

***Streptococcus pneumoniae* Gateway®
Clone Set, Recombinant in *Escherichia coli*, Plate 20****Catalog No. NR-19587**

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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.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-19587.

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-19587 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 20, NR-19587."

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:

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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 20 (YSPCU)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
79842	A01	SP1707	hypothetical protein SP_1707	970	NP_346145.1	4.01546392
80111	A02	SP0525	BlpS protein	558	NP_345043.1	1.59139785
79963	A03	SP0016	IS630-Spn1, transposase Orf2	102	NP_344569.1	-
80107	A04	SP0300	IS630-Spn1, transposase Orf2	366	NP_344838.1	3.18579235
79915	A05	SP0214	50S ribosomal protein L22	303	NP_344754.1	4.15511551
79769	A06	SP0345	IS630-Spn1 transposase	423	YP_873925.1	2.44917258
79831	A07	SP0818	IS630-Spn1 transposase	792	YP_873929.1	8.59090909
79925	A08	SP1131	transcriptional regulator	1125	NP_345601.1	10.7164444
79770	A09	SP0234	30S ribosomal protein S13	315	NP_344774.1	3.79047619
79890	A10	SP1010	large conductance mechanosensitive channel protein MscL	963	NP_345486.1	9.09241952
80004	A11	SP1846	-	304	-	2
79855	A12	SP1558	hypothetical protein SP_1558	256	NP_346005.1	4
79868	B01	SP1085	transposase	1050	-	9.66761905
79751	B02	SP1927	IS1381 transposase protein A	688	NP_346355.1	-
79994	B03	SP1424	hypothetical protein SP_1424	1944	NP_345881.1	12.9562757
79847	B04	SP0216	50S ribosomal protein L16	306	NP_344756.1	2
79826	B05	SP0271	30S ribosomal protein S12	351	NP_344809.1	2.84900285
80047	B06	SP2047	hypothetical protein SP_2047	1231	NP_346471.1	1.54102356
79906	B07	SP0256	acetyltransferase	342	NP_344795.1	3.25730994
80043	B08	SP1507	F0F1 ATP synthase subunit epsilon	184	NP_345958.1	3
79811	B09	SP0113	argininosuccinate synthase	234	-	12.9358974
79930	B10	SP1794	hypothetical protein SP_1794	175	NP_346227.1	1.98857143
79754	B11	SP1783	MutT/nudix family protein	163	NP_346216.1	2
79819	B12	SP1203	transcriptional repressor,	1212	NP_345670.1	6.82260726
80080	C01	SP0396	PTS system, mannitol-specific IIA component	465	NP_344920.1	5.77634409
80067	C02	SP1614	-	475	-	4
80086	C03	SP2172	adc operon repressor AdcR	1927	NP_346586.1	3.89154126
80037	C04	SP1863	MarR family transcriptional regulator	373	NP_346295.1	2
79976	C05	SP0294	50S ribosomal protein L13	363	NP_344832.1	3.75757576
79904	C06	SP2077	transcriptional repressor	1324	NP_346498.1	1.20845921
79758	C07	SP1465	hypothetical protein SP_1465	148	NP_345919.1	3

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
80040	C08	SP0909	hypothetical protein SP_0909	870	NP_345394.1	8.82298851
79815	C09	SP1619	PTS system, IIA component	499	NP_346060.1	2
79884	C10	SP1786	hypothetical protein SP_1786	166	NP_346219.1	2
80052	C11	SP0364	-	438	-	3.23515982
79970	C12	SP0928	lipoprotein signal peptidase	882	NP_345412.1	8.29931973
80024	D01	SP1878	CBS domain-containing protein	448	NP_346310.1	2
79840	D02	SP0893	transcriptional repressor	858	NP_345380.1	8.06060606
79776	D03	SP1019	acetyltransferase	972	NP_345494.1	9.01131687
80103	D04	SP1968	phosphopantetheine adenylyltransferase	817	NP_346395.1	2
79802	D05	SP0053	phosphoribosylaminoimidazole carboxylase catalytic subunit	180	NP_344602.1	-
79947	D06	SP1512	F0F1 ATP synthase subunit B	190	NP_345963.1	4
79874	D07	SP0307	PTS system, IIA component	372	NP_344844.1	1.83064516
79880	D08	SP1384	hypothetical protein SP_1384	1689	NP_345842.1	13.1598579
79986	D09	SP0309	hypothetical protein SP_0309	375	NP_344846.1	3.27733333
79913	D10	SP1453	hypothetical protein SP_1453	136	NP_345907.1	3.98529412
80293	D11	SP0939	hypothetical protein SP_0939	894	NP_345423.1	8.85682327
80285	D12	SP1858	TetR family transcriptional regulator	370	NP_346290.1	2
80299	E01	SP2234	TetR family transcriptional regulator	2371	NP_346641.1	3.82623366
80197	E02	SP0989	MutT/nudix family protein	948	NP_345468.1	8.75105485
80267	E03	SP1931	hypothetical protein SP_1931	712	NP_346359.1	2
80220	E04	SP1000	thioredoxin family protein	954	NP_345477.1	8.97169811
80380	E05	SP1237	acetyltransferase	1254	NP_345703.1	8.761563
80151	E06	SP0659	thioredoxin family protein	654	NP_345164.1	4.75382263
80163	E07	SP1816	anthranilate synthase component II	229	NP_346249.1	1.97816594
80243	E08	SP1308	-	1344	-	13.0811012
80260	E09	SP0993	DNA polymerase III subunit epsilon	951	NP_345472.1	8.99474238
80215	E10	SP1018	thymidine kinase	972	NP_345493.1	8.87654321
80400	E11	SP0387	DNA-binding response regulator	456	NP_344914.1	4.33552632
80159	E12	SP1704	ABC transporter ATP-binding protein	952	NP_346142.1	3.94537815
80276	F01	SP0550	tRNA (guanine-N(7)-)-methyltransferase	579	NP_345067.1	5.92746114
80321	F02	SP2166	L-fucose phosphate aldolase	1873	NP_346580.1	3.90336359
80132	F03	SP1830	phosphate transport system regulatory protein PhoU	262	NP_346263.1	2
80374	F04	SP1169	uracil-DNA glycosylase	1176	NP_345638.1	9.70153061
80485	F05	SP0388	-	456	-	4.35307018
80223	F06	SP1097	hypothetical protein SP_1097	1068	NP_345569.1	9.96910112
80143	F07	SP0608	amino acid ABC transporter permease	624	NP_345120.1	4.14102564
80394	F08	SP0143	hypothetical protein SP_0143	252	NP_344685.1	13.9642857
80313	F09	SP2232	-	2329	-	4.14426793
80271	F10	SP0545	immunity protein BlpY	576	NP_345062.1	4.41145833
80455	F11	SP1230	phosphopantothenate--cysteine ligase	1248	NP_345696.1	7.57532051
80237	F12	SP1267	licC protein	1296	NP_345731.1	13.2523148
80508	G01	SP0858	hypothetical protein SP_0858	828	NP_345346.1	9.17270531
80463	G02	SP0756	cell division ABC transporter ATP-binding protein FtsE	738	NP_345254.1	6.7303523
80475	G03	SP1104	hypothetical protein SP_1104	1080	NP_345575.1	9.59814815
80498	G04	SP0753	branched-chain amino acid ABC transporter ATP-binding protein	738	NP_345252.1	7.94173442
80461	G05	SP1171	HAD superfamily hydrolase	1176	NP_345640.1	8.7542517

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
80487	G06	SP1922	hypothetical protein SP_1922	667	NP_346350.1	2
80316	G07	SP0617	hypothetical protein SP_0617	627	NP_345129.1	4.76076555
80450	G08	SP1449	C3-degrading proteinase	136	NP_345903.1	4
80365	G09	SP1201	serine/threonine protein phosphatase	1212	NP_345668.1	7.54455446
80471	G10	SP2020	GntR family transcriptional regulator	1009	NP_346445.1	3.32210109
80389	G11	SP0522	ABC transporter ATP-binding protein	558	NP_345040.1	5.01075269
80340	G12	SP0824	amino acid ABC transporter ATP-binding protein	798	NP_345316.1	6.78320802
80425	H01	SP1362	adaptor protein	1515	NP_345820.1	13.2752475
80280	H02	SP1408	acyl-ACP thioesterase	1821	NP_345866.1	14.0192202
80342	H03	SP1973	spoU rRNA methylase family protein	835	NP_346400.1	1.99281437
80502	H04	SP1733	phosphatase	1138	NP_346169.1	4.43321617
80494	H05	SP1599	tRNA pseudouridine synthase A	430	NP_346043.1	3.99069767
80239	H06	SP2235	response regulator ComE	2371	NP_346642.1	3.17587516
80325	H07	SP1396	phosphate transporter ATP-binding protein	1758	NP_345854.1	12.6825939
80491	H08	SP1071	ABC transporter ATP-binding protein	1029	NP_345544.1	10.7444121
80348	H09	SP1051	hypothetical protein SP_1051	1005	NP_345525.1	9.79104478
80294	H10	SP1909	short chain dehydrogenase/reductase family oxidoreductase	553	NP_346338.1	2
80191	H11	SP0609	amino acid ABC transporter amino acid-binding protein	624	NP_345121.1	3.7099359
80184	H12	SP2233	hypothetical protein SP_2233	2368	NP_346640.1	3.91765203

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