

***Streptococcus pneumoniae* Gateway®
Clone Set, Recombinant in *Escherichia coli*, Plate 17****Catalog No. NR-19584**

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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-19584.

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-19584 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 17, NR-19584."

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 17 (YSPCR)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
68669	A01	SP1778	aquaporin	151	NP_346211.1	2
68665	A03	SP1914	hypothetical protein SP_1914	592	NP_346342.1	2
68505	A04	SP1633	DNA-binding response regulator	652	NP_346073.1	4.59816
68613	A05	SP2094	hypothetical protein SP_2094	1396	NP_346513.1	3.74785
68385	A06	SP1951	hypothetical protein SP_1951	772	NP_346379.1	2
68517	A07	SP0999	cytochrome c-type biogenesis protein CcdA	954	NP_345476.1	9.19392
68525	A08	SP2082	response regulator	1354	NP_346502.1	3.55465
68557	A09	SP0980	O-methyltransferase	933	NP_345461.1	7.56163
68421	A10	SP0917	pilin gene inverting-related protein	873	NP_345401.1	8.76403
68449	A11	SP2072	glutamine amidotransferase, class-I	1309	NP_346495.1	1.46142
68321	A12	SP2196	ABC transporter ATP-binding protein	2050	NP_346607.1	2.6278
68657	B01	SP0452	amino acid ABC transporter ATP-binding protein	504	NP_344973.1	4.37897
68497	B02	SP2198	ABC transporter permease	2056	NP_346609.1	3.85117
68361	B03	SP0963	dihydroorotate dehydrogenase electron transfer subunit	924	NP_345444.1	8.37121
68393	B04	SP1871	iron-compound ABC transporter ATP-binding protein	417	NP_346303.1	2
68381	B05	SP2087	phosphate transporter ATP-binding protein	1375	NP_346507.1	1.20291
68633	B06	SP0833	hypothetical protein SP_0833	801	NP_345324.1	8.56679
68453	B07	SP1574	triosephosphate isomerase	313	NP_346020.1	3
68969	B08	SP1578	hypothetical protein SP_1578	334	NP_346024.1	4
68769	B09	SP1156	ribonuclease HII	1155	NP_345625.1	9.05714
68841	B10	SP0717	hydroxyethylthiazole kinase	699	NP_345218.1	13.1044
69025	B11	SP1035	iron-compound ABC transporter ATP-binding protein	990	NP_345510.1	8.72121
68749	B12	SP1609	hypothetical protein SP_1609	463	NP_346053.1	3.85745
68737	C01	SP0777	hypothetical protein SP_0777	756	NP_345275.1	8.5582
68865	C02	SP1063	ABC transporter permease	1017	NP_345537.1	10.4238
68901	C03	SP1397	phosphate transporter ATP-binding protein	1758	NP_345855.1	14.3134
68693	C04	SP1859	transporter	370	NP_346291.1	2.86757

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
68945	C05	SP0949	-	906	-	8.75276
68729	C06	SP0320	gluconate 5-dehydrogenase	387	NP_344856.1	4.56589
68685	C07	SP0637	hypothetical protein SP_0637	639	NP_345147.1	5.39437
68789	C08	SP0826	hypothetical protein SP_0826	798	NP_345318.1	6.59649
68705	C09	SP1021	HemK protein	975	NP_345496.1	8.88718
68741	C10	SP1681	sugar ABC transporter permease	850	NP_346120.1	4.88471
68893	C11	SP0149	lipoprotein	255	NP_344691.1	14.8157
68745	C12	SP0946	hypothetical protein SP_0946	903	NP_345429.1	8.44408
68773	D01	SP2085	phosphate ABC transporter permease	1363	NP_346505.1	3.53338
68721	D02	SP0586	5,10-methylenetetrahydrofolate reductase	609	NP_345099.1	2.90312
68877	D03	SP0481	hypothetical protein SP_0481	528	NP_345000.1	3.80492
68833	D04	SP0922	carbon-nitrogen hydrolase family protein	876	NP_345406.1	8.83904
68937	D05	SP0605	fructose-bisphosphate aldolase	621	NP_345117.1	4.84058
68941	D06	SP1137	GTP-binding protein	1134	NP_345607.1	10.5247
69045	D07	SP1398	phosphate ABC transporter permease	1764	NP_345856.1	13.5454
68733	D08	SP2003	ABC transporter ATP-binding protein	910	NP_346430.1	3.31868
68753	D09	SP1711	primosomal protein Dnal	1033	NP_346149.1	4.02227
69005	D10	SP1989	transcriptional regulator PlcR	874	NP_346416.1	2
68873	D11	SP0282	PTS system, mannose-specific IID component	357	NP_344820.1	3.7535
68905	D12	SP1564	hypothetical protein SP_1564	271	NP_346011.1	4
68965	E01	SP2098	hypothetical protein SP_2098	1405	NP_346517.1	1.18719
68917	E02	SP1062	ABC transporter ATP-binding protein	1014	NP_345536.1	10.9112
69057	E03	SP1399	phosphate ABC transporter permease	1767	NP_345857.1	13.5976
68785	E04	SP1798	ABC transporter permease	181	NP_346231.1	2
68909	E05	SP0791	aldo/keto reductase family oxidoreductase	771	NP_345288.1	8.62646
69001	E06	SP0764	dihydroorotate dehydrogenase 1A	747	NP_345262.1	7.63454
68857	E07	SP1448	hypothetical protein SP_1448	133	NP_345902.1	3
69405	E08	SP1869	iron-compound ABC transporter permease	400	NP_346301.1	2
69389	E09	SP0386	sensor histidine kinase	456	NP_344913.1	5.03509
69097	E10	SP0284	PTS system, mannose-specific IIAB components	357	NP_344822.1	3.29972
69385	E11	SP0378	choline binding protein J	450	NP_344905.1	4.02667
69197	E12	SP1292	SAP domain-containing protein	1332	NP_345756.1	12.4512
69257	F01	SP0330	sugar binding transcriptional regulator RegR	396	NP_344866.1	2.87626
69249	F02	SP1799	Lacl family transcriptional regulator	187	NP_346232.1	2
69325	F03	SP1821	Lacl family transcriptional regulator	238	NP_346254.1	2
69301	F04	SP1025	hypothetical protein SP_1025	978	NP_345500.1	9.03272
69213	F05	SP1828	UDP-glucose 4-epimerase	259	NP_346261.1	2
69201	F06	SP1033	iron-compound ABC transporter permease	990	NP_345508.1	8.28081
69329	F07	SP0377	choline binding protein C	450	NP_344904.1	4.54667
69305	F08	SP0391	choline binding protein F	459	NP_344917.1	4.33551
69417	F09	SP0651	-	648	-	5.125
69321	F10	SP1032	iron-compound ABC transporter iron compound-binding protein	987	NP_345507.1	7.40426

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
69441	F11	SP1701	phospho-2-dehydro-3-deoxyheptonate aldolase	946	NP_346139.1	5.08774
69269	F12	SP0066	aldose 1-epimerase	192	NP_344615.1	2
69265	G01	SP1013	aspartate-semialdehyde dehydrogenase	966	NP_345489.1	8.66563
69369	G02	SP0253	glycerol dehydrogenase	336	NP_344792.1	1.85119
69133	G03	SP1258	2-isopropylmalate synthase,	1278	NP_345722.1	12.1002
69165	G04	SP1525	cystathionine gamma-synthase	202	NP_345975.1	4
69357	G05	SP1366	glycosyl transferase, group 1	1533	NP_345824.1	13.8376
69281	G06	SP0931	gamma-glutamyl kinase	882	NP_345415.1	9.17234
69381	G07	SP1493	hypothetical protein SP_1493	166	NP_345945.1	4
69413	G08	SP0553	transcription elongation factor NusA	585	NP_345069.1	5.28718
69181	G09	SP1378	hypothetical protein SP_1378	1677	NP_345836.1	13.3637
69429	G10	SP1552	cation efflux family protein	241	NP_345999.1	3.9668
69261	G11	SP1727	hydroxymethylglutaryl-CoA synthase	1072	NP_346164.1	4.39925
69105	G12	SP0176	3,4-dihydroxy-2-butanone 4-phosphate synthase/GTP cyclohydrolase II	279	NP_344717.1	3.41577
69229	H01	SP0351	capsular polysaccharide biosynthesis protein Cps4F	426	NP_344884.1	2.90376
69445	H03	SP0356	polysaccharide transporter	429	NP_344889.1	2.86014
69797	H04	SP0159	hypothetical protein SP_0159	261	NP_344701.1	12.7548
69657	H05	SP0411	seryl-tRNA synthetase	474	NP_344934.1	3.87764
69665	H06	SP1966	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	808	NP_346393.1	1.78713
69689	H07	SP2224	M16 family peptidase	2284	NP_346632.1	3.45841
69485	H08	SP0156	DNA-binding response regulator	261	NP_344698.1	14.9962
69817	H09	SP1402	NOL1/NOP2/sun family protein	1785	NP_345860.1	13.9524
69601	H10	SP2109	maltodextrin ABC transporter permease	1459	NP_346528.1	1.14873
69653	H11	SP0413	aspartate kinase	474	NP_344936.1	4.14346
69473	H12	SP1667	cell division protein FtsA	787	NP_346106.1	5.02922

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