

***Streptococcus pneumoniae* Gateway®  
Clone Set, Recombinant in *Escherichia coli*, Plate 5****Catalog No. NR-19572**

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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-19572.

**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-19572 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 5, NR-19572."

**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 5 (YSPCE)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22784	A01	SP0769	VanZF-related protein	753	NP_345267.1	9.520584
22785	A02	SP0985	regulatory protein	942	NP_345464.1	7.972399
22786	A03	SP1517	transcription elongation factor GreA	196	NP_345967.1	2.984694
22787	A04	SP0340	S-ribosylhomocysteinase	408	NP_344874.1	3.046569
22788	A05	SP1831	hypothetical protein SP_1831	262	NP_346264.1	2
22789	A06	SP0440	-	495	-	1.979798
22790	A07	SP2036	PTS system, IIA component	1123	NP_346461.1	3.926091
22791	A08	SP0423	acetyl-CoA carboxylase biotin carboxyl carrier protein subunit	480	NP_344946.1	3.6
22795	A09	SP1422	hypothetical protein SP_1422	1941	NP_345879.1	13.16332
22796	A10	SP0323	PTS system, IIB component	387	NP_344859.1	3.276486
22799	A11	SP1519	acetyltransferase	196	NP_345969.1	3
22800	A12	SP2217	rod shpae-determining protein MreD	2194	NP_346625.1	2.474476
22801	B01	SP1464	acetyltransferase	148	NP_345918.1	2
22802	B02	SP0227	30S ribosomal protein S5	312	NP_344767.1	4.785256
22805	B03	SP0967	metalloprotease	927	NP_345448.1	9.023732
22806	B04	SP0645	PTS system IIA component,	644	NP_345152.1	4.731366
22808	B05	SP0864	hypothetical protein SP_0864	820	NP_345351.1	9.159756
22809	B06	SP0732	transposase	711	-	13.69339
22810	B07	SP0950	acetyltransferase	909	NP_345432.1	9.086909
22811	B08	SP1745	isochorismatase family protein	1309	NP_346181.1	3.666157
22812	B09	SP1355	50S ribosomal protein L10	1485	NP_345813.1	12.47273
22813	B10	SP0794	MutT/nudix family protein	771	NP_345291.1	9.542153
22814	B11	SP1916	PAP2 family protein	601	NP_346344.1	2
22815	B12	SP0486	RNA methyltransferase	534	NP_345004.1	2.910112
22816	C01	SP0628	HIT family protein	633	NP_345139.1	3.456556
22817	C02	SP0204	acetyltransferase	297	NP_344744.1	4.26936
22818	C03	SP1571	dihydrofolate reductase	301	NP_346018.1	2
22821	C04	SP1194	-	1200	-	6.650833
22822	C05	SP0049	vanZ protein	174	NP_344598.1	2
22823	C06	SP1012	hypothetical protein SP_1012	963	NP_345488.1	8.915888
22825	C07	SP0580	acetyltransferase	606	NP_345094.1	4.29868
22827	C08	SP0767	hypothetical protein SP_0767	747	NP_345265.1	7.353414
22828	C09	SP1533	hypothetical protein SP_1533	205	NP_345981.1	3
22830	C10	SP0834	hemolysin-related protein	804	NP_345325.1	8.945274
22831	C11	SP1577	adenine phosphoribosyltransferase	322	NP_346023.1	1.993789

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22832	C12	SP1234	biotin repressor family transcriptional regulator	1254	NP_345700.1	8.229665
22833	D01	SP0022	hypothetical protein SP_0022	105	NP_344574.1	-
22837	D02	SP0430	hypothetical protein SP_0430	483	NP_344953.1	5.759834
22838	D03	SP1943	acetyltransferase	751	NP_346371.1	2
22839	D04	SP0778	16S rRNA-processing protein RimM	759	NP_345276.1	9.121212
22840	D05	SP1651	thiol peroxidase	709	NP_346090.3	5.122708
22841	D06	SP2211	transposase	2140	-	2.528037
22842	D07	SP1879	hypothetical protein SP_1879	451	NP_346311.1	2
22843	D08	SP1640	hypothetical protein SP_1640	667	NP_346080.1	5
22844	D09	SP1278	bifunctional pyrimidine regulatory protein PyrR/uracil phosphoribosyltransferase	1317	NP_345742.1	13.21488
22845	D10	SP0837	topology modulation protein	807	NP_345328.1	9.392813
22846	D11	SP0723	hypothetical protein SP_0723	702	NP_345224.1	11.0755
22847	D12	SP0516	heat shock protein GrpE	555	NP_345034.1	4.985586
22848	E01	SP0500	hypothetical protein SP_0500	540	NP_345018.1	3.177778
22849	E02	SP2191	hypothetical protein SP_2191	2023	NP_346602.1	3.702422
22850	E03	SP1750	hypothetical protein SP_1750	1342	NP_346186.1	3.201192
22851	E04	SP0371	hypothetical protein SP_0371	447	NP_344898.1	4.798658
22852	E05	SP2155	-	1726	-	2.35168
22853	E06	SP1463	methylated-DNA--protein-cysteine S-methyltransferase	148	NP_345917.1	2
22854	E07	SP0879	hypothetical protein SP_0879	846	NP_345366.1	8.040189
22855	E08	SP1903	hypothetical protein SP_1903	529	NP_346334.1	2
22856	E09	SP1511	F0F1 ATP synthase subunit delta	187	NP_345962.1	3
22857	E10	SP1572	non-heme iron-containing ferritin	310	NP_346019.1	4
22858	E11	SP0783	hypothetical protein SP_0783	762	NP_345280.1	8.472441
22859	E12	SP0180	DNA-3-methyladenine glycosylase I	282	NP_344721.1	3.687943
22861	F01	SP2007	transcription antitermination protein NusG	931	NP_346434.1	1.934479
22862	F02	SP0225	50S ribosomal protein L6	309	NP_344765.1	5.158576
22863	F03	SP1969	type II DNA modification methyltransferase,	820	NP_346396.1	2
22864	F04	SP2095	5-formyltetrahydrofolate cyclo-ligase family protein	1396	NP_346514.1	1.218481
22866	F05	SP1664	hypothetical protein SP_1664	784	NP_346103.1	5.159439
22867	F06	SP0830	hypothetical protein SP_0830	801	NP_345321.1	9.174782
22868	F07	SP1189	hypothetical protein SP_1189	1194	NP_345658.1	3.369347
22869	F08	SP1280	hypothetical protein SP_1280	1320	NP_345744.1	12.21591
22870	F09	SP0012	hypoxanthine-guanine phosphoribosyltransferase	99	NP_344565.1	-
22871	F10	SP0221	50S ribosomal protein L5	309	NP_344761.1	5.239482
22872	F11	SP0332	hypothetical protein SP_0332	399	NP_344867.1	2.85213
22874	F12	SP2222	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	2230	NP_346630.1	2.46009
22876	G01	SP0048	phosphoribosylglycinamide formyltransferase	171	NP_344597.1	2
22877	G02	SP0482	hypothetical protein SP_0482	531	NP_345001.1	3.446328
22878	G03	SP0405	hypothetical protein SP_0405	471	NP_344928.1	4.791932
22879	G04	SP0409	hypothetical protein SP_0409	474	NP_344932.1	4.763713

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22880	G05	SP2206	ribosomal subunit interface protein	2119	NP_346617.1	2.163756
22882	G06	SP1082	acetyltransferase	1047	NP_345555.1	8.142311
22883	G07	SP1231	phosphopantothenoylcysteine decarboxylase	1248	NP_345697.1	6.728365
22884	G08	SP0804	4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein,	777	NP_345301.1	9.368082
22885	G09	SP0291	GTP cyclohydrolase I	363	NP_344829.1	3.732782
22887	G10	SP1532	-	205	-	-
22888	G11	SP0652	hypothetical protein SP_0652	648	NP_345157.1	4.740741
22890	G12	SP1430	restriction endonuclease	2289	-	11.43687
22891	H01	SP0959	translation initiation factor IF-3	918	NP_345440.1	7.738562
22892	H02	SP0945	ribosome recycling factor	903	NP_345428.1	8.953488
22893	H03	SP0743	TetR family transcriptional regulator	726	NP_345242.1	10.99311
22894	H04	SP0074	acetyltransferase	198	NP_344623.1	-
22895	H05	SP0165	flavoprotein	264	NP_344707.1	14.35985
22897	H06	SP1284	hypothetical protein SP_1284	1326	NP_345748.1	13.07919
22898	H07	SP0435	elongation factor P	492	NP_344957.1	3.804878
22899	H08	SP1779	hypothetical protein SP_1779	154	NP_346212.1	-
22900	H09	SP1990	primase-related protein	880	NP_346417.1	1.928409
22901	H10	SP0566	acetyltransferase	594	NP_345082.1	4.415825
22902	H11	SP0663	hypothetical protein SP_0663	657	NP_345168.1	5.401826
22903	H12	SP1232	hypothetical protein SP_1232	1248	NP_345698.1	6.753205

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