

***Streptococcus pneumoniae* Gateway®  
Clone Set, Recombinant in *Escherichia coli*, Plate 13****Catalog No. NR-19580**

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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.<sup>1</sup> 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-19580.

**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-19580 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 agar 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 13, NR-19580."

**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](http://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.

ATCC® is a trademark of the American Type Culture Collection.



**Table 1: *Streptococcus pneumoniae* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 13 (YSPCM)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23894	A01	SP0474	PTS system, cellobiose-specific IIC component	522	NP_344993.1	4.888889
23895	A02	SP0250	PTS system, IIC component	330	NP_344789.1	2.706061
23896	A03	SP0290	dihydrofolate synthetase	363	NP_344828.1	2.862259
23903	A04	SP1250	hypothetical protein SP_1250	1269	NP_345715.1	7.038613
23904	A05	SP0604	sensor histidine kinase VncS	621	NP_345116.1	4.136876
23905	A06	SP1963	hypothetical protein SP_1963	799	NP_346390.1	2
23906	A07	SP2153	hypothetical protein SP_2153	1705	NP_346569.1	3.916716
23907	A08	SP2192	sensor histidine kinase	2026	NP_346603.1	2.850444
23908	A09	SP2083	sensor histidine kinase PnpS	1360	NP_346503.1	1.415441
23909	A10	SP0562	hypothetical protein SP_0562	591	NP_345078.1	5.898477
23910	A11	SP1521	UDP-N-acetylmuramate--L-alanine ligase	199	NP_345971.1	3
23911	A12	SP0281	aminopeptidase C	357	NP_344819.1	3.294118
23912	B01	SP0799	sensor histidine kinase CiaH	774	NP_345296.1	9.379845
23913	B02	SP0239	hypothetical protein SP_0239	318	NP_344779.1	3.27044
23914	B03	SP1690	ABC transporter substrate-binding protein	910	NP_346129.1	3.631868
23915	B04	SP1757	hypothetical protein SP_1757	1471	NP_346192.1	3.379334
23917	B05	SP0626	branched-chain amino acid transport system II carrier protein	633	NP_345137.1	5.082148
23918	B06	SP0527	sensor histidine kinase BlpH	558	NP_345045.1	3.473118
23919	B07	SP0761	DEAD/DEAH box helicase	744	NP_345259.1	6.459677
23920	B08	SP1589	hypothetical protein SP_1589	382	NP_346035.1	4
23921	B09	SP0591	cysteinyl-tRNA synthetase	612	NP_345104.1	5.096405
23922	B10	SP1542	asparaginyl-tRNA synthetase	223	NP_345990.1	3
23923	B11	SP1352	IS1380-Spn1 transposase	1482	NP_345810.1	12.18893
23924	B12	SP0328	IS1380-Spn1 transposase	393	NP_344864.1	3.16285
23925	C01	SP1306	glutamate dehydrogenase	1344	NP_345769.1	11.49405
23926	C02	SP0502	glutamine synthetase, type I	543	NP_345020.1	5.828729
23927	C03	SP1439	IS1380-Spn1 transposase	130	NP_345895.1	3
23928	C04	SP2179	IS1380-Spn1 transposase	1993	NP_346592.1	3.618665
23929	C05	SP1418	IS1380-Spn1, transposase	1938	NP_345875.1	13.49536
23930	C06	SP0343	IS1380-Spn1 transposase	411	NP_344877.1	3.729927
23933	C07	SP2201	choline binding protein D	2074	NP_346612.1	4.184185
23935	C08	SP1595	IS1380-Spn1 transposase	415	NP_346039.1	4

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23936	C09	SP0310	cellobiose phosphotransferase system IIC component	375	NP_344847.1	3.232
23937	C10	SP0714	IS1380-Spn1 transposase	699	NP_345215.1	9.467811
23938	C11	SP1503	IS1380-Spn1 transposase	181	NP_345954.1	2
23939	C12	SP2129	PTS system ascorbate-specific transporter subunit IIC	1585	NP_346547.1	3.34511
23940	D01	SP0495	IS1380-Spn1 transposase	540	NP_345013.1	5.053704
23942	D02	SP1226	sensory box sensor histidine kinase	1239	NP_345692.1	7.539144
23943	D03	SP0480	potassium transporter peripheral membrane component	527	NP_344999.1	4.931689
23945	D04	SP0688	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	681	NP_345193.1	12.04846
23949	D05	SP0529	BlpC ABC transporter	561	NP_345047.1	3.796791
23950	D06	SP1166	MATE efflux family protein	1171	NP_345635.1	9.622545
23955	D07	SP1939	MATE efflux family protein DinF	727	NP_346367.1	2
23961	D08	SP0078	Trk family potassium uptake protein	201	NP_344627.1	1.955224
23971	D09	SP0167	hypothetical protein SP_0167	264	NP_344709.1	10.83333
23972	D10	SP1001	amino acid permease family protein	954	NP_345478.1	8.281971
23973	D11	SP0374	hypothetical protein SP_0374	447	NP_344901.1	3.845638
23974	D12	SP0623	dipeptidase PepV	633	NP_345135.1	4.744076
23977	E01	SP2167	L-fucose kinase fucK	1885	NP_346581.1	3.567109
23981	E02	SP2021	glycosyl hydrolase family protein	1009	NP_346446.1	1.874133
23982	E03	SP0871	intein-containing protein	837	NP_345358.1	7.137395
23983	E04	SP0477	6-phospho-beta-galactosidase	525	NP_344996.1	4.339048
23985	E05	SP0578	6-phospho-beta-glucosidase	603	NP_345092.1	4.197347
23986	E06	SP1119	glyceraldehyde-3-phosphate dehydrogenase, NADP-dependent	1104	NP_345590.1	9.692935
23989	E07	SP2187	hypothetical protein SP_2187	2014	NP_346598.1	3.741807
23994	E08	SP0436	aspartyl/glutamyl-tRNA amidotransferase subunit B	492	NP_344958.1	4.333333
23996	E09	SP1894	sucrose phosphorylase	484	NP_346325.1	2
23997	E10	SP0346	capsular polysaccharide biosynthesis protein Cps4A	423	NP_344879.1	2.886525
23998	E11	SP1530	UDP-N-acetylmuramoylalanyl-D-glutamate--L-lysine ligase	205	NP_345979.1	3
24000	E12	SP1382	cytoplasmic alpha-amylase	1680	NP_345840.1	13.25536
24001	F01	SP2038	PTS system ascorbate-specific transporter subunit IIC	1126	NP_346463.1	3.80373
24006	F02	SP0437	aspartyl/glutamyl-tRNA amidotransferase subunit A	492	NP_344959.1	5.308943
24007	F03	SP0287	xanthine/uracil permease family protein	360	NP_344825.1	3.047222
24010	F04	SP0092	ABC transporter substrate-binding protein	216	NP_344639.1	3.875
24011	F05	SP0713	lysyl-tRNA synthetase	699	NP_345214.3	13.70815
24015	F06	SP1852	galactose-1-phosphate uridylyltransferase	358	NP_346284.1	2
24018	F07	SP0341	hypothetical protein SP_0341	408	NP_344875.1	2.806373
24019	F08	SP2066	threonine synthase	1297	NP_346489.1	3.22899
24020	F09	SP1243	glucose-6-phosphate 1-dehydrogenase	1257	NP_345708.1	7.774065
24021	F10	SP1272	polysaccharide biosynthesis protein,	1308	NP_345736.1	12.2974
24023	F11	SP1890	oligopeptide ABC transporter permease AmiC	481	NP_346321.1	1.91684

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
24024	F12	SP0897	pyruvate kinase	861	NP_345384.1	8.416957
24025	G01	SP2169	zinc ABC transporter zinc-binding lipoprotein	1900	NP_346583.1	3.902632
24026	G02	SP1510	F0F1 ATP synthase subunit alpha	187	NP_345961.1	3
24031	G03	SP2107	4-alpha-glucanotransferase	1450	NP_346526.1	1.317241
24032	G04	SP1684	PTS system, IIBC components	874	NP_346123.1	3.632723
24035	G05	SP0461	transcriptional regulator	513	NP_344981.1	4.460039
24036	G06	SP1761	hypothetical protein SP_1761	127	NP_346196.1	2
24037	G07	SP0846	sugar ABC transporter ATP-binding protein	816	NP_345337.1	9.093137
24038	G08	SP0770	ABC transporter ATP-binding protein	753	NP_345268.1	9.073041
24042	G09	SP2176	D-alanine--poly(phosphoribitol) ligase subunit 1	1984	NP_346590.1	3.855847
24046	G10	SP0453	amino acid ABC transporter amino acid-binding protein/permease	507	NP_344974.1	4.952663
63449	G11	SP0988	bifunctional N-acetylglucosamine-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyltransferase	945	NP_345467.1	8.544974
24067	G12	SP0155	sensor histidine kinase	258	NP_344697.1	15.39535
24068	H01	SP0575	helicase	603	NP_345089.1	3.74461
24070	H02	SP0966	adherence and virulence protein A	924	NP_345447.1	8.570346
24071	H03	SP0865	DNA polymerase III subunits gamma and tau	834	NP_345352.1	7.480815
24072	H04	SP0613	metallo-beta-lactamase superfamily protein	627	NP_345125.1	4.464115
24075	H05	SP0443	hypothetical protein SP_0443	498	NP_344964.1	3.39759
24078	H06	SP1526	ABC transporter ATP-binding protein	202	-	3
24079	H07	SP0478	PTS system, lactose-specific IIBC components	525	NP_344997.1	4.346667
24080	H08	SP2146	hypothetical protein SP_2146	1660	NP_346563.1	4.068072
24081	H09	SP0121	metallo-beta-lactamase superfamily protein	237	NP_344667.1	16
24082	H10	SP1040	resolvase family site-specific recombinase	996	NP_345515.1	2.804217
24083	H11	SP0483	ABC transporter ATP-binding protein	531	NP_345002.1	2.905838
24084	H12	SP0662	sensor histidine kinase	657	NP_345167.1	4.753425

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