

***Streptococcus pneumoniae* Gateway®
Clone Set, Recombinant in *Escherichia coli*, Plate 2**

Catalog No. NR-19569

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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.¹ 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-19569.

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-19569 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 2, NR-19569.”

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.

Disclaimers:

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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 2 (YSPCB)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22338	A01	SP0142	hypothetical protein SP_0142	252	NP_344684.1	16.9365079
22339	A02	SP0122	hypothetical protein SP_0122	237	NP_344668.1	13.8902954
22340	A03	SP0560	hypothetical protein SP_0560	588	NP_345076.1	4.28741497
22343	A04	SP0888	hypothetical protein SP_0888	858	NP_345375.1	8.10955711
22344	A05	SP0431	hypothetical protein SP_0431	486	NP_344954.1	4.75925926
22347	A06	SP1459	hypothetical protein SP_1459	142	NP_345913.1	4
22349	A07	SP0365	IS66 family Orf1	438	-	2.46803653
22350	A08	SP1443	IS66 family Orf1	130	NP_345897.1	3
22352	A09	SP0304	hypothetical protein SP_0304	369	NP_344841.1	3.68834688
22353	A10	SP0389	hypothetical protein SP_0389	459	NP_344915.1	3.80392157
22354	A11	SP0776	KH domain-containing protein	756	NP_345274.1	9.11243386
22355	A12	SP0782	hypothetical protein SP_0782	762	NP_345279.1	8.43175853
22357	B01	SP1806	hypothetical protein SP_1806	199	NP_346239.1	2
22358	B02	SP2174	D-alanine--poly(phosphoribitol) ligase subunit 2	1963	NP_346588.1	3.46001019
22359	B03	SP1539	30S ribosomal protein S18	220	NP_345987.1	3
22360	B04	SP1385	hypothetical protein SP_1385	1689	NP_345843.1	13.1367673
22361	B05	SP1299	50S ribosomal protein L31 type B	1341	NP_345763.1	12.7912006
22362	B06	SP0018	hypothetical protein SP_0018	102	NP_344570.1	-
22363	B07	SP1495	hypothetical protein SP_1495	169	NP_345947.1	4
22364	B08	SP1873	hypothetical protein SP_1873	423	NP_346305.1	2
22365	B09	SP0640	hypothetical protein SP_0640	642	NP_345150.1	4.12149533
22366	B10	SP1480	hypothetical protein SP_1480	160	NP_345934.1	3
22368	B11	SP0123	competence-induced protein Ccs1	237	NP_344669.1	14
22369	B12	SP0561	hypothetical protein SP_0561	591	NP_345077.1	4.11844332
22371	C01	SP0748	hypothetical protein SP_0748	729	NP_345247.1	13.0082305
22375	C02	SP1302	hypothetical protein SP_1302	1341	NP_345765.1	12.1603281
22376	C03	SP1059	hypothetical protein SP_1059	1014	NP_345533.1	10.8481262
22378	C04	SP0682	hypothetical protein SP_0682	678	NP_345187.1	5.06047198
22379	C05	SP1494	hypothetical protein SP_1494	166	NP_345946.1	3
22380	C06	SP0563	hypothetical protein SP_0563	591	NP_345079.1	4.85617597
22381	C07	SP1596	hypothetical protein SP_1596	415	NP_346040.1	3.87951807
22383	C08	SP1350	hypothetical protein SP_1350	1473	NP_345808.1	12.2830957
22384	C09	SP1740	hypothetical protein SP_1740	1240	NP_346176.1	3.41774194

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22385	C10	SP1223	hypothetical protein SP_1223	1233	NP_345689.1	7.55555556
22386	C11	SP0653	hypothetical protein SP_0653	648	NP_345158.1	5.68364198
22387	C12	SP1741	hypothetical protein SP_1741	1264	NP_346177.1	2.1914557
22388	D01	SP1473	hypothetical protein SP_1473	154	NP_345927.1	3
22389	D02	SP1658	hypothetical protein SP_1658	748	NP_346097.1	3.46925134
22390	D03	SP2049	hypothetical protein SP_2049	1237	NP_346473.1	1.5650768
22391	D04	SP0067	hypothetical protein SP_0067	195	NP_344616.1	3.96923077
22392	D05	SP1930	hypothetical protein SP_1930	706	NP_346358.1	2
22393	D06	SP0218	30S ribosomal protein S17	309	NP_344758.1	3.25566343
22394	D07	SP1663	hypothetical protein SP_1663	775	NP_346102.1	4.45419355
22395	D08	SP1177	phosphocarrier protein HPr	1182	NP_345646.1	8.95093063
22396	D09	SP0275	hypothetical protein SP_0275	354	NP_344813.1	3.14689266
22399	D10	SP2202	hypothetical protein SP_2202	2077	NP_346613.1	4.17862301
22402	D11	SP0201	hypothetical protein SP_0201	297	NP_344741.1	5.6026936
22403	D12	SP1132	hypothetical protein SP_1132	1128	NP_345602.1	10.3235816
22406	E01	SP0448	hypothetical protein SP_0448	501	NP_344969.1	4.39520958
22408	E02	SP1312	transposase	1344	-	13.0141369
22409	E03	SP0007	S4 domain-containing protein	96	NP_344560.1	-
22410	E04	SP0192	hypothetical protein SP_0192	291	NP_344733.1	4.82130584
22412	E05	SP0532	bacteriocin BlpJ	561	NP_345049.1	6.26559715
22414	E06	SP0587	hypothetical protein SP_0587	609	NP_345100.1	3.8226601
22416	E07	SP1626	30S ribosomal protein S15	622	NP_346066.1	4.67363344
22417	E08	SP1256	hypothetical protein SP_1256	1275	NP_345721.1	8.17176471
22418	E09	SP0910	hypothetical protein SP_0910	870	NP_345395.1	6.64137931
22419	E10	SP0775	30S ribosomal protein S16	756	NP_345273.1	8.6005291
22422	E11	SP0276	hypothetical protein SP_0276	354	NP_344814.1	3.67231638
22426	E12	SP2037	PTS system, IIB component	1126	NP_346462.1	1.51332149
22427	F01	SP0213	30S ribosomal protein S19	303	NP_344753.1	1.38283828
22429	F02	SP0639	hypothetical protein SP_0639	642	NP_345149.1	4.46417445
22430	F03	SP2130	PTS system, IIB component,	1594	NP_346548.1	3.62045169
22433	F04	SP1907	co-chaperonin GroES	541	NP_346337.1	2
22434	F05	SP1107	50S ribosomal protein L27	1089	NP_345578.1	10.1606979
22435	F06	SP1703	hypothetical protein SP_1703	952	NP_346141.1	4.82457983
22436	F07	SP0520	hypothetical protein SP_0520	555	NP_345038.1	4.95495495
22439	F08	SP1728	hypothetical protein SP_1728	1111	NP_346165.1	4.0810081
22440	F09	SP0800	hypothetical protein SP_0800	774	NP_345297.1	7.88372093
22441	F10	SP1102	hypothetical protein SP_1102	1080	NP_345573.1	10.5138889
22442	F11	SP2199	hypothetical protein SP_2199	2065	NP_346610.1	2.54188862
22443	F12	SP1541	30S ribosomal protein S6	220	NP_345989.1	3
22445	G01	SP0554	hypothetical protein SP_0554	585	NP_345070.1	5.64786325
22446	G02	SP0326	preprotein translocase, YajC subunit	387	NP_344862.1	3.30749354
22447	G03	SP1144	hypothetical protein SP_1144	1140	NP_345614.1	9.31578947
22448	G04	SP0211	50S ribosomal protein L23	297	NP_344751.1	3.48148148
22449	G05	SP0735	6-phospho-beta-glucosidase, truncation	711	-	13.0914205
22450	G06	SP1864	hypothetical protein SP_1864	373	NP_346296.1	1.98123324
22451	G07	SP1832	hypothetical protein SP_1832	265	NP_346265.1	2
22452	G08	SP0998	hypothetical protein SP_0998	954	NP_345475.1	8.94025157
22453	G09	SP1535	hypothetical protein SP_1535	211	NP_345983.1	3
22455	G10	SP0555	hypothetical protein SP_0555	585	NP_345071.1	5.08034188
22457	G11	SP0816	hypothetical protein SP_0816	792	NP_345309.1	8.52146465

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22458	G12	SP1912	hypothetical protein SP_1912	580	NP_346341.1	2
22459	H01	SP1496	transposase, IS630-Spn1 related, Orf2	172	NP_345948.1	2
22460	H02	SP0983	-	939	-	8.84025559
22462	H03	SP1913	hypothetical protein SP_1914	589		2
22463	H04	SP1635	hypothetical protein SP_1635	664	NP_346075.1	4
22465	H05	SP1197	hypothetical protein SP_1197	1209	NP_345664.1	6.09015715
63441	H06	SP1452	hypothetical protein SP_1452	136	NP_345906.1	3
22467	H07	SP0438	aspartyl/glutamyl-tRNA amidotransferase subunit C	495	NP_344960.1	2
22469	H08	SP0194	hypothetical protein SP_0194	291	NP_344734.1	3.3814433
22470	H09	SP0646	PTS system, IIB component,	645	NP_345153.1	4.94883721
22472	H10	SP0249	PTS system, IIB component	324	NP_344788.1	3.27160494
22473	H11	SP2023	PTS system, IIB component	1027	NP_346448.1	1.78870497
22474	H12	SP2178	conserved hypothetical protein, interruption	1990	-	2.69849246

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