Salmonella enterica subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4

Catalog No. NR-19525

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Contributor:

Pathogen Functional Genomics Resource Center at the J. Craig Venter Institute

Manufacturer:

BEI Resources

Product Description:

Clone plates are replicated using a BioMek® FX robot. 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 only confirms the clone plate orientation and viability of randomly picked clones. BEI Resources does not confirm or validate individual clone identities provided by the contributor.

The *Salmonella enterica* subsp. *enterica (S. enterica* subsp. *enterica)*, strain Ty2 (serovar Typhi), Gateway® clone set consists of approximately 3380 sequence validated clones from *S. enterica* subsp. *enterica*, strain Ty2, 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 no 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 *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR™221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 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.

Plate orientation and viability were confirmed for NR-19525.

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.

Packaging/Storage:

NR-19525 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: 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 24 hours.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: *Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4, NR-19525."

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.

Disclaimers:

You are authorized to use this product for research use only. It is not intended for human use.

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References:

1. Deng, W., et al. "Comparative Genomics of *Salmonella enterica* serovar Typhi strains Ty2 and CT18." J. Bacteriol. 185 (2003): 2330-2337. PubMed: 12644504.

Support Provided by NIAID

Table 1: *Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4 (ZSTDD)[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
83161	A01	t0045	30S ribosomal protein S20	298	NP_803929.1	2.825503
83185	A02	t0603	assembly protein for periplasmic nitrate reductase	298	NP_804460.1	2.996644
83301	A03	t2024	glutaredoxin 1	298	NP_805787.1	2
83257	A04	t2231	hypothetical protein t2231	298	NP_805974.1	2.855705
83333	A05	t2423	hypothetical protein t2423	298	NP_806153.1	2
83299	A06	t3276	hypothetical protein t3276	298	NP_806951.1	2.983221
83329	A07	t1019	hypothetical protein t1019	301	NP_804838.1	3
83187	A08	t1288	type III secretion protein	301	NP_805091.1	3
83209	A09	t2063	hypothetical protein t2063	301	NP_805825.1	2.890365
83259	A10	t2965	hypothetical protein t2965	301	NP_806657.1	2.996678
83179	A11	t3036	bacteriocin immunity protein	301	NP_806723.1	2
83249	A12	t3049	hypothetical protein t3049, partial	301	NP_806735.1	2
83219	B01	t4209	hypothetical protein t4209	301	NP_807813.1	3
83213	B02	t0897	flagellar biosynthesis protein FliQ	304	NP_804726.1	1.904605
83255	B03	t1386	hypothetical protein t1386	304	NP_805181.1	2.710526
83295	B04	t1604	hypothetical protein t1604	304	NP_805383.1	2
83325	B05	t3625	hypothetical protein t3625	304	NP_807266.1	2.924342
83155	B06	t3739	phosphocarrier protein of PTS system	304	NP_807371.1	-
83292	B07	t1908	damage-inducible protein	274	NP_805676.1	2
83198	B08	t3649	ATP-synthase F0F1 subunit C	274	NP_807286.1	1.967153
83312	B09	t4263	hypothetical protein t4263	274	NP_807861.1	2
83270	B10	t1199	cell division modulator	277	NP_805006.1	2
83164	B11	t1264	secretion system protein	277	NP_805067.1	2
83192	B12	t2673	hypothetical protein t2673	277	NP_806384.1	1.938628
83232	C01	t0670	hypothetical protein t0670	280	NP_804519.1	2
83200	C02	t2082	molybdopterin synthase small subunit	280	NP_805840.2	2
83310	C03	t2286	hypothetical protein t2286	283	NP_806027.1	2
83338	C04	t3064	hydrogenase 2 accessory protein HypG	283	NP_806750.1	-
83242	C05	t2945	endonuclease fragment, partial	286	NP_806638.1	1.968531
83314	C06	t1759	biofilm formation regulatory protein BssS	289	NP_805534.2	1.913495
83218	C07	t3324	twin-arginine translocation protein TatA	289	NP_806992.1	1.982699
83228	C08	t4074	30S ribosomal protein S17	289	NP_807681.1	2
83336	C09	t1706	hypothetical protein t1706	292	NP_805482.1	2
83204	C10	t3553	hypothetical protein t3553, partial	292	NP_807198.1	2

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
83298	C11	t1896	bacteriophage protein	295	NP_805664.1	2
83168	C12	t1116	outer membrane virulence protein	298	NP_804929.1	1.946309
83166	D01	t1061	cell division topological specificity factor MinE	301	NP_804878.1	2
83322	D02	t1912	bacteriophage protein	301	NP_805680.1	2
83324	D03	t3277	hypothetical protein t3277	301	NP_806952.1	1.946844
83182	D04	t3201	30S ribosomal protein S15	304	NP_806879.1	-
83709	D05	t4290	hypothetical protein t4290	304	NP_807888.1	2.9375
83493	D06	t1389	hypothetical protein t1389	307	NP_805184.1	3
83461	D07	t2409	DNA-binding ATP-dependent protease La	307	NP_806140.1	2.729642
83485	D08	t2758	hydrogenase assembly chaperone	307	NP_806459.1	2.824104
83565	D09	t3241	N-regulated PTS system phosphohistidinoprotein-hexose phosphotransferase Npr	307	NP_806917.1	2
83577	D10	t3278	hypothetical protein t3278	307	NP_806953.1	3
83597	D11	t3461	transcriptional regulator HU subunit alpha	307	NP_807117.1	3
83621	D12	t3949	hypothetical protein t3949	307	NP_807560.1	2
83361	E01	t4121	hypothetical protein t4121	307	NP_807725.1	3
83385	E02	t4262	hypothetical protein t4262	307	NP_807860.1	2
83569	E03	t4459	hypothetical protein t4459	307	NP_808046.1	3
83689	E04	t0484	hypothetical protein t0484	310	NP_804341.1	3
83377	E05	t0829	propanediol utilization protein PduJ	310	NP_804668.1	3
83409	E06	t1179	hypothetical protein t1179	310	NP_804987.1	2.767742
83629	E07	t3024	hypothetical protein t3024	310	NP_806716.1	3
83425	E08	t3777	DNA-directed RNA polymerase subunit omega	310	NP_807400.1	2.664516
83413	E09	t4440	hypothetical protein t4440	310	NP_808027.1	2
83669	E10	t0730	hypothetical protein t0730	313	NP_804574.1	2.984026
83681	E11	t1171	hypothetical protein t1171	313	NP_804979.1	3
83573	E12	t3038	bacteriocin immunity protein	313	NP_806724.1	3
83457	F01	t4069	30S ribosomal protein S19	313	NP_807676.1	3
83445	F02	t3388	peptidyl-prolyl cis-trans isomerase C	316	NP_807052.1	2
83389	F03	t0161	hypothetical protein t0161	319	NP_804044.1	3
83353	F04	t0630	50S ribosomal protein L25	319	NP_804482.1	2
83397	F05	t1952	integration host factor subunit beta	319	NP_805717.1	2.987461
83545	F06	t2424	hypothetical protein t2424	319	NP_806154.1	2.990596
83625	F07	t2473	hypothetical protein t2473	319	NP_806202.1	2.780564
83637	F08	t3179	PTS system galactitol-specific transporter subunit IIB	319	NP_806857.1	2.956113
83521	F09	t3607	hypothetical protein t3607	319	NP_807249.1	2.99373
83613	F10	t4484	hypothetical protein t4484	319	NP_808071.1	2.996865
83497	F11	t1039	hypothetical protein t1039	322	NP_804856.1	3
83401	F12	t1910	bacteriophage protein	322	NP_805678.1	2.981366
83665	G01	t2653	hypothetical protein t2653	322	NP_806364.1	2.987578
83489	G02	t3072	hypothetical protein t3072	322	NP_806758.1	2.798137
83429	G03	t3223	DNA-binding transcriptional regulator Nlp	322	NP_806899.1	2.86646
83549	G04	t3238	sigma(54) modulation protein	322	NP_806914.1	2.872671
83473	G05	t3735	PTS system transporter subunit IIB	322	NP_807368.1	3
83469	G06	t4056	sulfur transfer complex subunit TusB	322	NP_807663.1	2.885093
83357	G07	t4341	hypothetical protein t4341	322	NP_807934.1	2.78882
83673	G08	t4578	hypothetical protein t4578	322	NP_808154.1	2.990683
83649	G09	t0083	hypothetical protein t0083	325	NP_803967.1	2.996923

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
83433	G10	t1205	hypothetical protein t1205	325	NP_805012.1	2.787692
83509	G11	t2023	hypothetical protein t2023	325	NP_805786.1	2.535385
83453	G12	t2640	hypothetical protein t2640	325	NP_806351.2	3
83465	H01	t2804	hypothetical protein t2804	325	NP_806504.1	2.547692
83697	H02	t3014	hypothetical protein t3014	325	NP_806706.1	3
83441	H03	t3723	acetolactate synthase 1 regulatory subunit	325	NP_807356.1	2.846154
83477	H04	t0061	citrate lyase subunit gamma	328	NP_803945.1	1.987805
83481	H05	t2180	LexA regulated protein	328	NP_805930.1	2.734756
83501	H06	t3225	hypothetical protein t3225	328	NP_806901.1	2.844512
83585	H07	t4223	hypothetical protein t4223	328	NP_807825.1	1.728659
83601	H08	t4381	co-chaperonin GroES	328	NP_807972.1	2.807927
83381	H09	t1650	hypothetical protein t1650	331	NP_805428.1	3
83349	H10	t1922	host-nuclease inhibitor protein	331	NP_805689.1	3
83641	H11	t2811	hypothetical protein t2811	331	NP_806510.1	3
83557	H12	t3034	hypothetical protein t3034	331	NP_806722.1	2.746224

[1]All information in this table was provided by J. Craig Venter Institute at the time of deposition.

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