

Yersinia pestis, Strain KIM, Gateway® Clone Set, Recombinant in Escherichia coli, Plate 22

Catalog No. NR-19618

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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-19618 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 22, NR-19618."

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 22 (UYPVV)

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38796	A01	NTL02YP2769	hypothetical protein	1156	AAM85884.1	3.292387543
39105	A02	NTL02YP2751	putative histidine protein kinase sensor	1333	AAM85867.1	3.92348087
39113	A03	NTL02YP2079	hypothetical protein	1336	AAM85320.1	3.796407186
39333	A04	NTL02YP2086	3-oxoacyl-[acyl-carrier-protein] synthase II	1474	AAM85328.1	3.622116689
39342	A05	NTL02YP3838	hypothetical protein	1477	AAM86772.1	3.599187542
39380	A06	NTL02YP2096	putative shikimate 5-dehydrogenase	1516	AAM85337.1	2.980870712
39411	A07	NTL02YP2085	acyl carrier protein	1549	AAM85327.1	5.580374435
36833	A08	NTL02YP3843	putative sulfatase	472	AAM86777.1	4.911016949
36840	A09	NTL02YP3848	hypothetical protein	475	AAM86781.1	6.134736842
36973	A10	NTL02YP2081	fatty acid/phospholipid synthesis protein	514	AAM85322.1	3.982490272
37040	A11	NTL02YP2756	regulator protein	535	AAM86352.1	2
37090	B01	NTL02YP1670	hypothetical protein	550	AAM85266.1	2
37108	B02	NTL02YP3863	ATP-binding component of D-ribose high-affinity transport system	556	AAM86793.1	2.84352518
37113	B03	NTL02YP2097	hypothetical protein	559	AAM85338.1	2.792486583
37151	B04	NTL02YP3875	hypothetical protein	574	AAM86803.1	2.759581882
37195	B05	NTL02YP3871	hypothetical protein	586	AAM86801.1	2.805460751
39487	B06	NTL02YP3840	2-deoxy-D-gluconate 3-dehydrogenase	1639	AAM86774.1	2.954850519
39491	B07	NTL02YP3181	periplasmic D-galactose-binding ABC transport protein	1648	AAM86215.1	3.563106796
39500	B08	NTL02YP3866	hypothetical protein	1660	AAM86796.1	3.386144578
39526	B09	NTL02YP2774	putative prismane	1693	AAM86370.1	4.156526875
39546	B10	NTL02YP1666	spermidine N1-acetyltransferase	1720	AAM84977.1	3.493604651
39549	B11	NTL02YP2092	DNA polymerase III, delta prime subunit	1723	AAM85333.1	3.308763784
39552	B12	NTL02YP1668	phosphoribosylglycinamide formyltransferase 1	1729	AAM84978.1	3.526894158
39557	C01	NTL02YP2772	hypothetical protein	1732	AAM85887.1	6.020207852
39575	C02	NTL02YP2759	hypothetical protein	1765	AAM85873.1	3.363739377
39603	C03	NTL02YP2758	hypothetical protein	1825	AAM85874.1	3.901369863
37193	C04	NTL02YP1677	hypothetical protein	586	AAM84986.1	2.795221843
37286	C05	NTL02YP3851	hypothetical protein	616	AAM86783.1	2.826298701
37382	C06	NTL02YP2753	hypothetical protein	649	AAM85870.1	2.807395994
37443	C07	NTL02YP3876	hypothetical protein	667	AAM86804.1	2.818590705
37506	C08	NTL02YP3856	hypothetical protein	688	AAM86786.1	2.584302326
37606	C09	NTL02YP3869	hypothetical protein	721	AAM86799.1	6.769764216

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37629	C10	NTL02YP2078	hypothetical protein	733	AAM85319.1	2.795361528
38020	C12	NTL02YP0577	putative transposase	865	AAM84093.1	5.719075145
38120	D01	NTL02YP2745	probable formate transporter	898	AAM86341.1	2
38137	D02	NTL02YP0561	thiC protein	907	AAM84080.1	3.310915105
38143	D03	NTL02YP3819	carbohydrate kinase	907	AAM87415.1	3.663726571
38281	D04	NTL02YP1660	putative solute binding protein of ABC transporter	958	AAM85256.1	5.124217119
38325	D05	NTL02YP2726	possible protoporphyrinogen oxidase	973	AAM85848.1	6.091469681
38339	D06	NTL02YP1656	putative divalent cation transporter	979	AAM84967.1	6.362614913
38350	D07	NTL02YP3818	hypothetical protein	982	AAM86758.1	3.549898167
38358	D08	NTL02YP3816	D-ribose-binding periplasmic protein of ABC transporter	985	AAM87412.1	1.98680203
36037	D09	NTL02YP1639	hypothetical protein	199	AAM84953.1	3.929648241
36260	D10	NTL02YP2730	hypothetical protein	274	AAM85852.1	4.795620438
36271	D11	NTL02YP2727	peptide chain release factor RF-1	277	AAM85849.1	6.678700361
36317	D12	NTL02YP0556	thiH protein	298	AAM84076.1	2
36329	E01	NTL02YP1640	transcriptional response regulatory protein (sensor BaeS)	301	AAM84954.1	5.827242525
38366	E02	NTL02YP0550	50S ribosomal subunit protein L10	991	AAM84071.1	3.641775984
38398	E03	NTL02YP1638	hypothetical protein	1000	AAM84952.1	5.956
38497	E04	NTL02YP3815	putative carbonic anhydrase	1033	AAM86757.1	3.494675702
38506	E05	NTL02YP3822	putative chondroitin lyase	1036	AAM86761.1	3.477799228
38543	E06	NTL02YP1641	hypothetical protein	1051	AAM85237.1	3.402473834
38611	E08	NTL02YP0566	endonuclease V (deoxyinosine 3endoduclease)	1078	AAM84086.1	3.474025974
38653	E09	NTL02YP0568	quinone oxidoreductase	1093	AAM84164.1	5.766697164
38709	E10	NTL02YP0570	hypothetical protein	1120	AAM84089.1	3.391071429
38727	E11	NTL02YP2740	putative recombinase	1126	AAM85858.1	3.418294849
36490	E12	NTL02YP0575	hypothetical protein	358	AAM84171.1	4.75698324
36639	F01	NTL02YP0563	hypothetical protein	412	AAM84082.1	5.951456311
36643	F02	NTL02YP2729	putative glutamyl-tRNA dehydrogenase	412	AAM85851.1	2
36655	F03	NTL02YP3832	putative tagatose 6-phosphate kinase 2	415	AAM86767.1	2
36654	F04	NTL02YP3830	hypothetical protein	415	AAM87426.1	2
36747	F05	NTL02YP3827	hypothetical protein	445	AAM87423.1	2
36900	F06	NTL02YP0549	50S ribosomal subunit protein L1	496	AAM84070.1	2
37064	F07	NTL02YP1650	4-aminobutyrate aminotransferase	544	AAM84962.1	2
37068	F08	NTL02YP3825	putative transposase	544	AAM86763.1	2
38751	F10	NTL02YP2742	hypothetical protein	1135	AAM85860.1	3.34185022
38772	F11	NTL02YP3829	aspartate-semialdehyde dehydrogenase	1144	AAM87425.1	3.448426573
38820	F12	NTL02YP1649	putative transcriptional regulator	1168	AAM84961.1	3.098458904
38946	G01	NTL02YP0571	phosphoribosylglycinamide synthetase	1234	AAM84090.1	3.174230146
39001	G02	NTL02YP1659	polyphosphate kinase	1267	AAM84970.1	3.089187056
39123	G03	NTL02YP1645	hypothetical protein	1345	AAM84957.1	3.108550186
39158	G04	NTL02YP3824	putative transposase	1357	AAM86762.1	3.708179808
39180	G05	NTL02YP2739	5-enolpyruvylshikimate-3-phosphate synthetase	1372	AAM86335.1	3.050291545
39296	G06	NTL02YP0557	thiG protein	1441	AAM84077.1	2.970853574
37106	G07	NTL02YP2737	peptidyl-tRNA hydrolase	556	AAM85856.1	2.415467626
37111	G08	NTL02YP0565	uroporphyrinogen decarboxylase	559	AAM84085.1	2.821109123
37140	G09	NTL02YP1655	outer membrane protein X	571	AAM85251.1	2.826619965
37174	G10	NTL02YP1657	hypothetical protein	583	AAM84968.1	2.825042882

Clone	Well Position	Locus ID	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37249	G11	NTL02YP0560	thiE protein	616	AAM84079.1	2.8204
37277	G12	NTL02YP0552	RNA polymerase, beta subunit	625	AAM84073.1	2.8101
37319	H01	NTL02YP3828	hypothetical protein	625	AAM86765.1	6.7232
37308	H02	NTL02YP0551	50S ribosomal subunit protein L7/L12	625	AAM84072.1	2.8096
37465	H03	NTL02YP0553	RNA polymerase, beta prime subunit	679	AAM84074.1	2.804123711
37529	H04	NTL02YP1647	ATP hydrolase of ABC transporter	697	AAM84959.1	2.806312769
39307	H05	NTL02YP0569	DNA-binding protein HU-alpha (HU-2)	1447	AAM84088.1	3.612992398
39329	H06	NTL02YP3837	glucose-1-phosphate adenylyl-transferase	1471	AAM87433.1	1.39225017
39340	H07	NTL02YP2731	hypothetical protein	1477	AAM85853.1	5.680433311
39392	H08	NTL02YP1661	putative inner membrane permease of high-affinity phosphate-specific	1531	AAM84971.1	3.548007838
39485	H09	NTL02YP3811	putative general secretion protein	1636	AAM86753.1	3.371026895
39561	H10	NTL02YP3834	PTS family enzyme IIB component 2 (EIIB-AGA)	1738	AAM86769.1	2.881472957
39584	H11	NTL02YP2733	phosphoribosylpyrophosphate synthetase	1789	AAM85854.1	3.26607043
37609	H12	NTL02YP3817	conserved hypothetical protein	724	AAM87413.1	6.435082873