Streptococcus pneumoniae Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 3

Catalog No. NR-19570

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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. pneumonia*, 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 *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR™221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 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-19570.

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-19570 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 3, NR-19570."

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.

Disclaimers:

You are authorized to use this product for research use only. It is not intended for human use.

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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.

Support Provided by NIAID

Table 1: *Streptococcus pneumoniae* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 3 (YSPCC)[1]

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22475	A01	SP1141	hypothetical protein SP_1141	1137	NP_345611.1	9.516271
22476	A02	SP0404	hypothetical protein SP_0404	468	NP_344927.1	5.760684
22477	A03	SP1955	hypothetical protein SP_1955	784	NP_346382.1	2
22478	A04	SP1737	DNA-directed RNA polymerase subunit omega	1207	NP_346173.1	3.275891
22479	A05	SP2102	hypothetical protein SP_2102	1414	NP_346521.1	1.336634
22481	A06	SP1748	hypothetical protein SP_1748	1321	NP_346184.1	3.654807
22482	A07	SP1428	hypothetical protein SP_1428	2220	NP_345885.1	12.29595
22483	A08	SP1060	hypothetical protein SP_1060	1014	NP_345534.1	9.06213
22484	A09	SP0031	hypothetical protein SP_0031	108	NP_344581.1	-
22486	A10	SP0305	cellobiose phosphotransferase system IIB component	370	NP_344842.1	3.689189
22487	A11	SP0308	cellobiose phosphotransferase system IIA component	375	NP_344845.1	3.288
22488	A12	SP1986	hypothetical protein SP_1986	871	NP_346413.1	2
22489	B01	SP1776	thioredoxin	142	NP_346209.1	2
22490	B02	SP1186	PTS system, lactose-specific IIA component	1191	NP_345655.1	5.712846
22491	B03	SP1911	thioredoxin,	577	NP_346340.1	2
22492	B04	SP0937	DNA replication intiation control protein YabA	888	NP_345421.1	8.056306
22493	B05	SP1047	hypothetical protein SP_1047	1005	NP_345521.1	9.833831
22494	B06	SP0335	cell division protein FtsL	402	NP_344870.1	3.674129
22495	B07	SP0114	hypothetical protein SP_0114	234	NP_344660.1	16
22496	B08	SP0108	hypothetical protein SP_0108	231	NP_344655.1	8.930736
22497	B09	SP0650	hypothetical protein SP_0650	648	NP_345156.1	5.669753
22498	B10	SP1318	V-type ATP synthase subunit F	1344	NP_345776.1	12.41295
22499	B11	SP0248	PTS system, IIA component	324	NP_344787.1	2.858025
22500	B12	SP0781	hypothetical protein SP_0781	762	NP_345278.1	9.586614
22501	C01	SP0789	hypothetical protein SP_0789	768	NP_345286.1	9.536458
22506	C02	SP1497	-	172	NP_345948.1	3
22507	C03	SP2051	competence protein CglC	1273	-	1.362137
22508	C04	SP1618	PTS system, IIB component	481	NP_346059.1	4
22509	C05	SP0100	hypothetical protein SP_0100	228	NP_344647.1	8.960526
22510	C06	SP2024	PTS system, IIA component	1045	NP_346449.1	3.113876

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22511	C07	SP0030	competence-induced protein Ccs16	108	NP_344580.1	-
22518	C08	SP1288	DNA-binding protein	1329	NP_345752.1	12.78179
22532	C09	SP1602	phnA protein	433	NP_346046.1	2.990762
22533	C10	SP0344	IS630-Spn1, transposase Orf2	411	NP_344878.1	3.717762
22534	C11	SP1372	hypothetical protein SP_1372	1644	NP_345830.1	13.12774
22535	C12	SP2125	hypothetical protein SP_2125	1555	NP_346543.1	4.106109
22536	D01	SP0634	hypothetical protein SP_0634	639	NP_345144.1	4.760563
22538	D02	SP1106	hypothetical protein SP_1106	1083	NP_345577.1	9.779317
22539	D03	SP0476	PTS system, lactose-specific IIA component	525	NP_344995.1	4.401905
22541	D04	SP1679	hypothetical protein SP_1679	844	NP_346118.1	4.822275
22542	D05	SP1293	50S ribosomal protein L19	1335	NP_345757.1	12.46442
22543	D06	SP1499	bacterocin transport accessory protein	178	NP_345950.1	-
22544	D07	SP0299	IS630-Spn1, transposase Orf1, authentic frameshift	366	NP_344837.1	3.699454
22545	D08	SP1093	hypothetical protein SP_1093	1065	NP_345565.1	8.042254
22548	D09	SP0731	hypothetical protein SP_0731	708	NP_345232.1	13.03814
22549	D10	SP0514	hypothetical protein SP_0514	555	NP_345032.1	4.118919
22554	D12	SP0557	ribosome-binding factor A	585	NP_345073.1	5.982906
22555	E01	SP0703	hypothetical protein SP_0703	693	NP_345207.1	12.68975
22556	E02	SP0131	-	243	-	11.84774
22558	E03	SP1856	MerR family transcriptional regulator	364	NP_346288.1	2
22560	E04	SP1462	hypothetical protein SP_1462	145	NP_345916.1	2
22561	E05	SP0501	MerR family transcriptional regulator	540	NP_345019.1	4.437037
22562	E06	SP0226	50S ribosomal protein L18	312	NP_344766.1	3.432692
22563	E07	SP1054	Tn5252, ORF 10 protein	1008	NP_345528.1	10.89087
22564	E08	SP0449	hypothetical protein SP_0449	501	NP_344970.1	3.806387
22565	E09	SP1255	hypothetical protein SP_1255	1272	NP_345720.1	5.492138
22566	E10	SP0961	50S ribosomal protein L20	921	NP_345442.1	8.235613
22567	E11	SP2061	hypothetical protein SP_2061	1291	NP_346485.1	1.88536
22568	E12	SP1261	hypothetical protein SP_1261	1284	NP_345725.1	13.06308
22569	F01	SP1935	hypothetical protein SP_1935	724	NP_346363.1	2
22570	F02	SP1537	hypothetical protein SP_1537	211	NP_345985.1	3
22571	F03	SP1917	ABC transporter ATP-binding protein	601	NP_346345.1	2
22572	F04	SP1699	4'-phosphopantetheinyl transferase	946	NP_346137.1	3.343552
22573	F05	SP0633	hypothetical protein SP_0633	639	NP_345143.1	5.103286
22574	F06	SP0302	hypothetical protein SP_0302	369	NP_344839.1	3.948509
22575	F07	SP1143	hypothetical protein SP_1143	1140	NP_345613.1	5.905263
22576	F08	SP1281	hypothetical protein SP_1281	1320	NP_345745.1	11.57348
22577	F09	SP0442	hypothetical protein SP_0442	496	NP_344963.1	3.800403
22579	F10	SP1543	-	225	-	3
22580	F11	SP1714	GntR family transcriptional regulator	1036	NP_346152.1	4.124517
22581	F12	SP1055	Tn5252, ORF 9 protein	1008	NP_345529.1	10.63988
22582	G01	SP1354	50S ribosomal protein L7/L12	1485	NP_345812.1	12.38519
22583	G02	SP0219	50S ribosomal protein L14	309	NP_344759.1	3.080906
22584	G03	SP0008	hypothetical protein SP_0008	96	NP_344561.1	-
22585	G04	SP1822	hypothetical protein SP_1822	241	NP_346255.1	2
22586	G05	SP2226	hypothetical protein SP_2226	2293	NP_346634.1	4.10205
22588	G06	SP0293	hypothetical protein SP_0293	363	NP_344831.1	2.688705
22591	G07	SP2054	hypothetical protein SP_2054	1285	NP_346478.1	1.501167

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Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
22592	G08	SP0728	hypothetical protein SP_0728	708	NP_345229.1	11.04802
22593	G09	SP1719	-	1045	-	3.494737
22594	G10	SP1295	camphor resistance protein CrcB	1335	NP_345759.1	11.95655
22595	G11	SP1173	phosphotransferase mannose-specific family component IIA	1179	NP_345642.1	8.471586
22596	G12	SP1289	hypothetical protein SP_1289	1332	NP_345753.1	12.83408
22597	H01	SP1841	hypothetical protein SP_1841	301	NP_346274.1	-
22599	H02	SP1053	hypothetical protein SP_1053	1008	NP_345527.1	9.805556
22601	H03	SP1348	hypothetical protein SP_1348	1470	NP_345806.1	11.92789
22603	H04	SP0115	hypothetical protein SP_0115	234	NP_344661.1	15.94444
22605	H05	SP0696	hypothetical protein SP_0696	690	NP_345201.1	12.02319
22606	H06	SP0678	hypothetical protein SP_0678	675	NP_345183.1	3.645926
22609	H07	SP1411	hypothetical protein SP_1411	1869	NP_345869.1	13.8031
22611	H08	SP0597	-	615	-	4.452033
22612	H09	SP0237	50S ribosomal protein L17	318	NP_344777.1	4.232704
22617	H10	SP0537	IS1381 transposase protein A	567	NP_345054.1	4.412698
22618	H11	SP0844	cytidine deaminase	816	NP_345335.1	9.030637
22619	H12	SP1630	hypothetical protein SP_1630	637	NP_346070.1	5

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

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