

***Streptococcus pneumoniae* Gateway®  
Clone Set, Recombinant in *Escherichia coli*, Plate 4**

**Catalog No. NR-19571**

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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-19571 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 4, NR-19571.”

**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 4 (YSPCD)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22620	A01	SP0538	IS1381 transposase protein B	567	NP_345055.1	6.88
22621	A02	SP0490	hypothetical protein SP_0490	534	NP_345008.1	3.481
22626	A03	SP1476	hypothetical protein SP_1476	157	NP_345930.1	4
22629	A04	SP0434	hypothetical protein SP_0434	492	NP_344956.1	4.258
22630	A05	SP1410	hypothetical protein SP_1410	1842	NP_345868.1	13.22
22632	A06	SP1908	single-stranded DNA-binding protein	547	YP_873936.1	2
22633	A07	SP0564	hypothetical protein SP_0564	592	NP_345080.1	4.796
22637	A08	SP0544	immunity protein BlpX	573	NP_345061.1	3.991
22640	A09	SP0224	30S ribosomal protein S8	309	NP_344764.1	3.819
22642	A10	SP0727	transcriptional repressor	705	NP_345228.1	10.04
22644	A11	SP1405	transcriptional regulator Spx	1806	NP_345863.1	13.88
22645	A12	SP0536	immunity protein BlpL	567	NP_345053.1	5.713
22646	B01	SP2050	competence protein CglD	1267	NP_346474.1	3.23
22647	B02	SP0064	PTS system, IIA component	189	NP_344613.1	1.952
22649	B03	SP0884	hypothetical protein SP_0884	852	NP_345371.1	7.016
22650	B04	SP1477	hypothetical protein SP_1477	157	NP_345931.1	4
22651	B05	SP1995	hypothetical protein SP_1995	889	NP_346422.1	1.993
22652	B06	SP1142	hypothetical protein SP_1142	1140	NP_345612.1	9.636
22653	B07	SP2027	hypothetical protein SP_2027	1060	NP_346452.1	1.826
22655	B08	SP1924	hypothetical protein SP_1924	670	NP_346352.1	2
22656	B09	SP0521	HIT family protein	555	NP_345039.1	3.459
22657	B10	SP1641	hypothetical protein SP_1641	670	NP_346081.1	3.819
22658	B11	SP1959	nucleoside diphosphate kinase	796	NP_346386.1	2
22674	B12	SP1193	galactose-6-phosphate isomerase subunit LacA	1197	NP_345662.1	6.572
22675	C01	SP2089	transposase, IS1380-Spn1 related, truncation	1381	-	1.207
22676	C02	SP2062	MarR family transcriptional regulator	1291	NP_346486.1	1.341
22677	C03	SP1934	hypothetical protein SP_1934	714	NP_346362.1	2
22678	C04	SP0630	50S ribosomal protein L11	636	NP_345141.1	5.27
22681	C05	SP1516	acetyltransferase	196	NP_345966.1	3
22682	C06	SP1620	PTS system, nitrogen regulatory component IIA	526	NP_346061.1	3.992
22683	C07	SP2028	phosphotyrosine protein phosphatase	1066	NP_346453.1	1.805
22686	C08	SP1545	hypothetical protein SP_1545	229	NP_345992.1	3.9
22687	C09	SP1011	GtrA family protein	963	NP_345487.1	7.264

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22688	C10	SP1023	acetyltransferase	978	NP_345498.1	8.585
22689	C11	SP2164	PTS system, IIA component	1810	NP_346578.1	2.204
22690	C12	SP0321	PTS system, IIA component	387	NP_344857.1	2.868
22692	D01	SP2068	cytidine/deoxycytidylate deaminase family protein	1303	NP_346491.1	1.487
22693	D02	SP0033	hypothetical protein SP_0033	108	NP_344583.1	-
22695	D03	SP0128	ribosomal-protein-alanine acetyltransferase,	240	NP_344674.1	13.83
22701	D04	SP0161	hypothetical protein SP_0161	264	NP_344703.1	8.807
22702	D05	SP0870	NifU family protein	837	NP_345357.1	7.612
22703	D06	SP1760	hypothetical protein SP_1760	118	NP_346195.1	1.992
22704	D07	SP2090	transcriptional regulator	1381	NP_346509.1	1.398
22709	D08	SP0021	deoxyuridine 5'-triphosphate nucleotidohydrolase	105	NP_344573.1	-
22713	D09	SP1437	hypothetical protein SP_1437	130	NP_345893.1	3
22715	D10	SP1944	hypothetical protein SP_1944	757	NP_346372.1	2
22721	D11	SP1807	acetyltransferase	199	NP_346240.1	-
22722	D12	SP1730	hypothetical protein SP_1730	1123	NP_346166.1	3.308
22723	E01	SP1915	hypothetical protein SP_1915	598	NP_346343.1	2
22725	E02	SP0565	hypothetical protein SP_0565	594	NP_345081.1	4.072
22726	E03	SP1920	MarR family transcriptional regulator	625	NP_346348.1	2
22728	E04	SP1135	hypothetical protein SP_1135	1134	NP_345605.1	10.22
22729	E05	SP1691	hypothetical protein SP_1691	910	NP_346130.1	4.993
22730	E06	SP1996	universal stress protein	892	NP_346423.1	2
22731	E07	SP1680	hypothetical protein SP_1680	849	NP_346119.1	5.349
22733	E08	SP2204	50S ribosomal protein L9	2098	NP_346615.1	2.686
63461	E09	SP1442	IS66 family Orf2	130	NP_345896.1	-
22736	E10	SP0812	transposase	789	-	8.942
22737	E11	SP0740	MutT/nudix family protein	720	NP_345239.1	13.06
22738	E12	SP0119	MutT/nudix family protein	237	NP_344665.1	14
22739	F01	SP0595	hypothetical protein SP_0595	615	NP_345108.1	3.839
22740	F02	SP1327	hypothetical protein SP_1327	1368	NP_345785.1	12.77
22741	F03	SP2195	transcriptional regulator CtsR	2032	NP_346606.1	2.442
22742	F04	SP0198	hypothetical protein SP_0198	294	NP_344738.1	1.99
22743	F05	SP0160	hypothetical protein SP_0160	264	NP_344702.1	17.31
22744	F06	SP2048	hypothetical protein SP_2048	1234	NP_346472.1	4.033
22746	F07	SP2081	hypothetical protein SP_2081	1348	NP_346501.1	1.388
22748	F08	SP1774	transcriptional regulator	142	NP_346207.1	2
22750	F09	SP1597	hypothetical protein SP_1597	415	NP_346041.1	4
22752	F10	SP1168	mutator MutT protein	1176	NP_345637.1	8.032
22753	F11	SP1777	7-cyano-7-deazaguanine reductase	145	NP_346210.1	2
22754	F12	SP1235	MutT/nudix family protein	1254	NP_345701.1	9.364
22756	G01	SP0175	6,7-dimethyl-8-ribityllumazine synthase	276	NP_344716.1	3.775
22758	G02	SP0976	SsrA-binding protein	933	NP_345457.1	7.846
22760	G03	SP0744	cytidine and deoxycytidylate deaminase family protein	726	NP_345243.1	12.05
22761	G04	SP2163	PTS system, IIB component	1801	NP_346577.1	2.68
22762	G05	SP1785	hypothetical protein SP_1785	166	NP_346218.1	2
22763	G06	SP1540	single-stranded DNA-binding protein	220	NP_345988.1	3
22764	G07	SP0158	flavoprotein NrdI	261	NP_344700.1	17

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22766	G08	SP0272	30S ribosomal protein S7	354	NP_344810.1	2.836
22767	G09	SP1064	IS200 family transposase	1017	NP_345538.1	10.59
22768	G10	SP1622	IS200 family transposase	544	NP_346062.1	3.994
22769	G11	SP1713	transcriptional regulator NrdR	1033	NP_346151.1	3.495
22770	G12	SP0982	IS3-Spn1, transposase	936	-	9.1
22771	H01	SP1370	shikimate kinase	1377	NP_345828.1	2.73
22772	H02	SP1050	transcriptional regulator,	1005	NP_345524.1	10.58
22773	H03	SP0446	acetolactate synthase 3 regulatory subunit	498	NP_344967.1	3.781
22774	H04	SP1604	hypothetical protein SP_1604	451	NP_346048.1	3.996
22775	H05	SP1321	V-type ATP synthase subunit K	1344	NP_345779.1	12.82
22776	H06	SP1926	hypothetical protein SP_1926	676	NP_346354.1	2
22777	H07	SP0313	glutathione peroxidase	378	NP_344850.1	2.788
22778	H08	SP0061	PTS system, IIB component	186	NP_344610.1	2
22779	H09	SP2006	transcriptional regulator ComX2	928	NP_346433.1	2
22781	H10	SP0014	transcriptional regulator ComX1	99	NP_344567.1	-
22782	H11	SP0552	hypothetical protein SP_0552	585	NP_345068.1	3.232
22783	H12	SP2238	rRNA large subunit methyltransferase	2446	NP_346645.1	3.434

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