

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 11**

Catalog No. NR-19607

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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-19607 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 11, NR-19607.”

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 11 (UYPVK)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39044	A01	NTL02YP3475	putative transport	1257	AAM87071.1	3.194294526
39077	A02	NTL02YP0790	glutamate-1-semialdehyde aminotransferase	1281	AAM84386.1	3.878122634
39305	A03	NTL02YP3468	outer membrane channel protein	1404	AAM87064.1	3.707063712
39323	A04	NTL02YP3456	suppressor of ftsI	1425	AAM87052.1	3.632764505
37197	A05	NTL02YP0782	dnaK suppressor protein	549	AAM84378.1	1.994906621
37220	A06	NTL02YP1886	vitamin B12-binding periplasmic protein of vitamin B12	555	AAM85482.1	2.796638655
37221	A07	NTL02YP2368	hypothetical protein	555	AAM85964.1	5.490756303
37278	A08	NTL02YP0784	hypothetical protein	576	AAM84380.1	2.805194805
37279	A09	NTL02YP1268	RNA polymerase, sigma-E factor	576	AAM84864.1	2.784090909
37300	A10	NTL02YP2369	hypothetical protein	582	AAM85965.1	2.762057878
37318	A11	NTL02YP3464	hypothetical protein	585	AAM87060.1	2.8096
37317	A12	NTL02YP3461	modulator of drug activity B	585	AAM87057.1	2.6848
37456	B01	NTL02YP3467	hypothetical protein	633	AAM87063.1	2.757800892
37522	B02	NTL02YP3472	3,4 dihydroxy-2-butanone-4-phosphate synthase	654	AAM87068.1	3.587896254
37533	B03	NTL02YP2364	yersiniabactin thioesterase	657	AAM85960.1	3.292682927
39350	B04	NTL02YP3476	putative kinase	1446	AAM87072.1	1.432032301
39378	B05	NTL02YP0779	poly(A) polymerase I	1476	AAM84375.1	3.682717678
39427	B06	NTL02YP0797	deoxyguanosine triphosphate triphosphohydrolase	1521	AAM84393.1	3.779628443
39469	B07	NTL02YP3445	hypothetical protein	1557	AAM87041.1	3.71884784
39612	B08	NTL02YP1273	GTP-binding elongation factor	1800	AAM84869.1	3.883695652
39649	B09	NTL02YP3463	DNA topoisomerase IV subunit B	1896	AAM87059.1	10.29442149
37526	B10	NTL02YP1269	sigma-E factor, negative regulatory protein	657	AAM84865.1	4.262553802
37548	B11	NTL02YP0794	hypothetical protein	663	AAM84390.1	3.544807966
37557	B12	NTL02YP3449	hypothetical protein	663	AAM87045.1	4.536273115
37598	C01	NTL02YP1275	RNase III, ds RNA	681	AAM84871.1	6
37607	C02	NTL02YP0781	hypothetical protein	684	AAM84377.1	2.306629834
37751	C03	NTL02YP3458	1-acyl-sn-glycerol-3-phosphate acyltransferase	732	AAM87045.1	5.251295337
37745	C04	NTL02YP1277	recO protein	732	AAM84873.1	1.998704663
37829	C05	NTL02YP1887	ATP-binding component of vitamin B12 transport system	762	AAM85483.1	5.182044888

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37860	C06	NTL02YP3442	hypothetical protein	771	AAM87038.1	5.803945746
37822	C07	NTL02YP1266	putative enzyme	759	AAM84862.1	4.921151439
37859	C08	NTL02YP3422	flagellar biosynthesis protein	771	AAM87018.1	3.218249075
37857	C09	NTL02YP2335	putative DEOR-type transcriptional regulator	771	AAM85931.1	3.085080148
37873	C10	NTL02YP1254	putative lactam utilization protein	777	AAM84850.1	2.651162791
37887	C11	NTL02YP3424	putative flagellar biosynthetic protein	780	AAM87020.1	3.407317073
37985	C12	NTL02YP3440	hypothetical protein	813	AAM87036.1	5.82883939
38073	D01	NTL02YP2345	putative citrate lyase	843	AAM85941.1	3.621744054
38107	D02	NTL02YP3436	hypothetical protein	855	AAM87032.1	5.530726257
38150	D03	NTL02YP2340	hypothetical protein	870	AAM85936.1	6.235164835
36180	D04	NTL02YP2331	hypothetical protein	204	AAM85927.1	3.995901639
36554	D05	NTL02YP0173	hypothetical protein	339	AAM83769.1	4.200527704
38236	D06	NTL02YP2344	putative transcriptional regulator LYSR-type	897	AAM85940.1	6.395944504
38249	D07	NTL02YP3420	hypothetical protein	900	AAM87016.1	5.813829787
38330	D08	NTL02YP0176	putative membrane protein	936	AAM83772.1	5.012295082
38329	D09	NTL02YP0159	aspartate carbamoyltransferase, catalytic subunit	936	AAM83755.1	5.792008197
38376	D10	NTL02YP0163	repressor of treA,B,C	954	AAM83759.1	4.967806841
38505	D11	NTL02YP3428	hypothetical protein	996	AAM87024.1	2.838803089
38576	D12	NTL02YP2334	putative glutaminase	1023	AAM85930.1	3.483537159
38600	E01	NTL02YP3419	response regulator of ato, ornithine decarboxylase antizyme	1029	AAM87015.1	5.29373246
38613	E02	NTL02YP1249	hypothetical protein	1038	AAM84845.1	3.43135436
36669	E03	NTL02YP3418	hypothetical protein	381	AAM87014.1	3.698337292
36694	E04	NTL02YP0167	cytochrome b(562)	393	AAM83763.1	3.877598152
36776	E05	NTL02YP3421	hypothetical protein	414	AAM87017.1	4.883259912
36772	E06	NTL02YP2330	periplasmic protein	414	AAM85926.1	4.262114537
36790	E07	NTL02YP1256	hypothetical protein	420	AAM84852.1	5.426086957
36802	E08	NTL02YP3434	hypothetical protein	423	AAM87030.1	2
36807	E09	NTL02YP0161	hypothetical protein	426	AAM83757.1	4.650214592
36892	E10	NTL02YP3437	hypothetical protein	450	AAM87033.1	4.285714286
36954	E11	NTL02YP0160	aspartate carbamoyltransferase, regulatory subunit	471	AAM83756.1	2
36967	E12	NTL02YP0172	putative ribonuclease	474	AAM83768.1	4.461089494
38777	F01	NTL02YP3430	putative adhesin	1107	AAM87026.1	3.39581517
38829	F02	NTL02YP0174	succinate-semialdehyde dehydrogenase	1134	AAM83770.1	5.348381601
38833	F03	NTL02YP3425	putative flagellar biosynthetic protein	1134	AAM87021.1	3.10988075
38941	F04	NTL02YP2337	putative aminotransferase	1188	AAM85933.1	3.238599349
39015	F05	NTL02YP3438	hypothetical protein	1233	AAM87034.1	3.056559309
39054	F06	NTL02YP2355	putative prophage integrase	1263	AAM85951.1	3.923254029
39073	F07	NTL02YP2341	putative major facilitator superfamily (MFS) transport protein	1278	AAM85937.1	3.025796662
39094	F08	NTL02YP3439	putative secretion NTP hydrolase	1287	AAM87035.1	3.713639789
39128	F09	NTL02YP2356	anthranilate synthase	1305	AAM85952.1	4.005947955
39166	F10	NTL02YP2347	putative Coenzyme A transferase	1323	AAM85943.1	3.556859868
39169	F11	NTL02YP1265	ATP-dependent RNA helicase	1326	AAM84861.1	6.043923865
36974	F12	NTL02YP2343	hypothetical protein	474	AAM85939.1	4.441634241
36982	G01	NTL02YP0162	hypothetical protein	477	AAM83758.1	2
37004	G02	NTL02YP1246	hypothetical protein	483	AAM84842.1	5.391969407
37189	G03	NTL02YP1251	putative carboxylase	546	AAM84847.1	4.42662116

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
37214	G04	NTL02YP0170	putative alpha helix protein	555	AAM83766.1	4.134453782
37233	G05	NTL02YP2342	hypothetical protein	561	AAM85938.1	2.81530782
37262	G06	NTL02YP2350	putative fimbrial precursor	570	AAM85946.1	2.813114754
37294	G07	NTL02YP3427	hypothetical protein	579	AAM87023.1	2.783521809
37347	G08	NTL02YP1257	conserved hypothetical protein	597	AAM84853.1	2.814756672
37364	G09	NTL02YP1241	ATPase of high-affinity potassium transport system, C-chain	603	AAM84837.1	2.768273717
37432	G10	NTL02YP2338	putative oxidoreductase	624	AAM85934.1	2.792168675
39190	G11	NTL02YP0169	PmbA/TldD family protein	1341	AAM83765.1	3.095582911
39209	G12	NTL02YP2353	hypothetical protein	1350	AAM85949.1	1.58705036
39361	H01	NTL02YP2329	putative integral membrane protein	1455	AAM85925.1	2.371237458
39369	H02	NTL02YP1248	deoxyribodipyrimidine photolyase (photoreactivation)	1464	AAM84843.1	3.585106383
39440	H03	NTL02YP2336	L-asparagine permease	1530	AAM85932.1	3.144585987
39510	H04	NTL02YP1267	quinolinate synthetase, B protein	1638	AAM84863.1	3.592967819
39514	H05	NTL02YP2333	putative transport protein	1641	AAM85929.1	5.334919691
39661	H06	NTL02YP2332	putative integral membrane protein	1920	AAM85928.1	3.657142857
39677	H07	NTL02YP0175	hypothetical protein	1956	AAM83771.1	3.143787575
37491	H08	NTL02YP2351	putative pilin chaperone	645	AAM85947.1	3.22189781
37499	H09	NTL02YP1258	putative pyrrolidone-carboxylate peptidase	648	AAM84854.1	4.203488372
37508	H10	NTL02YP2346	putative transcriptional regulator	651	AAM85942.1	7.149059334
37525	H11	NTL02YP1263	putative accessory protein for YplA	657	AAM84859.1	4.901004304
37680	H12	NTL02YP1259	uracil-DNA-glycosylase	711	AAM84855.1	2.399467377

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.