Product Information Sheet for NR-19529

Salmonella enterica subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 8

Catalog No. NR-19529

This reagent is the tangible property of the U.S. Government.

For research use only. Not for human use.

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-19529.

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-19529 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 8, NR-19529."

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.

Table 1: *Salmonella enterica* subsp. *enterica*, Strain Ty2 (Serovar Typhi), Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 8 (ZSTDH)[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
85617	A01	t0645	hypothetical protein t0645	439	NP_804497.1	3
85741	A02	t1086	hydrogenase-1 operon protein HyaE	439	NP_804901.1	2.419134
85701	A03	t1542	cytochrome	439	NP_805326.1	3
85645	A04	t1645	hypothetical protein t1645	439	NP_805423.1	1.856492
85629	A05	t1920	DNA-binding protein	439	NP_805687.1	2.91344
85753	A06	t2821	regulatory protein	439	NP_806518.1	3
85901	A07	t3263	cytochrome d ubiquinol oxidase subunit III	439	NP_806938.1	3
85649	A08	t4421	hypothetical protein t4421	439	NP_808010.1	2.833713
85909	A09	t1303	glyoxalase I	442	NP_805104.1	3
85877	A10	t1887	bacteriophage protein	442	NP_805655.1	2.927602
85949	A11	t2797	virulence-associated secretory protein	442	NP_806498.1	3
85689	A12	t1551	heat-inducible protein	445	NP_805334.1	3
85669	B01	t1822	hypothetical protein t1822	445	NP_805594.1	3
85905	B02	t2251	nucleoside diphosphate kinase regulator	445	NP_805993.1	3
85833	B03	t2703	ribonucleotide reductase stimulatory protein	445	NP_806410.1	3
85953	B04	t2949	hypothetical protein t2949	445	NP_806642.1	3
85777	B05	t3075	hypothetical protein t3075	445	NP_806760.1	2.894382
85809	B06	t4177	hypothetical protein t4177	445	NP_807781.1	3
85773	B07	t1107	toxin subunit	448	NP_804921.1	3
85805	B08	t1662	global DNA-binding transcriptional dual regulator H-NS	448	NP_805439.1	3
85817	B09	t0719	hypothetical protein t0719	451	NP_804565.1	2.802661
85897	B10	t1180	pyrimidine (deoxy)nucleoside triphosphate pyrophosphohydrolase	451	NP_804988.1	2
85770	B11	t4493	hypothetical protein t4493	421	NP_808080.1	2
85606	B12	t0660	DNA-binding protein	424	NP_804511.1	2
85830	C01	t1901	prophage membrane protein	424	NP_805669.1	2
85598	C02	t2144	succinate dehydrogenase cytochrome b556 large membrane subunit	424	NP_805898.1	2
85866	C03	t3260	30S ribosomal protein S9	427	NP_806935.1	2
85890	C04	t4272	hypothetical protein t4272	427	NP_807870.1	2
85706	C05	t0141	nucleoside triphosphate pyrophosphohydrolase	430	NP_804024.1	2
85674	C06	t0950	universal stress protein UspC	430	NP_804774.1	2
85782	C07	t1022	hypothetical protein t1022	430	NP_804841.1	2

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
85946	C08	t1798	hypothetical protein t1798	430	NP_805571.1	2
85762	C09	t3562	hypothetical protein t3562	430	NP_807207.1	2
85738	C10	t1510	hypothetical protein t1510	433	NP_805296.1	2
85658	C11	t2407	hypothetical protein t2407	433	NP_806137.1	1.60739
85846	C12	t2943	plasmid maintenance protein	433	NP_806636.1	1.411085
85938	D01	t4425	hypothetical protein t4425	433	NP_808012.1	2
85678	D02	t2531	DNA-binding transcriptional regulator Crl	436	NP_806255.1	-
85858	D03	t3203	ribosome-binding factor A	436	NP_806881.1	2
85854	D04	t0011	hypothetical protein t0011	439	NP_803896.1	2
85638	D05	t2132	acyl-CoA thioester hydrolase	439	NP_805886.1	2
85602	D06	t2652	hypothetical protein t2652	439	NP_806363.1	2
85750	D07	t0916	flagellar protein FliS	442	NP_804745.1	2
85786	D08	t2543	hypothetical protein t2543	442	NP_806267.1	1.997738
85850	D09	t3871	transcriptional regulator	442	NP_807489.1	2
85874	D10	t2748	formate hydrogenlyase maturation protein	445	NP_806449.1	2
85870	D11	t4072	50S ribosomal protein L16	445	NP_807679.1	2
85826	D12	t0900	flagellar motor switch protein FliN	448	NP_804729.1	2
85970	E01	t3709	heat shock protein lbpA	448	NP_807344.1	2
85922	E02	t4094	large-conductance mechanosensitive channel	448	NP_807701.1	2
85842	E03	t1242	cysteine desufuration protein SufE	451	NP_805048.1	2
86233	E04	t1270	pathogenicity island effector protein	451	NP_805073.1	3
86101	E05	t1780	curli assembly protein CsgF	451	NP_805554.1	2.997783
86141	E06	t1842	hypothetical protein t1842	451	NP_805611.1	2.993348
85973	E07	t2361	DNA-binding transcriptional regulator CueR	451	NP_806093.1	2.991131
86045	E08	t2574	hypothetical protein t2574	451	NP_806293.1	3
86241	E09	t3009	Holliday junction resolvase-like protein	451	NP_806701.1	2.824834
86097	E10	t0104	hypothetical protein t0104	454	NP_803987.1	2
86185	E11	t0261	thioredoxin	454	NP_804138.1	1.887665
85977	E12	t0724	hypothetical protein t0724	454	NP_804570.1	3
86117	F01	t1020	acetyltransferase	454	NP_804839.1	3
86133	F02	t3655	ATP synthase F0F1 subunit epsilon	454	NP_807292.1	1.810573
86229	F03	t4269	hypothetical protein t4269	454	NP_807867.1	2.848018
86161	F04	t0242	peptidyl-tRNA hydrolase domain-containing protein	457	NP_804122.1	1.796499
86237	F05	t2598	hypothetical protein t2598, partial	457	NP_806315.1	1.971554
86169	F06	t0568	hypothetical protein t0568	460	NP_804425.1	2
86085	F07	t1602	periplasmic protein	460	NP_805382.1	3
86257	F08	t2990	hypothetical protein t2990	460	NP_806682.1	2.254348
86305	F09	t3078	biopolymer transport protein ExbD	460	NP_806763.1	1.584783
86125	F10	t3746	PTS system protein	460	NP_807376.1	1.873913
86005	F11	t4418	transcriptional repressor NsrR	460	NP_808007.1	2.795652
86189	F12	t3387	hypothetical protein t3387	463	NP_807051.1	2.695464
86181	G01	t1478	osmotically inducible protein C	466	NP_805267.1	3
86293	G02	t2700	hypothetical protein t2700	466	NP_806407.1	2.61588
86201	G03	t3816	hypothetical protein t3816	466	NP_807438.1	2
86221	G04	t3925	universal stress protein A	469	NP_807538.1	3
86281	G05	t0150	major pilin subunit	472	NP_804033.1	3
86193	G06	t1525	phosphotransferase	472	NP_805311.1	1.533898
86037	G07	t1541	hypothetical protein t1541	472	NP_805325.1	2.754237
86313	G08	t2573	hypothetical protein t2573	472	NP_806292.1	2.944915
86277	G09	t4109	hypothetical protein t4109	472	NP_807713.1	3

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
86129	G10	t4600	DNA polymerase III subunit psi	472	NP_808172.1	2.809322
86017	G11	t0101	IS element transposase	475	NP_803985.1	3
86289	G12	t0179	PTS system transporter subunit IIA	475	NP_804062.1	2.850526
86013	H01	t1819	homoprotocatechuate degradative operon repressor	475	NP_805591.1	1.72
86073	H02	t2295	hypothetical protein t2295	475	NP_806036.1	2.608421
86121	H03	t0017	hypothetical protein t0017	478	NP_803902.1	2.633891
86209	H04	t0734	hypothetical protein t0734	478	NP_804578.1	2.838912
86285	H05	t2795	virulence-associated secretory protein	478	NP_806496.1	3
86217	H06	t4267	lipoprotein	478	NP_807866.1	2.882845
86317	H07	t1066	hypothetical protein t1066	481	NP_804883.2	3
86321	H08	t1366	hypothetical protein t1366	481	NP_805162.1	3
86138	H09	t1746	flagellar basal-body rod protein FlgB	451	NP_805521.1	2
86029	H10	t4156	hypothetical protein t4156	451	NP_807760.1	2.977827
86246	H11	t4504	ornithine carbamoyltransferase subunit I	451	NP_808090.1	1.993348
86298	H12	t0880	DNA polymerase V subunit UmuD	454	NP_804710.1	2

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

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