

***Streptococcus pneumoniae* Gateway®  
Clone Set, Recombinant in *Escherichia coli*, Plate 10****Catalog No. NR-19577**

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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.<sup>1</sup> 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-19577.

**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-19577 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 10, NR-19577."

**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/bmbli5/index.htm](http://www.cdc.gov/biosafety/publications/bmbli5/index.htm).

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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 10 (YSPCJ)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23471	A01	SP1475	glycyl-tRNA synthetase subunit alpha	154	NP_345929.1	3
23472	A02	SP1329	N-acetylneuraminate lyase	1389	NP_345787.1	21.97480202
23473	A03	SP1797	ABC transporter permease	178	NP_346230.1	2
23475	A04	SP1110	bifunctional riboflavin kinase/FMN adenylyltransferase	1095	NP_345581.1	10.76712329
23479	A05	SP1002	adhesion lipoprotein	957	NP_345479.1	9.143155695
23480	A06	SP0839	pantothenate kinase	807	NP_345330.1	9.148698885
23481	A07	SP2210	cysteine synthase	2131	NP_346621.1	2.220553731
23482	A08	SP0420	acyl-carrier-protein S-malonyltransferase	477	NP_344943.1	4.870020964
23483	A09	SP0091	ABC transporter permease	210	NP_344638.1	1.952380952
23485	A10	SP0859	hypothetical protein SP_0859	829	NP_345347.1	9.142340169
23486	A11	SP1470	thiamine biosynthesis protein ApbE	154	NP_345924.1	2
23487	A12	SP1980	cmp-binding-factor 1	859	NP_346407.1	1.995343423
23489	B01	SP1975	OxaA-like protein precursor	844	NP_346402.1	3.626777251
23490	B02	SP1887	oligopeptide ABC transporter ATP-binding protein AmiF	473	NP_346318.1	2
23491	B03	SP1889	oligopeptide ABC transporter permease AmiD	478	NP_346320.1	2
23493	B04	SP1952	hypothetical protein SP_1952	772	NP_346380.1	2
23494	B05	SP1191	tagatose-6-phosphate kinase	1197	NP_345660.1	6.461152882
23495	B06	SP1650	manganese ABC transporter manganese-binding adhesion liprotein	706	NP_346089.1	3.985835694
23496	B07	SP0674	ribonuclease Z	669	NP_345179.1	3.161434978
23497	B08	SP2127	transketolase, C-terminal subunit	1576	NP_346545.1	4.289340102
23499	B09	SP0660	bifunctional methionine sulfoxide reductase A/B protein	657	NP_345165.1	4.091324201
23500	B10	SP1298	DHH subfamily 1 protein	1341	NP_345762.1	12.34601044
23502	B11	SP1014	dihydrodipicolinate synthase	966	NP_345490.1	8.651138716
23503	B12	SP1735	methionyl-tRNA formyltransferase	1147	NP_346171.1	3.741063644
23504	C01	SP0236	DNA-directed RNA polymerase subunit alpha	315	NP_344776.1	5.298412698
23505	C02	SP1534	manganese-dependent inorganic pyrophosphatase	205	NP_345982.1	3

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23507	C03	SP1359	bifunctional methionine sulfoxide reductase A/B protein	1503	NP_345817.1	12.30738523
23509	C04	SP0964	dihydroorotate dehydrogenase 1B	924	NP_345445.1	9.017316017
23510	C05	SP2113	hypothetical protein SP_2113	1498	NP_346532.1	2.47329773
23511	C06	SP0981	foldase protein PrsA	936	NP_345462.1	8.926282051
23513	C07	SP1576	homoserine O-succinyltransferase	319	NP_346022.1	3.388714734
23514	C08	SP0289	dihydropteroate synthase	363	NP_344827.1	3.724517906
23516	C09	SP0736	mannose-6-phosphate isomerase	714	NP_345235.1	12.6372549
23517	C10	SP2151	carbamate kinase	1680	NP_346567.1	3.929166667
23518	C11	SP1782	ribosomal protein L11 methyltransferase	160	NP_346215.1	2
23519	C12	SP0334	S-adenosyl-methyltransferase MraW	402	NP_344869.1	3.315920398
23520	D01	SP1390	UDP-N-acetylenolpyruvoylglucosamine reductase	1719	NP_345848.1	13.11867365
23521	D02	SP0978	competence protein CoiA	933	NP_345459.1	7.34619507
23523	D03	SP2045	hypothetical protein SP_2045	1201	NP_346470.1	1.434637802
23524	D04	SP1754	hypothetical protein SP_1754	1435	NP_346189.1	2.488501742
23526	D05	SP0848	sugar ABC transporter permease,	822	NP_345339.1	8.931873479
23527	D06	SP1937	autolysin	724	NP_346365.1	2
23528	D07	SP0751	branched-chain amino acid ABC transporter permease	735	NP_345250.1	11.06122449
23529	D08	SP2189	NifR3 family TIM-barrel protein	2020	NP_346600.1	2.463861386
23530	D09	SP1870	iron-compound ABC transporter permease	412	NP_346302.1	2
23531	D10	SP1095	ribose-phosphate pyrophosphokinase	1065	NP_345567.1	10.20938967
23532	D11	SP0090	ABC transporter permease	207	NP_344637.1	2.990338164
23534	D12	SP0668	glucokinase	663	NP_345173.2	3.681749623
23535	E01	SP1606	glycosyl transferase family protein	457	NP_346050.1	3.940919037
23536	E02	SP1998	L-asparaginase	895	NP_346425.1	2
23537	E03	SP1563	pyridine nucleotide-disulphide oxidoreductase family protein	265	NP_346010.1	2
23538	E04	SP1725	sucrose operon repressor	1060	NP_346162.1	3.65754717
23539	E05	SP0890	phage integrase family integrase/recombinase	858	NP_345377.1	8.764568765
23540	E06	SP1872	iron-compound ABC transporter iron-compound-binding protein	421	NP_346304.1	2
23541	E07	SP0676	transcriptional regulator	675	NP_345181.1	4.767407407
23542	E08	SP0027	ribose-phosphate pyrophosphokinase	108	NP_344578.1	-
23545	E09	SP1164	acetoin dehydrogenase, E1 component, alpha subunit	1167	NP_345633.1	9.373607541
23546	E10	SP0417	3-oxoacyl-(acyl carrier protein) synthase III	474	NP_344940.1	3.367088608
23547	E11	SP0419	enoyl-(acyl-carrier-protein) reductase	477	NP_344942.1	2.899371069
23550	E12	SP1027	hypothetical protein SP_1027	984	NP_345502.1	8.856707317
23552	F01	SP1565	hypothetical protein SP_1565	272	NP_346012.1	4
23553	F02	SP1482	Gfo/ldh/MocA family oxidoreductase	160	NP_345936.1	2.9625
23554	F03	SP2013	hypothetical protein SP_2013	976	NP_346440.1	1.651639344
23556	F04	SP0247	transcriptional regulator	324	NP_344786.1	3.962962963
23557	F05	SP1695	acetyl xylan esterase	919	NP_346133.1	5.011969532
23558	F06	SP0337	phospho-N-acetylmuramoyl-pentapeptide-transferase	405	NP_344872.1	2.308641975

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23559	F07	SP2112	maltose operon transcriptional repressor	1498	NP_346531.1	2.304405875
23560	F08	SP2040	jag protein	1156	NP_346465.1	1.694636678
23561	F09	SP0095	hypothetical protein SP_0095	219	NP_344642.1	2
23562	F10	SP1249	guanosine 5'-monophosphate oxidoreductase	1266	NP_345714.1	8.982622433
23563	F11	SP1365	glycosyl transferase family protein	1533	NP_345823.1	11.98238748
23564	F12	SP1220	L-lactate dehydrogenase	1230	NP_345686.1	7.043902439
23565	G01	SP1160	lipoate-protein ligase	1164	NP_345629.1	6.708762887
23566	G02	SP1163	acetoin dehydrogenase, E1 component, beta subunit	1164	NP_345632.1	9.524914089
23567	G03	SP0037	glycerol-3-phosphate acyltransferase PlsX	111	NP_344587.1	-
23568	G04	SP0636	ABC transporter ATP-binding protein	639	NP_345146.1	4.461658842
23570	G05	SP1970	asparagine synthetase AsnA	823	NP_346397.1	2
23571	G06	SP1612	hypothetical protein SP_1612	473	NP_346056.1	2
23572	G07	SP0915	IS1239 transposase	873	NP_345399.1	7.840778923
23574	G08	SP0259	Holliday junction DNA helicase RuvB	342	NP_344797.1	3.263157895
23576	G09	SP0667	pneumococcal surface protein	663	NP_345172.1	4.494720965
23581	G10	SP0318	carbohydrate kinase	384	NP_344854.1	1.9921875
23582	G11	SP0582	hypothetical protein SP_0582	606	NP_345096.1	4.686468647
23584	G12	SP1815	anthranilate phosphoribosyltransferase	223	NP_346248.1	2
23585	H01	SP1515	-	193	-	2
23586	H02	SP0896	6-phosphofructokinase	858	NP_345383.1	7.763403263
23587	H03	SP1034	iron-compound ABC transporter permease	990	NP_345509.1	8.767676768
23588	H04	SP1854	galactose operon repressor	364	NP_346286.1	2
23589	H05	SP2012	glyceraldehyde-3-phosphate dehydrogenase	970	NP_346439.1	1.594845361
23592	H06	SP2132	hypothetical protein SP_2132	1606	NP_346550.1	3.985678705
23593	H07	SP0383	phosphomevalonate kinase	453	NP_344910.1	5.293598234
23595	H08	SP1999	catabolite control protein A	901	NP_346426.1	1.874583796
23596	H09	SP0129	DNA-binding/iron metalloprotein/AP endonuclease	240	NP_344675.1	17
23597	H10	SP0034	hypothetical protein SP_0034	108	NP_344584.1	-
23600	H11	SP1825	ABC transporter ATP-binding protein	250	NP_346258.1	2
23603	H12	SP1506	hypothetical protein SP_1506	184	NP_345957.1	4

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