

***Streptococcus pneumoniae* Gateway®  
Clone Set, Recombinant in *Escherichia coli*, Plate 1**

**Catalog No. NR-19568**

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**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 *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-19568.

**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-19568 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 1, NR-19568.”

**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](http://www.cdc.gov/biosafety/publications/bmbl5/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 1 (YSPCA)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22040	A01	SP1028	hypothetical protein SP_1028	984	NP_345503.1	8.94410569
22062	A02	SP0684	hypothetical protein SP_0684	681	NP_345189.1	5.09985316
22066	A03	SP0747	hypothetical protein SP_0747	729	NP_345246.1	12.4828532
22067	A04	SP0934	hypothetical protein SP_0934	888	NP_345418.1	8.29617117
22068	A05	SP0612	hypothetical protein SP_0612	627	NP_345124.1	3.25039872
22074	A06	SP1678	hypothetical protein SP_1678	838	NP_346117.1	4.81622912
22075	A07	SP0699	hypothetical protein SP_0699	690	NP_345203.1	12.3768116
22076	A08	SP0195	hypothetical protein SP_0194	294	NP_344735.1	4.7755102
22080	A09	SP0821	hypothetical protein SP_0821	795	NP_345313.1	9.35345912
22081	A10	SP0407	hypothetical protein SP_0407	471	NP_344930.1	4.30997877
22083	A11	SP0070	hypothetical protein SP_0070	195	NP_344619.1	1.95384615
22086	A12	SP0654	hypothetical protein SP_0654	651	NP_345159.1	4.78341014
22089	B01	SP1120	hypothetical protein SP_1120	1104	NP_345591.1	10.7336957
22090	B02	SP0414	hypothetical protein SP_0414	474	NP_344937.1	4.80379747
22091	B03	SP1788	hypothetical protein SP_1788	169	NP_346221.1	1.6035503
22094	B04	SP0172	hypothetical protein SP_0172	270	NP_344713.1	14.9444444
22098	B05	SP0316	hypothetical protein SP_0316	381	NP_344852.1	2.69553806
22102	B06	SP1481	hypothetical protein SP_1481	160	NP_345935.1	3
22105	B07	SP1353	hypothetical protein SP_1353	1482	NP_345811.1	11.5121457
22106	B08	SP1351	hypothetical protein SP_1351	1479	NP_345809.1	10.8133874
22109	B09	SP0094	hypothetical protein SP_0094	216	NP_344641.1	2.89814815
22110	B10	SP0244	hypothetical protein SP_0244	323	NP_344783.1	3.94736842
22111	B11	SP1868	hypothetical protein SP_1868	388	NP_346300.1	2
22112	B12	SP0497	hypothetical protein SP_0497	540	NP_345015.1	4.07407407
22114	C01	SP1138	hypothetical protein SP_1138	1134	NP_345608.1	9.27513228
22115	C02	SP2200	hypothetical protein SP_2200	2071	NP_346611.1	3.16224046
22116	C03	SP0621	hypothetical protein SP_0621	630	NP_345133.1	4.16190476
22117	C04	SP0512	hypothetical protein SP_0512	552	NP_345030.1	2.93478261
22119	C05	SP1158	hypothetical protein SP_1158	1161	NP_345627.1	9.68906115
22122	C06	SP0093	hypothetical protein SP_0093	216	NP_344640.1	2
22123	C07	SP0072	hypothetical protein SP_0072	198	NP_344621.1	-
22125	C08	SP0815	hypothetical protein SP_0815	789	NP_345308.1	9.55006337

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22126	C09	SP1049	hypothetical protein SP_1049	1005	NP_345523.1	10.2199005
22127	C10	SP0052	hypothetical protein SP_0052	177	NP_344601.1	1.94915254
22128	C11	SP0594	-	615	-	4.8796748
22129	C12	SP1791	integrase-related protein	169	NP_346224.1	2
22130	D01	SP0693	hypothetical protein SP_0693	687	NP_345198.1	12.7103348
22231	D02	SP1108	hypothetical protein SP_1108	1092	NP_345579.1	9.06868132
22235	D03	SP0472	hypothetical protein SP_0472	519	NP_344991.1	4.42003854
22236	D04	SP1562	hypothetical protein SP_1562	262	NP_346009.1	2
22238	D05	SP2008	preprotein translocase subunit SecE	943	NP_346435.1	1.95864263
22239	D06	SP0311	hypothetical protein SP_0311	378	NP_344848.1	3.25396825
22242	D07	SP1077	hypothetical protein SP_1077	1035	NP_345550.1	9.24541063
22246	D08	SP1338	hypothetical protein SP_1338	1422	NP_345796.1	16.8691983
22247	D09	SP1017	4-oxalocrotonate tautomerase	972	NP_345492.1	8.96604938
22248	D10	SP0559	hypothetical protein SP_0559	588	NP_345075.1	2
22249	D11	SP0228	50S ribosomal protein L30	312	NP_344768.1	4.20512821
22250	D12	SP1818	hypothetical protein SP_1818	232	NP_346251.1	2
22251	E01	SP2134	50S ribosomal protein L32	1630	NP_346552.1	1.17177914
22256	E02	SP0132	-	243	-	12.9547325
22258	E03	SP1949	hypothetical protein SP_1949	769	NP_346377.1	2
22260	E04	SP1656	hypothetical protein SP_1656	742	NP_346095.1	5.31536388
22261	E05	SP0441	50S ribosomal protein L28	495	NP_344962.1	2
22263	E06	SP1455	hypothetical protein SP_1455	139	NP_345909.1	-
22264	E07	SP1401	hypothetical protein SP_1401	1773	NP_345859.1	13.9430344
22266	E08	SP0513	hypothetical protein SP_0513	554	NP_345031.1	4.34837545
22270	E09	SP0333	transcriptional regulator	402	NP_344868.1	2.87313433
22271	E10	SP0926	hypothetical protein SP_0926	882	NP_345410.1	9.50680272
22273	E11	SP1723	hypothetical protein SP_1723	1060	NP_346160.1	4.61698113
22275	E12	SP1042	hypothetical protein SP_1042	999	NP_345517.1	8.79179179
22276	F01	SP0679	hypothetical protein SP_0679	675	NP_345184.1	4.77333333
22278	F02	SP0997	hypothetical protein SP_0997	954	NP_345474.1	8.48637317
22280	F03	SP2133	hypothetical protein SP_2133	1615	NP_346551.1	3.95356037
22281	F04	SP0960	50S ribosomal protein L35	921	NP_345441.1	7.93159609
22282	F05	SP2118	hypothetical protein SP_2118	1516	NP_346537.1	3.04023747
22283	F06	SP1006	hypothetical protein SP_1006	960	NP_345482.1	8.36875
22284	F07	SP2183	hypothetical protein SP_2183	2008	NP_346594.1	3.80677291
22285	F08	SP1805	hypothetical protein SP_1805	199	NP_346238.1	2
22286	F09	SP0772	hypothetical protein SP_0772	756	NP_345270.1	8.82804233
22289	F10	SP2104	hypothetical protein SP_2104	1420	NP_346523.1	1.26830986
22290	F11	SP0217	50S ribosomal protein L29	306	NP_344757.1	3.85620915
22292	F12	SP1965	hypothetical protein SP_1965	802	NP_346392.1	2
22295	G01	SP1787	hypothetical protein SP_1787	169	NP_346220.1	2
22297	G02	SP1037	type II restriction endonuclease	990	NP_345512.1	7.51111111
22299	G03	SP0147	hypothetical protein SP_0147	252	NP_344689.1	14.3293651
22300	G04	SP0025	hypothetical protein SP_0025	105	NP_344576.1	-
22301	G05	SP1628	hypothetical protein SP_1628	628	NP_346068.1	4.39649682
22303	G06	SP1206	exodeoxyribonuclease VII small subunit	1218	NP_345673.1	7.5681445
22308	G07	SP0232	translation initiation factor IF-1	315	NP_344772.1	3.33333333
22309	G08	SP1300	hypothetical protein SP_1300	1341	NP_345764.1	12.7129008
22310	G09	SP0487	hypothetical protein SP_0487	534	NP_345005.1	4.36516854
22314	G10	SP1789	hypothetical protein SP_1789	169	NP_346222.1	2
22315	G11	SP0924	hypothetical protein SP_0924	876	NP_345408.1	8.34246575

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22316	G12	SP1657	hypothetical protein SP_1657	742	NP_346096.1	5.24797844
22319	H01	SP1755	hypothetical protein SP_1755	1438	NP_346190.1	3.054242
22322	H02	SP0951	hypothetical protein SP_0951	909	NP_345433.1	8.84818482
22328	H03	SP0279	hypothetical protein SP_0279	357	NP_344817.1	3.70028011
63442	H04	SP0541	bacteriocin BlpO	570	NP_345058.1	6.31578947
22330	H05	SP0861	hypothetical protein SP_0861	831	NP_345349.1	8.14681107
22331	H06	SP2115	hypothetical protein SP_2115	1510	NP_346534.1	3.62781457
22332	H07	SP0822	hypothetical protein SP_0822	795	NP_345314.1	8.15974843
22333	H08	SP1834	hypothetical protein SP_1834	268	NP_346267.1	2
22334	H09	SP0038	acyl carrier protein	111	NP_344588.1	-
22335	H10	SP0974	preprotein translocase subunit SecG	933	NP_345455.1	9.07609861
22336	H11	SP0029	hypothetical protein SP_0029	108	NP_344579.1	-
22337	H12	SP0171	ROK family protein	267	NP_344712.1	14.340824

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