

***Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7**

Catalog No. NR-19528

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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 *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.

Plate orientation and viability were confirmed for NR-19528.

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-19528 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 7, NR-19528."

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:

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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.

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Table 1: *Salmonella enterica* subsp. *enterica*, Strain Ty2 (Seroovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 7 (ZSTDG)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
85429	A01	t2512	lipoprotein	394	NP_806238.1	2.989848
85449	A02	t3430	phage baseplate assembly protein	394	NP_807093.1	2
85293	A03	t4392	fumarate reductase subunit D	394	NP_807983.1	3
85421	A04	t3392	hypothetical protein t3392	397	NP_807056.1	2.632242
85565	A05	t3713	hypothetical protein t3713	397	NP_807347.1	2.843829
85313	A06	t3830	hypothetical protein t3830	397	NP_807451.1	1.984887
85389	A07	t4264	hypothetical protein t4264	397	NP_807862.1	2
85229	A08	t4475	hypothetical protein t4475	397	NP_808062.1	2.63728
85309	A09	t3475	50S ribosomal protein L7/L12	400	NP_807131.1	2.7625
85349	A10	t0489	hypothetical protein t0489	403	NP_804346.1	2.717122
85505	A11	t1237	iron-sulfur cluster assembly scaffold protein	403	NP_805043.1	2.637717
85589	A12	t1888	bacteriophage protein	403	NP_805656.1	2.848635
85409	B01	t4092	hypothetical protein t4092	403	NP_807699.1	2.704715
85569	B02	t4142	diacylglycerol kinase	403	NP_807746.1	2.652605
85405	B03	t3969	hypothetical protein t3969	406	NP_807579.1	2.568966
85545	B04	t4075	50S ribosomal protein L14	406	NP_807682.1	3
85529	B05	t4383	hypothetical protein t4383	406	NP_807974.1	2.997537
85501	B06	t0491	bacteriophage protein	409	NP_804348.1	3
85573	B07	t1285	type III secretion protein	409	NP_805088.1	3
85322	B08	t1714	lipoprotein	409	NP_805490.1	1.977995
85585	B09	t1767	hypothetical protein t1767	409	NP_805541.1	3
85493	B10	t1919	DNA-binding protein	409	NP_805686.1	2.987775
85417	B11	t2386	hypothetical protein t2386	409	NP_806116.1	3
85385	B12	t2407	peptidyl-prolyl cis-trans isomerase D	409	NP_806138.1	3
85369	C01	t4057	30S ribosomal protein S12	409	NP_807664.1	2.899756
85253	C02	t4565	hypothetical protein t4565	409	NP_808143.1	2.938875
85285	C03	t1110	hypothetical protein t1110	412	NP_804924.1	3
85517	C04	t1986	integrase remnant	412	NP_805749.1	2.776699
85497	C05	t2025	hypothetical protein t2025	412	NP_805788.1	2.881068
85241	C06	t3425	hypothetical protein t3425	412	NP_807088.1	2.946602
85525	C07	t4398	hypothetical protein t4398	412	NP_807989.1	3
85245	C08	t3344	hypothetical protein t3344	415	NP_807012.1	1.877108
85373	C09	t3647	F0F1 ATP synthase subunit I	415	NP_807284.1	2.99759
85341	C10	t4282	hypothetical protein t4282	415	NP_807880.1	2.522892

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
85297	C11	t1261	pathogenicity island secreted effector protein	418	NP_805064.1	2.901914
85577	C12	t2036	biofilm formation regulatory protein BssR	418	NP_805799.1	2.801435
85537	D01	t3798	hypothetical protein t3798	418	NP_807420.1	2.535885
85353	D02	t4218	hypothetical protein t4218	418	NP_807820.1	2.889952
85401	D03	t4526	phage immunity repressor protein	418	NP_808111.1	2.784689
85553	D04	t0865	hypothetical protein t0865	421	NP_804698.1	2.534442
85357	D05	t4271	hypothetical protein t4271	421	NP_807869.1	2.71734
85438	D06	t3497	hypothetical protein t3497	394	NP_807145.1	2
85562	D07	t4289	hypothetical protein t4289	394	NP_807887.1	2
85266	D08	t4308	phage baseplate assembly protein	394	NP_807904.1	2
85226	D09	t0165	hypothetical protein t0165	397	NP_804048.1	2
85290	D10	t0444	hypothetical protein t0444	397	NP_804309.1	2
85442	D11	t1149	hypothetical protein t1149	397	NP_804960.1	1.994962
85382	D12	t1402	multidrug efflux system protein MdtJ	397	NP_805197.1	1.806045
85534	E01	t1807	copper sensitivity suppressor membrane protein A	397	NP_805580.1	2
85318	E02	t2303	bactoprenol-linked glucose translocase	397	NP_806042.1	2
85362	E03	t2735	PTS-system glucitol/sorbitol-specific transporter subunit IIA	397	NP_806436.1	2
85426	E04	t2850	6-pyruvoyl tetrahydrobiopterin synthase	397	NP_806547.1	2
85394	E05	t3126	bifunctional dihydroneopterin aldolase/dihydroneopterin triphosphate 2'-epimerase	397	NP_806809.1	2
85466	E06	t0125	cell division protein FtsL	400	NP_804008.1	-
85558	E07	t2454	hypothetical protein t2454	400	NP_806184.1	2
85486	E08	t0915	flagellar biosynthesis protein FlIT	403	NP_804744.1	2
85274	E09	t2289	hypothetical protein t2289	403	NP_806030.1	2
85262	E10	t0092	ApaG protein	412	NP_803976.1	2
85234	E11	t0419	hypothetical protein t0419	412	NP_804288.1	2
85270	E12	t0899	flagellar biosynthesis protein FliO	412	NP_804728.1	2
85326	F01	t1897	hypothetical protein t1897	412	NP_805665.1	2
85250	F02	t2378	hypothetical protein t2378	412	NP_806109.1	2
85366	F03	t4293	hypothetical protein t4293	412	NP_807890.1	2
85302	F04	t0181	aspartate alpha-decarboxylase	415	NP_804064.1	2
85454	F05	t0280	4'-phosphopantetheinyl transferase	415	NP_804156.1	1.995181
85238	F06	t3734	hypothetical protein t3734	415	NP_807367.1	2
85522	F07	t0264	autonomous glycyl radical cofactor GrcA	418	NP_804141.1	2
85470	F08	t1440	DNA-binding transcriptional activator MarA	418	NP_805233.2	2
85334	F09	t2237	camphor resistance protein CrcB	418	NP_805979.1	2
85458	F10	t3147	hypothetical protein t3147	418	NP_806828.1	2
85330	F11	t0212	hypothetical protein t0212	421	NP_804094.1	2
85462	F12	t4455	hypothetical protein t4455	421	NP_808042.1	-
85965	G01	t4473	soluble cytochrome b562	421	NP_808060.1	2
85765	G02	t0205	iron-sulfur cluster insertion protein ErpA	424	NP_804087.1	3
85721	G03	t0237	hypothetical protein t0237	424	NP_804117.1	2.764151
85917	G04	t0468	bactoprenol-linked glucose transferase	424	NP_804328.1	2.997642
85621	G05	t0961	chemotaxis regulatory protein CheY	424	NP_804785.1	2.912736
85730	G06	t1102	transcriptional regulator	424	NP_804916.1	1.957547
85837	G07	t1397	bacteriophage transcriptional regulator	424	NP_805192.1	1.728774
85641	G08	t1885	bacteriophage protein	424	NP_805653.1	2
85745	G09	t4088	30S ribosomal protein S11	424	NP_807695.1	3
85793	G10	t0965	flagellar protein FlhE	427	NP_804789.1	2.896956

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
85789	G11	t1234	acyl-CoA esterase	427	NP_805040.1	3
85625	G12	t2972	glycine cleavage system protein H	427	NP_806664.1	2.508197
85633	H01	t4079	30S ribosomal protein S8	427	NP_807686.1	1.995316
85861	H02	t0069	DNA-binding transcriptional activator CaiF	430	NP_803953.1	3
85881	H03	t2889	hypothetical protein t2889	430	NP_806585.1	2.967442
85693	H04	t3185	hypothetical protein t3185	430	NP_806863.1	3
85709	H05	t4442	30S ribosomal protein S6	430	NP_808029.1	3
85681	H06	t4573	endoribonuclease SymE	430	NP_808150.1	2.488372
85913	H07	t0674	hypothetical protein t0674	433	NP_804523.1	3
85613	H08	t2526	hypothetical protein t2526	433	NP_806251.1	2.87067
85801	H09	t1648	acyl-CoA thioester hydrolase	436	NP_805426.1	2.78211
85813	H10	t4009	ribosome-associated heat shock protein Hsp15	436	NP_807619.1	2.995413
85893	H11	t4017	hypothetical protein t4017	436	NP_807627.1	3
85697	H12	t0247	outer membrane lipoprotein	439	NP_804127.1	1.701595

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