

***Streptococcus pneumoniae* Gateway®
Clone Set, Recombinant in *Escherichia coli*, Plate 14****Catalog No. NR-19581**

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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 *Streptococcus pneumoniae* (*S. pneumoniae*) Gateway® clone set consists of approximately 2029 sequence validated clones from *S. pneumoniae*, strain TIGR4 cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells.¹ Each open reading frame was constructed in vector pDONR™221 (Invitrogen™) with a native 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-19581.

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-19581 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 containing 50 µg/mL kanamycin

LB 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 18 to 24 hours.

Citation:

Acknowledgment for publications should read "The following reagent was obtained through BEI Resources, NIAID, NIH: *Streptococcus pneumoniae* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 14, NR-19581."

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. Kwon, K., et al. "A Correlation Analysis of Protein Characteristics Associated with Genome-Wide High Throughput Expression and Solubility of *Streptococcus pneumoniae* Proteins." *Protein Expr. Purif.* 55 (2007): 368-378. PubMed: 17703947.

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Table 1: *Streptococcus pneumoniae* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 14 (YSPCN)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
24085	A01	SP2078	arginyl-tRNA synthetase	1345	NP_346499.1	1.407435
24086	A02	SP1185	PTS system, lactose-specific IIBC components	1188	NP_345654.1	8.510943
24090	A03	SP2126	dihydroxy-acid dehydratase	1555	NP_346544.1	4.03537
24091	A04	SP1161	acetoin dehydrogenase complex, E3 component, dihydrolopoamide dehydrogenase	1164	NP_345630.1	6.78866
24092	A05	SP1498	phosphoglucumutase	172	NP_345949.1	3
24093	A06	SP0665	chorismate binding enzyme	660	NP_345170.1	3.79697
24095	A07	SP0807	septation ring formation regulator EzrA	783	NP_345304.1	9.338442
24097	A08	SP1046	-	1005	-	8.140299
24101	A09	SP1839	ABC transporter ATP-binding protein/permease	286	NP_346272.1	2
24102	A10	SP1434	ABC transporter ATP-binding protein/permease	2403	NP_345890.1	12.61465
24103	A11	SP1072	DNA primase	1032	NP_345545.1	10.91085
24105	A12	SP2073	ABC transporter ATP-binding protein/permease	1312	NP_346496.1	3.131098
24107	B01	SP0394	PTS system, mannitol-specific IIBC components	462	NP_344918.1	4.530303
24108	B02	SP0994	hypothetical protein SP_0994	951	NP_345473.1	8.911672
24110	B03	SP1317	V-type ATP synthase subunit A	1344	NP_345775.1	13.0744
24111	B04	SP0060	Beta-galactosidase 3	186	NP_344609.1	1.989247
24113	B05	SP1780	oligoendopeptidase F	157	NP_346213.1	2
24114	B06	SP0979	oligoendopeptidase F	933	NP_345460.1	8.768489
24115	B07	SP0266	glucosamine--fructose-6-phosphate aminotransferase		NP_344804.1	
24116	B08	SP2057	hypothetical protein SP_2057	1291	NP_346481.1	3.39117
24118	B09	SP1200	GTP-binding protein LepA	1212	NP_345667.1	6.777228
24119	B10	SP1056	Tn5252, relaxase	1011	NP_345530.1	10.54698
24122	B11	SP0681	elongation factor Tu family protein	675	NP_345186.1	5.140741
24123	B12	SP0618	excinuclease ABC subunit C	627	NP_345130.1	3.5311
24127	C01	SP1553	ABC transporter ATP-binding protein	241	NP_346000.1	3.950207
24128	C02	SP1222	type II restriction endonuclease	1231	NP_345688.1	7.571893

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
24129	C03	SP2141	glycosyl hydrolase-related protein	1642	NP_346558.1	3.014616
24133	C04	SP1647	endopeptidase O	685	NP_346087.1	4.389781
24134	C05	SP1114	ABC transporter ATP-binding protein	1097	NP_345585.1	10.40474
24137	C06	SP1251	endonuclease	1269	NP_345716.1	9.022065
24138	C07	SP0475	hypothetical protein SP_0475	522	NP_344994.1	5.666667
24139	C08	SP1343	prolyl oligopeptidase family protein	1443	NP_345801.1	16.64796
24141	C09	SP1631	threonyl-tRNA synthetase	646	NP_346071.1	4.02322
24142	C10	SP0806	DNA gyrase subunit B	777	NP_345303.1	9.158301
24178	C11	SP1263	DNA topoisomerase I	1284	NP_345727.1	12.65187
24190	C12	SP0202	anaerobic ribonucleoside triphosphate reductase	297	NP_344742.1	2.262626
24194	D01	SP1326	neuraminidase	1359	NP_345784.1	11.91759
24202	D02	SP1118	pullulanase	1101	NP_345589.1	8.319709
24203	D03	SP1087	ATP-dependent DNA helicase PcrA	1053	NP_345559.1	9.815764
24205	D04	SP0878	SpoE family protein	846	NP_345365.1	8.066194
24206	D05	SP0459	formate acetyltransferase	510	NP_344979.1	4.717647
24214	D06	SP0581	phenylalanyl-tRNA synthetase subunit beta	606	NP_345095.1	2.929043
24215	D07	SP1175	hypothetical protein SP_1175	1179	NP_345644.1	9.63274

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