.69699
37528	G09	NTL02YP1540	ATP binding protein of heme exporter A	657	AAM85136.1	2.79197
37546	G10	NTL02YP0446	hypothetical protein	663	AAM84042.1	2.79232
37570	G11	NTL02YP2628	putative ATP-binding ABC transporter protein	669	AAM86224.1	2.79126
37614	G12	NTL02YP1541	heme exporter protein B	687	AAM85137.1	2.36726
37650	H01	NTL02YP0443	hypothetical protein	702	AAM84039.1	1.81132
37696	H02	NTL02YP2621	GTP cyclohydrolase I	717	AAM86217.1	2.79128
37762	H03	NTL02YP1542	heme exporter protein C	738	AAM85138.1	6.42031
37782	H04	NTL02YP0455	ferrisiderophore reductase	744	AAM84051.1	2.42985
37814	H05	NTL02YP0442	COQ5 methyltransferase	756	AAM84038.1	6.5402
37874	H06	NTL02YP1549	lipoprotein precursor	777	AAM85145.1	6.61812
38157	H07	NTL02YP0436	putative carboxymethylenebutenolidase	873	AAM84032.1	3.65608
38224	H08	NTL02YP2589	glucose-1-phosphate uridylyltransferase	891	AAM86185.1	4.23738
38431	H09	NTL02YP3684	putative transposase	972	AAM87280.1	3.63142
38449	H10	NTL02YP3688	3-phosphoserine phosphatase	981	AAM87284.1	4.99412
36394	H11	NTL02YP1515	hypothetical protein	282	AAM85111.1	5.59938
36431	H12	NTL02YP3700	hypothetical protein	294	AAM87296.1	4.82335

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.