

Streptococcus pneumoniae Gateway® Clone Set, Recombinant in Escherichia coli, Plate 12

Catalog No. NR-19579

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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-19579.

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-19579 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 12, NR-19579."

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 12 (YSPCL)¹

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23742	A01	SP1712	hypothetical protein SP_1712	1033	NP_346150.1	4.1036
23743	A02	SP0140	UDP-glucose 6-dehydrogenase	252	-	13.393
23745	A03	SP1005	conserved domain protein	957	-	9.1923
23746	A04	SP0741	hypothetical protein SP_0741	720	NP_345240.1	13.653
23747	A05	SP0168	macrolide efflux protein	267	NP_344710.1	15.258
23748	A06	SP2216	hypothetical protein SP_2216	2192	NP_346624.1	2.4243
23749	A07	SP1153	hypothetical protein SP_1153	1149	NP_345622.1	8.9843
23750	A08	SP1853	galactokinase	361	NP_346285.1	2
23751	A09	SP1116	transporter	1101	NP_345587.1	10.678
23752	A10	SP2239	serine protease	2473	NP_346646.1	3.351
23753	A11	SP0464	cell wall surface anchor family protein	516	NP_344984.1	3.8275
23754	A12	SP0958	hypothetical protein SP_0958	918	NP_345439.1	8.573
23755	B01	SP1214	transulfuration enzyme family protein	1224	-	6.0809
23756	B02	SP0360	UDP-N-acetylglucosamine 2-epimerase	435	NP_344893.1	2.4368
23759	B03	SP1544	aspartate aminotransferase	226	NP_345991.1	3
23760	B04	SP2044	acetate kinase	1201	NP_346469.1	2.9001
23761	B05	SP0322	glucuronyl hydrolase	387	NP_344858.1	3.7261
23763	B06	SP1145	hypothetical protein SP_1145	1142	NP_345615.1	9.3879
23764	B07	SP0762	S-adenosylmethionine synthetase	744	NP_345260.1	6.0215
23765	B08	SP1893	hypothetical protein SP_1893	484	NP_346324.1	2
23768	B09	SP1489	elongation factor Tu	166	NP_345941.1	2.9819
23769	B10	SP1765	glycosyl transferase family protein	130	NP_346200.1	2
23771	B11	SP1716	hypothetical protein SP_1716	1036	NP_346153.1	3.528
23772	B12	SP0690	cell division protein DivIB	687	NP_345195.1	13.426
23773	C01	SP0972	multi-drug resistance efflux pump	927	NP_345453.1	9.0043
23776	C02	SP0606	oxidoreductase	621	NP_345118.1	4.1111
23780	C03	SP1504	hypothetical protein SP_1504	181	NP_345955.1	2
23781	C04	SP0829	phosphopentomutase	801	NP_345320.1	7.633
23782	C05	SP1994	aminotransferase AlaT	886	NP_346421.1	1.6569
23783	C06	SP1770	glycosyl transferase family protein	139	NP_346204.1	2
23784	C07	SP0881	thiamine biosynthesis protein ThiI	846	NP_345368.1	7.4267
23785	C08	SP1763	preprotein translocase subunit SecY	127	NP_346198.1	2
23786	C09	SP0615	beta-lactam resistance factor	627	NP_345127.1	2.8947

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23787	C10	SP1766	glycosyl transferase family protein	133	NP_346201.1	2
23788	C11	SP1008	peptidase T	960	NP_345484.1	8.6625
23789	C12	SP1812	tryptophan synthase subunit beta	211	NP_346245.1	2
23790	D01	SP1336	type II DNA modification methyltransferase Spn5252IP	1410	NP_345794.1	21.133
23791	D02	SP0473	ROK family protein	522	NP_344992.1	5.5958
23792	D03	SP0803	rod shape-determining protein RodA,	774	NP_345300.1	8.624
23793	D04	SP0145	hypothetical protein SP_0145	252	NP_344687.1	14
23794	D05	SP1587	ATP-dependent RNA helicase	373	NP_346033.1	4
23795	D06	SP1837	capsular polysaccharide biosynthesis protein	283	NP_346270.1	2
23796	D07	SP0869	aminotransferase, class-V	837	NP_345356.1	7.4492
23797	D08	SP2148	arginine deiminase	1666	NP_346565.1	3.3812
23798	D09	SP0359	capsular polysaccharide biosynthesis protein Cps4K	435	NP_344892.1	2.9034
23800	D10	SP1067	cell division protein FtsW	1020	NP_345540.1	9.7127
23803	D11	SP0379	hypothetical protein SP_0379	450	NP_344906.1	3.3311
23804	D12	SP1417	IS1380-Spn1 transposase	1929	-	13.471
23805	E01	SP2065	MATE efflux family protein	1294	NP_346488.1	1.4011
23806	E02	SP0422	3-oxoacyl-(acyl carrier protein) synthase II	477	NP_344945.1	4.7505
23808	E03	SP0278	aminopeptidase PepS	354	NP_344816.1	1.8559
23810	E04	SP2175	dltB protein	1978	NP_346589.1	3.0147
23812	E05	SP1472	oxidoreductase	154	NP_345926.1	4
23813	E06	SP2122	hypothetical protein SP_2122	1546	NP_346541.1	3.6656
23814	E07	SP1978	diaminopimelate decarboxylase	850	NP_346405.1	2
23815	E08	SP0450	threonine dehydratase	501	NP_344971.1	4.3792
23818	E09	SP0197	dihydrofolate synthetase	294	NP_344737.1	4.619
23819	E10	SP1941	competence damage-inducible protein A	745	NP_346369.1	2
23821	E11	SP2181	-	2002	-	2.5215
23823	E12	SP2100	tyrosyl-tRNA synthetase	1414	NP_346519.1	1.355
23826	F01	SP0257	-	342	-	3.1404
23828	F02	SP1262	IS1167, transposase	1284	NP_345726.1	11.731
23832	F03	SP0263	eep protein	345	NP_344801.1	3.6522
23836	F04	SP0919	hypothetical protein SP_0919	876	NP_345403.1	8.3139
23837	F05	SP1666	cell division protein FtsZ	787	NP_346105.1	5.2427
23838	F06	SP1081	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	1041	NP_345554.1	10.883
23842	F07	SP0868	hypothetical protein SP_0868	837	NP_345355.1	7.9558
23843	F08	SP1848	xanthine permease	340	NP_346280.1	2
23845	F09	SP0460	IS1167, transposase	510	NP_344980.1	5.0118
23848	F10	SP0737	sodium-dependent transporter	714	NP_345236.1	11.006
23849	F11	SP1393	hypothetical protein SP_1393	1725	NP_345851.1	12.993
23850	F12	SP2108	maltose/maltodextrin ABC transporter maltose/maltodextrin-binding protein	1459	NP_346527.1	2.682
23854	G01	SP1368	psr protein	1548	NP_345826.1	13.072
23855	G02	SP1213	hypothetical protein SP_1213	1224	NP_345680.1	7.5866
23859	G03	SP2067	hypothetical protein SP_2067	1297	NP_346490.1	1.2621
23861	G04	SP2144	hypothetical protein SP_2144	1651	NP_346561.1	3.5966
23863	G05	SP0400	trigger factor	468	NP_344923.1	3.7628

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23864	G06	SP1371	3-phosphoshikimate 1-carboxyvinyltransferase	1644	NP_345829.1	13.319
23868	G07	SP0019	adenylosuccinate synthetase	105	NP_344571.1	-
23869	G08	SP1429	U32 family peptidase	2277	NP_345886.1	12.287
23870	G09	SP1361	homoserine dehydrogenase	1503	NP_345819.1	13.568
23871	G10	SP1244	signal recognition particle-docking protein FtsY	1257	NP_345709.1	7.0764
23873	G11	SP0200	competence-induced protein Ccs4	297	NP_344740.1	3.862
23874	G12	SP2022	PTS system, IIC component	1015	NP_346447.1	1.3892
23875	H01	SP2208	helicase	2125	NP_346619.1	2.4381
23876	H02	SP0056	adenylosuccinate lyase	180	NP_344605.1	2.9389
23877	H03	SP1290	hypothetical protein SP_1290	1332	NP_345754.1	11.45
23879	H04	SP1128	phosphopyruvate hydratase	1119	NP_345598.1	10.421
23880	H05	SP1079	GTPase ObgE	1041	NP_345552.1	10.887
23884	H06	SP1709	GTP-binding protein EngA	1009	NP_346147.1	3.8642
23885	H07	SP0230	preprotein translocase subunit SecY	312	NP_344770.1	3.4038
23887	H08	SP1901	RNA methyltransferase	523	NP_346332.1	2
23889	H09	SP1588	oxalate:formate antiporter	379	NP_346034.1	3
23890	H10	SP1795	sucrose-6-phosphate hydrolase	175	NP_346228.1	1.7486
23891	H11	SP1340	hypothetical protein SP_1340	1440	NP_345798.1	18.217
23893	H12	SP0408	sodium:alanine symporter family protein	473	NP_344931.1	4.8013

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