

***Yersinia pestis*, Strain KIM, Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 15**

Catalog No. NR-19611

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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-19611 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 15, NR-19611.”

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 15 (UYPVO)

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
39006	A01	NTL02YP1820	putative alanine racemase	1230	AAM85416.1	2.522047244
39072	A02	NTL02YP3990	hypothetical protein	1275	AAM87586.1	4.137642586
39109	A03	NTL02YP0740	putative prophage P4 integrase	1296	AAM84336.1	3.214071856
37112	A04	NTL02YP1836	hypothetical protein	519	AAM85432.1	2
37176	A05	NTL02YP1832	hypothetical protein	543	AAM85428.1	4.212692967
37204	A06	NTL02YP0754	regulates ampC	552	AAM84350.1	2
37273	A07	NTL02YP2924	hypothetical protein	573	AAM86520.1	7.106035889
37312	A08	NTL02YP1831	hypothetical protein	585	AAM85427.1	2
37328	A09	NTL02YP4017	hypothetical protein	588	AAM87613.1	2
37450	A10	NTL02YP2906	putative epimerase/aldolase	630	AAM86502.1	4.63880597
37464	A11	NTL02YP4009	putative outer membrane usher protein	636	AAM87605.1	2
37494	A12	NTL02YP4011	putative fimbrial-like protein	645	AAM87607.1	4.827737226
39146	B01	NTL02YP2907	hypothetical protein	1314	AAM86503.1	1.259970458
39362	B02	NTL02YP4006	xylulokinase	1455	AAM87602.1	3.068227425
39445	B03	NTL02YP4003	putative ATP-binding protein of xylose ABC transport	1533	AAM87599.1	3.77813096
39467	B04	NTL02YP0751	putative integral membrane protein	1557	AAM84347.1	3.507201002
37520	B05	NTL02YP2925	positive response regulator for colanic capsule biosynthesis	654	AAM86521.1	2.786743516
37588	B06	NTL02YP4013	putative transposase	675	AAM87609.1	4.825174825
37720	B07	NTL02YP2909	putative phage repressor protein cl	723	AAM86505.1	1.766710354
37806	B08	NTL02YP1830	putative pilus assembly chaperone	753	AAM85426.1	6.078184111
37779	B10	NTL02YP2888	putative regulator	741	AAM86484.1	2.768245839
37884	B11	NTL02YP2889	hypothetical protein	780	AAM86485.1	10.1695122
38062	C01	NTL02YP0706	putative sugar transport permease	840	AAM84302.1	6.207954545
36214	C02	NTL02YP2882	hypothetical protein	213	AAM86478.1	5.656126482
36253	C03	NTL02YP2881	hypothetical protein	231	AAM86477.1	5.778597786
36258	C04	NTL02YP1790	hypothetical protein	234	AAM85386.1	7.598540146
36334	C05	NTL02YP2891	hypothetical protein	261	AAM86487.1	4.6910299
38210	C06	NTL02YP1794	proton conductor component of motor	888	AAM85390.1	8.298491379
38259	C07	NTL02YP0727	putative ATP-binding component of dipeptide transport system	909	AAM84323.1	3.753424658
38500	C08	NTL02YP0698	putative collagenase	996	AAM84294.1	1.941119691
38637	C09	NTL02YP1788	putative oxidoreductase	1047	AAM85384.1	3.149034039
38655	C10	NTL02YP1812	protein methylesterase	1053	AAM85407.1	3.43915828
36618	C11	NTL02YP1797	hypothetical protein	363	AAM85393.1	3.977667494

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
36636	C12	NTL02YP2900	hypothetical protein	369	AAM86496.1	5.875305623
36652	D01	NTL02YP2890	hypothetical protein	375	AAM86486.1	6.089156627
36745	D02	NTL02YP2899	hypothetical protein	405	AAM86495.1	3.878651685
36752	D03	NTL02YP1801	hypothetical protein	408	AAM85397.1	4
38748	D04	NTL02YP0707	ATP-binding component of sn-glycerol 3-phosphate transport system	1095	AAM84303.1	3.364757709
38840	D05	NTL02YP2892	hypothetical protein	1137	AAM86488.1	3.294817332
38991	D06	NTL02YP0703	hypothetical protein	1221	AAM84299.1	2.981760508
36836	D07	NTL02YP0724	anaerobic ribonucleotide reductase activating protein	435	AAM84320.1	-
36888	D08	NTL02YP1785	putative regulator	450	AAM85381.1	4
37048	D09	NTL02YP1799	positive regulator of CheA protein activity	498	AAM85395.1	3.890334572
37050	D10	NTL02YP2884	hypothetical protein	498	AAM86480.1	1.992565056
37070	D11	NTL02YP0700	hypothetical protein	507	AAM84296.1	5.66179159
37147	D12	NTL02YP1787	hypothetical protein	534	AAM85383.1	2.81184669
37311	E01	NTL02YP1793	regulator of flagellar biosynthesis	585	AAM85389.1	6.344
37348	E02	NTL02YP2894	hypothetical protein	597	AAM86490.1	1.778649922
39371	E03	NTL02YP2887	6-phospho-beta-glucosidase A	1464	AAM86483.1	3.440824468
39398	E04	NTL02YP2897	hypothetical protein	1494	AAM86493.1	3.31029987
39493	E05	NTL02YP1809	methyl-accepting chemotaxis protein IV, peptide sensor receptor	1611	AAM85405.1	2.898849182
39567	E06	NTL02YP3986	putative urocanase	1707	AAM87582.1	3.849456211
39683	E07	NTL02YP0702	hypothetical protein	1971	AAM84298.1	4.755345599
37468	E08	NTL02YP0710	hypothetical protein	639	AAM84306.1	7.008836524
37487	E09	NTL02YP1814	chemotactic response CheY protein phosphatase	645	AAM85410.1	2.8
37558	E10	NTL02YP3981	response regulator	663	AAM87577.1	2.832147937
37694	E11	NTL02YP0726	dipeptide ABC transporter, ATP binding protein	717	AAM84322.1	6.678996037
37703	E12	NTL02YP0715	ATP-binding component of phosphonate ABC transporter	720	AAM84311.1	5.268421053
38022	F01	NTL02YP2257	hypothetical protein	825	AAM85853.1	3.068208092
38039	F02	NTL02YP2264	hypothetical protein	831	AAM85860.1	2
38038	F03	NTL02YP2252	possible protoporphyrinogen oxidase	831	AAM85848.1	2.621125144
38072	F04	NTL02YP2266	hypothetical protein	843	AAM85862.1	3.610419026
38104	F05	NTL02YP2249	2-dehydro-3-deoxyphosphooctulonate aldolase	855	AAM85845.1	3.605586592
38115	F06	NTL02YP1778	putative oxidoreductase	858	AAM85374.1	6.765033408
38173	F07	NTL02YP3377	hypothetical protein	876	AAM86973.1	6.197598253
38178	F08	NTL02YP1172	putative magnesium and cobalt efflux protein	879	AAM84768.1	6.163220892
38242	F09	NTL02YP0697	hypothetical protein	900	AAM84293.1	5.054255319
36011	F10	NTL02YP1173	hypothetical protein	153	AAM84769.1	3.953367876
36089	F11	NTL02YP2272	hypothetical protein	174	AAM85868.1	5.859813084
36093	F12	NTL02YP3345	hypothetical protein	174	AAM86941.1	3.953271028
36182	G01	NTL02YP3355	hypothetical protein	204	AAM86951.1	3.954918033
38256	G02	NTL02YP2276	hypothetical protein	906	AAM85872.1	5.559196617
38279	G03	NTL02YP1170	solute-binding periplasmic protein of glutamate/aspartate ABC transporter	918	AAM84766.1	4.897703549
38324	G04	NTL02YP2278	hypothetical protein	933	AAM85873.1	4.816032888
38419	G05	NTL02YP2258	phosphoribosylpyrophosphate synthetase	966	AAM85854.1	5.880715706
38659	G07	NTL02YP0692	putative enzyme	1056	AAM84288.1	3.384124088

Clone	Well Position	Locus ID ¹	Description (Gene name)	ORF Length	Accession Number	Average Depth of Coverage
38699	G08	NTL02YP2275	hypothetical protein	1074	AAM85871.1	5.400359066
38719	G09	NTL02YP2253	peptide chain release factor RF-1	1083	AAM85849.1	2.893143366
38744	G10	NTL02YP2269	hypothetical protein	1092	AAM85865.1	3.248233216
36216	G11	NTL02YP1783	hypothetical protein	216	AAM85379.1	3.96484375
36373	G12	NTL02YP2259	hypothetical protein	273	AAM85855.1	3.728434505
36388	H01	NTL02YP3367	hypothetical protein	279	AAM86963.1	4.833855799
36479	H02	NTL02YP0691	hypothetical protein	312	AAM84287.1	4.914772727
36537	H03	NTL02YP3365	hypothetical protein	333	AAM86961.1	4.587131367
36620	H04	NTL02YP2273	hypothetical protein	363	AAM85869.1	5.171215881
36633	H05	NTL02YP0690	hypothetical protein	369	AAM84286.1	5.66992665
38743	H06	NTL02YP2261	putative GTP-binding protein	1092	AAM85857.1	3.438162544
38787	H07	NTL02YP1175	putative ATP-binding protein in pho regulon	1113	AAM84771.1	3.391153513
38881	H08	NTL02YP0694	acridine efflux pump	1161	AAM84290.1	2.665278934
39014	H09	NTL02YP3357	possible peptidase	1233	AAM86953.1	3.177533386
39075	H10	NTL02YP3346	putative drug efflux protein	1278	AAM86942.1	3.89908953
39155	H11	NTL02YP2254	glutamyl-tRNA reductase	1317	AAM85850.1	3.822402358
39204	H12	NTL02YP3374	hypothetical protein	1347	AAM86970.1	3.82408075

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.