

***Streptococcus pneumoniae* Gateway®  
Clone Set, Recombinant in *Escherichia coli*, Plate 9**

**Catalog No. NR-19576**

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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. 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-19576.

**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-19576 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 9, NR-19576."

**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](http://www.cdc.gov/biosafety/publications/bmb15/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.

ATCC® is a trademark of the American Type Culture Collection.



**Table 1: *Streptococcus pneumoniae* Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 9 (YSPCI)<sup>1</sup>**

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23326	A01	SP0882	hypothetical protein SP_0882	849	NP_345369.1	8.0742
23327	A02	SP2041	SpollIJ family protein	1159	NP_346466.1	1.5962
23328	A03	SP1420	NAD synthetase	1938	NP_345877.1	12.63
23330	A04	SP1979	pur operon repressor	850	NP_346406.1	2
23331	A05	SP1451	Cof family protein	136	NP_345905.1	2
23335	A06	SP0574	hypothetical protein SP_0574	600	NP_345088.1	2.8067
23336	A07	SP0148	ABC transporter substrate-binding protein	252	NP_344690.1	15.913
23337	A08	SP0484	hypothetical protein SP_0484	534	NP_345003.1	2.8071
23338	A09	SP2223	hypothetical protein SP_2223	2275	NP_346631.1	3.5257
23339	A10	SP0392	-	459	-	4.3268
23340	A11	SP0212	50S ribosomal protein L2	300	NP_344752.1	4.2267
23341	A12	SP1688	ABC transporter permease	898	NP_346127.1	4.7171
23344	B01	SP0619	hypothetical protein SP_0619	627	NP_345131.1	3.7927
63467	B02	SP0814	IS3-Spn1, transposase	789	-	9.3523
23350	B03	SP1500	amino acid ABC transporter amino acid-binding protein	181	NP_345951.1	3
23352	B04	SP1112	degV family protein	1095	NP_345583.1	9.9927
23353	B05	SP0576	transcription antiterminator Lict	603	NP_345090.1	3.8176
23354	B06	SP0669	thymidylate synthase	663	NP_345174.1	3.4525
23355	B07	SP2220	cobalt transporter ATP-binding subunit	2215	NP_346628.1	2.4546
23356	B08		-	801	-	7.4182
23358	B09	SP1985	dimethyladenosine transferase	868	NP_346412.1	2
23360	B10	SP0986	hypothetical protein SP_0986	942	NP_345465.1	8.7569
23361	B11	SP2110	maltodextrin ABC transporter permease	1474	NP_346529.1	2.2123
23362	B12	SP1478	aldo/keto reductase family oxidoreductase	157	NP_345932.1	3
23364	C01	SP0457	undecaprenyl pyrophosphate phosphatase	510	NP_344977.1	3.4745
23366	C02	SP2103	rRNA (guanine-N1-)-methyltransferase	1420	NP_346522.1	3.6451
23367	C03	SP1130	transcriptional regulator	1125	NP_345600.1	10.722
23368	C04	SP1369	prephenate dehydratase	1563	NP_345827.1	13.058
23369	C05	SP1557	degV family protein	250	NP_346004.1	2
23370	C06	SP1649	manganese ABC transporter permease	703	YP_873934.1	4.9701
23371	C07	SP1111	hypothetical protein SP_1111	1095	NP_345582.1	10.737

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23375	C08	SP1155	ribosomal biogenesis GTPase	1149	NP_345624.1	8.7833
23376	C09	SP1674	phosphosugar-binding transcriptional regulator	829	NP_346113.1	5.7382
23380	C10	SP1044	hydrolase	1002	NP_345519.1	8.6796
23382	C11	SP0649	-	645	-	4.0977
23384	C12	SP2128	transketolase, N-terminal subunit	1582	NP_346546.1	1.201
23386	D01	SP0390	choline binding protein G	459	NP_344916.1	4.7473
23387	D02	SP0657	ribonuclease BN	654	NP_345162.1	4.445
23388	D03	SP1084	methionine aminopeptidase	1050	NP_345557.1	9.92
23389	D04	SP0096	hypothetical protein SP_0096	219	NP_344643.1	2.9954
23390	D05	SP0977	tellurite resistance protein TehB	933	NP_345458.1	8.3023
23391	D06	SP1899	msm operon regulatory protein	505	NP_346330.1	2
23392	D07	SP1266	DNA processing protein DprA	1293	NP_345730.1	13.071
23394	D08	SP1946	transcriptional regulator PlcR	763	NP_346374.1	2
23395	D09	SP2034	L-xylulose 5-phosphate 3-epimerase	1114	NP_346459.1	1.4991
23396	D10	SP1115	transcriptional regulator MutR	1098	NP_345586.1	10.362
23398	D11	SP0141	transcriptional regulator	252	NP_344683.1	12.504
23402	D12	SP0163	transcriptional regulator PlcR	264	NP_344705.1	14.932
23403	E01	SP0426	acetyl-CoA carboxylase subunit beta	480	NP_344949.1	3.7688
23405	E02	SP1491	glycerol uptake facilitator protein	166	NP_345943.1	2.9819
23406	E03	SP0938	tetrapyrrole methylase family protein	894	NP_345422.1	9.2271
23407	E04	SP2142	ROK family protein	1651	NP_346559.1	3.8019
23408	E05	SP1360	homoserine kinase	1503	NP_345818.1	12.3
23409	E06	SP0708	-	696	-	12.415
23410	E07	SP0105	L-serine dehydratase, iron-sulfur-dependent, alpha subunit	228	NP_344652.1	14.89
23411	E08	SP2188	Hsp33-like chaperonin	2017	NP_346599.1	3.2424
23412	E09	SP2016	nicotinate-nucleotide pyrophosphorylase	988	NP_346443.1	1.9787
23413	E10	SP2052	competence protein CglB	1276	NP_346476.1	2.7759
23414	E11	SP0899	hypothetical protein SP_0899	861	NP_345385.1	8.59
23415	E12	SP0136	glycosyl transferase family protein	249	NP_344679.1	17.928
23418	F01	SP0380	hypothetical protein SP_0380	348	NP_344907.1	2.5086
23420	F02	SP2084	phosphate ABC transporter phosphate-binding protein	1360	NP_346504.1	1.4228
23421	F03	SP2011	ribosomal large subunit pseudouridine synthase D	961	NP_346438.1	1.9813
23423	F04	SP0697	-	690	-	11.586
23425	F05	SP0381	mevalonate kinase	453	NP_344908.1	4.298
23426	F06	SP1268	licB protein	1296	NP_345732.1	11.441
23427	F07	SP1509	F0F1 ATP synthase subunit gamma	184	NP_345960.1	4
23428	F08	SP1984	ribosome-associated GTPase	868	NP_346411.1	2
23429	F09	SP1212	tRNA pseudouridine synthase B	1221	NP_345679.1	8.3874
23430	F10	SP1400	phosphate ABC transporter phosphate-binding protein	1767	NP_345858.1	14.194
23431	F11	SP0403	ribonuclease HIII	468	NP_344926.1	5.7415
23433	F12	SP1675	ROK family protein	832	NP_346114.1	5.7656
23435	G01	SP0671	tRNA delta(2)-isopentenylpyrophosphate transferase	666	NP_345176.1	4.018
23436	G02	SP1045	hypothetical protein SP_1045	1004	NP_345520.1	9.6524

Clone	Well Position	Locus ID	Description	ORF Length	Accession Number	Average Depth of Coverage
23437	G03	SP0590	acetyltransferase	612	NP_345103.1	4.4314
23438	G04	SP0593	hypothetical protein SP_0593	612	NP_345106.1	4.4069
23439	G05	SP1689	ABC transporter permease	901	NP_346128.1	4.0644
23442	G06	SP1721	fructokinase	1057	NP_346158.1	3.3046
23443	G07	SP0929	ribosomal large subunit pseudouridine synthase D	882	NP_345413.1	8.271
23444	G08	SP0936	DNA polymerase III subunit delta'	888	NP_345420.1	9.4628
23445	G09	SP1324	ROK family protein	1350	NP_345782.1	12.187
23446	G10	SP1896	sugar ABC transporter permease	490	NP_346327.1	2
23447	G11	SP1566	hypothetical protein SP_1566	280	NP_346013.1	4
23449	G12	SP1682	sugar ABC transporter permease	853	NP_346121.1	4.8957
23451	H01	SP1099	ribosomal large subunit pseudouridine synthase D	1074	NP_345571.1	10.766
23454	H02	SP1857	cation efflux system protein	369	NP_346289.1	2
23455	H03	SP1283	heat shock protein HtpX	1326	NP_345747.1	12.333
23456	H04	SP2092	UTP-glucose-1-phosphate uridylyltransferase	1384	NP_346511.1	1.1705
23458	H05	SP0410	exfoliative toxin	474	NP_344933.1	4.8228
23459	H06	SP0905	hypothetical protein SP_0905	867	NP_345390.1	8.5802
23460	H07	SP0062	PTS system, IIC component	186	NP_344611.1	2
23461	H08	SP1764	glycosyl transferase family protein	130	NP_346199.1	2
23462	H09	SP1751	CorA family protein	1399	NP_346187.1	3.4618
23464	H10	SP0927	LysR family transcriptional regulator	882	NP_345411.1	8.1054
23466	H11	SP0876	1-phosphofructokinase	846	NP_345363.1	7.6879
23470	H12	SP0098	hypothetical protein SP_0098	222	NP_344645.1	3.9099

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