

## Streptococcus pneumoniae Gateway® Clone Set, Recombinant in Escherichia coli, Plate 11

### Catalog No. NR-19578

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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 *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.

#### 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-19578 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 11, NR-19578."

#### 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.

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**Table 1: *Streptococcus pneumoniae* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 11 (YSPCK)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23604	A01	SP2091	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	1384	NP_346510.1	1.40029
23605	A02	SP0243	iron ABC transporter iron-binding protein	318	NP_344782.1	4.78931
23606	A03	SP1942	transcriptional regulator	748	NP_346370.1	2
23607	A04	SP0081	-	201	-	1.98507
23608	A05	SP2150	ornithine carbamoyltransferase	1675	NP_346566.1	4.08597
23609	A06	SP1075	glycosyl transferase CpoA	1032	NP_345548.1	9.91279
23611	A07	SP1607	UDP-glucose 4-epimerase	457	NP_346051.1	2.99562
23612	A08	SP0285	alcohol dehydrogenase	360	NP_344823.1	3.25833
23613	A09	SP0047	phosphoribosylaminoimidazole synthetase	171	NP_344596.1	2
23616	A10	SP1270	alcohol dehydrogenase, zinc-containing	1302	NP_345734.1	13.0937
23617	A11	SP0856	branched-chain amino acid aminotransferase	828	NP_345345.1	9.15821
23621	A12	SP1416	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	1899	NP_345874.1	13.7062
23623	B01	SP1700	phospho-2-dehydro-3-deoxyheptonate aldolase	946	NP_346138.1	2.51268
23625	B02	SP0182	methylcrotonoyl-CoA carboxylase	285	NP_344723.1	4
23626	B03	SP0458	DNA polymerase IV	510	NP_344978.1	3.9902
23628	B04	SP0515	heat-inducible transcription repressor	555	NP_345033.1	5.92252
23629	B05	SP1069	hypothetical protein SP_1069	1026	NP_345542.1	9.57895
23630	B06	SP0627	hypothetical protein SP_0627	633	NP_345138.1	5.37757
23631	B07	SP1967	hypothetical protein SP_1967	814	NP_346394.1	2
23636	B08	SP2214	elongation factor Ts	2164	NP_346622.1	3.90481
23637	B09	SP1162	dihydrolipoamide acetyltransferase	1164	NP_345631.1	10.4072
23638	B10	SP1671	D-alanyl-alanine synthetase A	793	NP_346110.1	5.28499
23639	B11	SP1264	hypothetical protein SP_1264	1287	NP_345728.1	12.1795
23641	B12	SP0523	ABC transporter permease	558	NP_345041.1	5.63441
23642	C01	SP0267	hypothetical protein SP_0267	348	NP_344805.1	2.85345
23643	C02	SP0084	sensor histidine kinase	204	NP_344632.1	-
23644	C03	SP0845	lipoprotein	816	NP_345336.1	8.93137
23645	C04	SP0358	capsular polysaccharide biosynthesis protein Cps4J	432	NP_344891.1	3.33565

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23646	C05	SP2055	alcohol dehydrogenase, zinc-containing	1291	NP_346479.1	3.99535
23647	C06	SP0689	undecaprenyldiphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	684	NP_345194.1	11.4678
23648	C07	SP0847	sugar ABC transporter permease	822	NP_345338.1	9.1837
23652	C08	SP0097	hypothetical protein SP_0097	222	NP_344644.1	2
23653	C09	SP0102	glycosyl transferase	228	NP_344649.1	14.9254
23654	C10	SP1375	3-dehydroquinate synthase	1659	NP_345833.1	12.5316
23655	C11	SP1888	oligopeptide ABC transporter ATP-binding protein AmiE	475	NP_346319.1	2
23656	C12	SP1826	ABC transporter substrate-binding protein	253	NP_346259.1	2
23657	D01	SP1386	spermidine/putrescine ABC transporter spermidine/putrescine-binding protein	1689	NP_345844.1	12.9876
23658	D02	SP1159	site-specific tyrosine recombinase XerS	1161	NP_345628.1	9.65891
23660	D03	SP1634	hypothetical protein SP_1634	652	NP_346074.1	4.38804
23661	D04	SP0352	capsular polysaccharide biosynthesis protein Cps4G	426	NP_344885.1	2.87089
23664	D05	SP1276	carbamoyl phosphate synthase small subunit	1314	NP_345740.1	13.0875
23666	D06	SP1483	DEAD/DEAH box helicase	163	NP_345937.1	3
23667	D07	SP0355	hypothetical protein SP_0355	429	NP_344888.1	3.331
23668	D08	SP1094	aminotransferase, class-V	1065	NP_345566.1	9.33521
23670	D09	SP0921	agmatine deiminase	876	NP_345405.1	9.19178
23672	D10	SP1617	PTS system, IIC component	478	NP_346058.1	3.97071
23675	D11	SP0242	ABC transporter ATP-binding protein	318	NP_344781.1	4.84277
23679	D12	SP1009	ferrochelatase	963	NP_345485.1	7.45067
23681	E01	SP0755	peptide chain release factor 2	738	YP_873927.1	3.42005
23682	E02	SP2227	recombination protein F	2293	NP_346635.1	3.88181
23683	E03	SP2001	sensor histidine kinase	904	NP_346428.1	1.98119
23684	E04	SP1742	hypothetical protein SP_1742		NP_346178.1	
23685	E05	SP0357	UDP-N-acetylglucosamine-2-epimerase	432	NP_344890.1	2.43519
23686	E06	SP0952	acetyltransferase	915		6.21202
23687	E07	SP0178	riboflavin biosynthesis protein RibD	279	NP_344719.1	3.41577
23689	E08	SP1698	alanine racemase	934	NP_346136.1	4.92934
23690	E09	SP1608	oxidoreductase, DadA family protein	457	NP_346052.1	2
23692	E10	SP1686	Gfo/Idh/MocA family oxidoreductase	889	NP_346125.1	5.63555
23693	E11	SP0166	pyridoxal-dependent decarboxylase	264	NP_344708.1	10.8106
23694	E12	SP1749	GTP-binding protein YqeH	1339	NP_346185.1	3.46378
23697	F01	SP1073	RNA polymerase sigma factor RpoD	1032	NP_345546.1	9.99903
23698	F02	SP0873	hypothetical protein SP_0873	840	NP_345360.1	8.15238
23699	F03	SP2063	LysM domain-containing protein	1294	YP_873938.1	1.31917
23701	F04	SP1126	hypothetical protein SP_1126	1113	NP_345596.1	9.65768
23702	F05	SP0004	GTP-dependent nucleic acid-binding protein EngD	96	NP_344557.1	-
23703	F06	SP0353	capsular polysaccharide biosynthesis protein Cps4H	429	NP_344886.1	2.40326
23704	F07	SP0887	type I restriction-modification system, S subunit	855	NP_345374.1	8.82456
23707	F08	SP1438	ABC transporter ATP-binding protein	130	NP_345894.1	4
23708	F09	SP0655	sodium/hydrogen exchanger family protein	651	NP_345160.2	4.74194

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23709	F10	SP0920	carboxynorspermidine decarboxylase	876	NP_345404.1	8.76826
23710	F11	SP1580	sugar ABC transporter ATP-binding protein	358	NP_346026.1	4
23711	F12	SP2096	M20/M25/M40 family peptidase	1402	NP_346515.1	1.09201
23712	G01	SP1409	coproporphyrinogen III oxidase	1839	NP_345867.1	13.8249
23713	G02	SP0397	mannitol-1-phosphate 5-dehydrogenase	465	NP_344921.1	5.34194
23715	G03	SP0519	chaperone protein DnaJ	555	NP_345037.1	5.27207
23716	G04	SP0002	DNA polymerase III subunit beta	93	NP_344555.1	-
23717	G05	SP0715	lactate oxidase	699	NP_345216.1	12.3877
23718	G06	SP1325	Gfo/Idh/MocA family oxidoreductase	1359	NP_345783.1	11.5217
23719	G07	SP1123	glycogen biosynthesis protein GlgD	1110	NP_345594.1	10.7045
23720	G08	SP2058	queuine tRNA-ribosyltransferase	1291	NP_346482.1	3.94423
23721	G09	SP0880	aminotransferase, class-V	846	NP_345367.1	7.54728
23722	G10	SP1122	glucose-1-phosphate adenylyltransferase	1107	NP_345593.1	9.97019
23723	G11	SP1753	-	1435	-	3.60697
23724	G12	SP1228	A/G-specific adenine glycosylase	1242	NP_345694.1	5.93076
23725	H01	SP1809	transcriptional regulator	205	NP_346242.1	2
23726	H02	SP2157	alcohol dehydrogenase, iron-containing	1735	NP_346571.1	3.7072
23727	H03	SP2056	N-acetylglucosamine-6-phosphate deacetylase	1291	NP_346480.1	1.41905
23728	H04	SP1600	hypothetical protein SP_1600	430	NP_346044.1	1.92093
23730	H05	SP0373	hypothetical protein SP_0373	447	NP_344900.1	4.76734
23731	H06	SP0749	branched-chain amino acid ABC transporter amino acid-binding protein	729	NP_345248.1	12.8189
23732	H07	SP0599	transmembrane protein Vexp1	618	NP_345111.1	4.77832
23733	H08	SP1129	phage integrase family integrase/recombinase	1122	NP_345599.1	10.7077
23734	H09	SP1524	aminotransferase, class II	199	NP_345974.1	2
23735	H10	SP1505	hypothetical protein SP_1505	181	NP_345956.1	4
23739	H11	SP0101	transporter	147	NP_344648.1	11.0544
23740	H12	SP1940	recombinase A	739	NP_346368.1	3.3816

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