

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 5**

Catalog No. NR-19601

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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-19601 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 5, NR-19601.”

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.

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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 5 (UYPVE)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38938	A01	NTL02YP1411	putative enzyme	1188	AAM85007.1	5.758957655
39177	A02	NTL02YP0290	heat shock protein, ATPase subunit	1332	AAM83886.1	4.674198251
39183	A03	NTL02YP0316	putative oxidoreductase	1335	AAM83878.1	4.088
39233	A04	NTL02YP2500	hypothetical 4-hydroxyphenylacetate permease	1368	AAM86096.1	4.575284091
39294	A05	NTL02YP2506	putative 5-carboxy-2-hydroxyuconate semialdehyde dehydrogenase	1398	AAM86102.1	4.448539638
37121	A07	NTL02YP0291	heat shock protein, proteasome-related peptidase subunit	525	AAM83887.1	3.808849558
37194	A08	NTL02YP2483	hypothetical protein	546	AAM86079.1	2.093856655
37190	A09	NTL02YP1381	spermidine N1-acetyltransferase	546	AAM84977.1	2.817406143
37198	A10	NTL02YP1413	hypothetical protein	549	AAM85009.1	2.797962649
37310	A11	NTL02YP1414	hypothetical protein	585	AAM85010.1	3.7408
37352	A12	NTL02YP0300	putative transposase	600	AAM83896.1	1.9875
37397	B01	NTL02YP0309	secreted hemophore	618	AAM83905.1	1.981762918
39454	B02	NTL02YP0329	putative 2-component regulator	1545	AAM83925.1	4.23533123
39473	B03	NTL02YP3597	2-isopropylmalate synthase	1563	AAM87193.1	4.134747349
39472	B04	NTL02YP2499	putative component B of 4-hydroxyphenylacetic acid-hydroxylase	1563	AAM84984.1	3.84404242
39479	B05	NTL02YP1388	hypothetical protein	1578	AAM84761.1	5.563658838
39543	B06	NTL02YP1410	putative sulfatase	1674	AAM85006.1	4.127187865
39601	B07	NTL02YP3592	acetolactate synthase III, large subunit	1782	AAM87188.1	3.885839737
39616	B08	NTL02YP3593	putative fatty acid biosynthesis protein	1806	AAM87189.1	4.503791983
39650	B09	NTL02YP0333	dihydroxyacid dehydratase	1899	AAM83929.1	5.090252708
39669	B10	NTL02YP2045	RNase II, mRNA degradation	1935	AAM85641.1	4.259240506
37469	B11	NTL02YP1382	phosphoribosylglycinamide formyltransferase 1	639	AAM84978.1	3.72017673
37474	B12	NTL02YP0301	putative transposase	642	AAM83897.1	5.089442815
37498	C01	NTL02YP0317	hypothetical protein	648	AAM83913.1	3.763081395
37538	C02	NTL02YP1384	uracil phosphoribosyltransferase	660	AAM84980.1	1.801428571
37551	C03	NTL02YP1417	nitrate/nitrite response regulator	663	AAM85013.1	1.995732575
37591	C04	NTL02YP1402	hypothetical protein	678	AAM84998.1	3.380222841
37636	C05	NTL02YP1391	hypothetical protein	696	AAM84987.1	3.362771739
37688	C06	NTL02YP1397	phosphoribosylaminoimidazole-succinocarboxamide synthetase	714	AAM84993.1	3.75994695

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37706	C07	NTL02YP1386	putative DNA replication factor	720	AAM84982.1	2
37740	C08	NTL02YP0314	peroxiredoxin family protein	732	AAM83910.1	6.67357513
37855	C09	NTL02YP2011	hypothetical protein	771	AAM85607.1	4.628853268
37864	C10	NTL02YP0933	putative amidotransferase	774	AAM84529.1	4.626535627
37863	C11	NTL02YP0911	hypothetical protein	774	AAM84507.1	9.843980344
37939	D01	NTL02YP2042	putative transaldolase	798	AAM85638.1	3.721957041
37958	D02	NTL02YP2040	L-ribulose-5-phosphate 4-epimerase	804	AAM85636.1	5.79028436
38117	D03	NTL02YP2030	hypothetical protein	858	AAM85626.1	4.599109131
38113	D04	NTL02YP0938	Na-translocating NADH ubiquinone oxidoreductase, gamma chain	858	AAM84534.1	1.944320713
35948	D05	NTL02YP0925	hypothetical protein	120	AAM84521.1	2.9875
36033	D06	NTL02YP0916	hypothetical protein	159	AAM84512.1	2
36105	D07	NTL02YP0935	hypothetical protein	180	AAM84531.1	2.845454545
36117	D08	NTL02YP0915	hypothetical protein	183	AAM84511.1	3.950672646
36219	D09	NTL02YP2039	osmotically inducible lipoprotein	216	AAM85635.1	4.96484375
36218	D10	NTL02YP2012	hypothetical protein	216	AAM85608.1	4.93359375
36217	D11	NTL02YP2001	hypothetical protein	216	AAM85597.1	4
36306	D12	NTL02YP2026	hypothetical protein	252	AAM85622.1	6.52739726
38255	E01	NTL02YP1998	oligopeptide ABC transporter permease protein	906	AAM85594.1	7.261099366
38266	E02	NTL02YP0946	probable LysR-type transcriptional regulatory protein	912	AAM84542.1	6.441176471
38332	E03	NTL02YP2020	putative enzyme	936	AAM85616.1	7.111680328
38361	E04	NTL02YP0943	hypothetical protein	948	AAM84539.1	6.737854251
38440	E05	NTL02YP2029	positive transcriptional regulator for cysteine regulon	975	AAM85625.1	6.608866995
38522	E06	NTL02YP2000	ATP-binding protein of oligopeptide ABC transporter	1002	AAM85596.1	4.41074856
38521	E07	NTL02YP1999	ATP-binding protein of oligopeptide ABC transporter	1002	AAM85595.1	4.419385797
38609	E09	NTL02YP2022	hypothetical protein	1035	AAM85618.1	3.349767442
38639	E10	NTL02YP2025	putative protease	1047	AAM85621.1	4.480220791
36438	E11	NTL02YP2006	hypothetical protein	297	AAM85602.1	2
36485	E12	NTL02YP2014	hypothetical protein	315	AAM85610.1	4
36515	F01	NTL02YP2034	hypothetical protein	324	AAM85630.1	5.313186813
36521	F02	NTL02YP2038	hypothetical protein	327	AAM85634.1	5.811989101
36528	F03	NTL02YP2043	hypothetical protein	330	AAM85639.1	6.043243243
36563	F04	NTL02YP0910	hypothetical protein	342	AAM84506.1	2
36650	F05	NTL02YP2002	hypothetical protein	375	AAM85598.1	7.638554217
36731	F06	NTL02YP0950	transcriptional regulator of cryptic csgA gene for	402	AAM84546.1	6.846153846
36753	F07	NTL02YP2027	hypothetical protein	408	AAM85623.1	1.997767857
36913	F08	NTL02YP0948	guanine-hypoxanthine phosphoribosyltransferase	459	AAM84544.1	2
38689	F09	NTL02YP0944	damage-inducible protein P putative tRNA synthetase	1071	AAM84540.1	4.335733573
38715	F10	NTL02YP0942	hypothetical protein	1083	AAM84538.1	4.261798753
38767	F11	NTL02YP0951	gamma-glutamate kinase	1104	AAM84547.1	4.212412587
38813	F12	NTL02YP2008	putative transposase	1125	AAM85604.1	4.182832618
38900	G01	NTL02YP2035	putative heat shock protein	1170	AAM85631.1	4.410743802
38956	G02	NTL02YP0912	putative permease, major facilitator superfamily	1200	AAM84508.1	3.292741935

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38994	G03	NTL02YP0941	Na-translocating NADH ubiquinone oxidoreductase, beta chain	1224	AAM84537.1	4.039556962
39027	G04	NTL02YP0937	Na-translocating NADH ubiquinone oxidoreductase:subunit B	1242	AAM84533.1	4.070202808
39058	G05	NTL02YP0949	hypothetical protein	1266	AAM84545.1	3.951761103
36947	G06	NTL02YP0913	hypothetical protein	468	AAM84509.1	3.998031496
37117	G07	NTL02YP0955	putative biotin synthesis protein	522	AAM84551.1	4.428825623
37122	G08	NTL02YP0957	shikimate kinase II	525	AAM84553.1	3.732743363
37155	G09	NTL02YP0909	regulator of plasmid mcrB operon (microcin B17)	537	AAM84505.1	3.814558059
37178	G10	NTL02YP2010	hypothetical protein	543	AAM85606.1	3.794168096
37298	G11	NTL02YP0932	phosphoheptose isomerase	582	AAM84528.1	2.781350482
37322	G12	NTL02YP0956	hypothetical protein	588	AAM84552.1	3.792993631
37334	H01	NTL02YP2023	cob(I)alamin adenosyltransferase	591	AAM85619.1	2
37367	H02	NTL02YP2032	GTP cyclohydrolase II	603	AAM85628.1	7.152410575
37361	H03	NTL02YP0940	hypothetical protein	603	AAM84536.1	3.782270607
37416	H04	NTL02YP2021	hypothetical protein	621	AAM85617.1	2
39091	H05	NTL02YP2017	tryptophan synthase, beta protein	1287	AAM85613.1	3.854559156
39222	H06	NTL02YP0936	Na-translocating NADH ubiquinone oxidoreductase:subunit A	1362	AAM84532.1	4.514265335
39289	H07	NTL02YP0914	putative glutamyl-tRNA(gln) amidotransferase subunit A	1398	AAM84510.1	4.337969402
39326	H08	NTL02YP2018	N-(5-phosphoribosyl)anthranilate isomerase	1428	AAM85614.1	4.08106267
39365	H09	NTL02YP0945	aminoacyl-histidine dipeptidase (peptidase D)	1461	AAM84541.1	4.2751499
39490	H10	NTL02YP0947	hypothetical protein	1605	AAM84543.1	4.041337386
39512	H11	NTL02YP1996	oligopeptide ABC transporter periplasmic binding protein	1638	AAM85592.1	4.190107271
39606	H12	NTL02YP0926	putative membrane protein, C-terminal part of adhesin	1791	AAM84522.1	4.592572365

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.