

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4**

**Catalog No. NR-19500**

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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:**

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 does not confirm or validate individual mutants provided by the contributor.

The methicillin-resistant *Staphylococcus aureus* (*S. aureus*), strain COL Gateway® clone set consists of 25 plates which contain 2343 sequence validated clones from *S. aureus* strain COL cloned in *Escherichia coli* (*E. coli*) DH10B-T1 cells. 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.

**Material Provided:**

Every 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-19500 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 or agar containing 50 µg/mL kanamycin.

Incubation:

Temperature: *E. coli*, strain DH10B-T1 clones should be grown at 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: *Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 4, NR-19500.”

**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](http://www.cdc.gov/biosafety/publications/bmbl5/index.htm).

**Disclaimers:**

You are authorized to use this product for research use only. It is not intended for human use.

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**References:**

- Gill, S. R., et al. "Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an Early Methicillin-Resistant *Staphylococcus aureus* Strain and a Biofilm-Producing Methicillin-Resistant *Staphylococcus epidermidis* Strain." *J. Bacteriol.* 187 (2005): 2426-2438. PubMed: 15774886.

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



**Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 4 (ZSAJD)**

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
671	A01	286	SACOL1466	conserved domain protein	YP_186314.1	2
675	A03	286	SACOL2299	conserved hypothetical protein	YP_187106.1	2
677	A04	286	SACOL2405	addiction module antitoxin, Axe family	YP_187208.1	-
679	A05	289	SACOL0590	30S ribosomal protein L7 Ae	YP_185476.1	3.283737024
681	A06	289	SACOL1131	conserved domain protein	YP_185995.1	3.3183391
683	A07	289	SACOL2044	acetolactate synthase, small subunit, truncation	YP_186861.1	3.301038062
685	A08	289	SACOL2112	ribosomal protein L31	YP_186927.1	3.294117647
687	A09	292	SACOL0349	conserved hypothetical protein	YP_185241.1	3.301369863
690	A10	292	SACOL0929	conserved hypothetical protein	YP_185799.1	2.609589041
691	A11	292	SACOL1842	conserved hypothetical protein TIGR00278	YP_186673.1	3.260273973
693	A12	292	SACOL2465	addiction module antitoxin, Axe family	YP_187263.1	3.270547945
695	B01	292	SACOL2559	hypothetical protein	YP_187351.1	3.304794521
697	B02	295	SACOL0035	hypothetical protein	YP_184946.1	3.294915254
699	B03	295	SACOL0048	conserved hypothetical protein	YP_184958.1	3.274576271
701	B04	295	SACOL0062	conserved hypothetical protein	YP_184967.1	2.640677966
703	B05	295	SACOL0336	conserved hypothetical protein	YP_185228.1	3.291525424
707	B06	295	SACOL0865	hypothetical protein	YP_185738.1	3.308474576
709	B07	295	SACOL1581	conserved hypothetical protein	YP_186421.1	3.301694915
711	B08	295	SACOL1672	conserved hypothetical protein	YP_186512.1	3.281355932
713	B09	295	SACOL1693	preprotein translocase, YajC subunit	YP_186532.1	3.26779661
717	B10	298	SACOL0333	conserved hypothetical protein	YP_185225.1	3.295302013
719	B11	298	SACOL0445	conserved domain protein	YP_185335.1	3.285234899
722	B12	298	SACOL0537	conserved hypothetical protein	YP_185425.1	2
724	C01	298	SACOL0550	S4 domain protein	YP_185438.1	3.244966443
726	C02	298	SACOL0891	transcriptional regulator, putative	YP_185762.1	3.244966443
727	C03	298	SACOL1076	phosphoribosylformylglycinamide synthase, PurS protein	YP_185940.1	2.275167785
729	C04	298	SACOL2230	ribosomal protein S17	YP_187040.1	3.238255034
732	C05	301	SACOL0790.1	ribonucleoside-diphosphate reductase 2, NrdH-redoxin, putative	YP_185664.1	2.222591362
733	C06	301	SACOL1091	phosphocarrier protein HPr	YP_185955.1	3.325581395
735	C07	301	SACOL1151	conserved hypothetical protein	YP_186014.1	3.285714286
737	C08	301	SACOL1342	hypothetical protein	YP_186196.1	3.279069767
739	C09		SACOL2404	CLONE IS NOT AVAILABLE <sup>1</sup>	YP_187207.1	
741	C10		SACOL2464	CLONE IS NOT AVAILABLE <sup>1</sup>	YP_187262.1	
743	C11	301	SACOL2502	hypothetical protein	YP_187297.1	3.255813953
745	C12	304	SACOL0508	conserved hypothetical protein	YP_185396.1	3.296052632
747	D01	304	SACOL0624	conserved hypothetical protein	YP_185509.1	3.286184211
749	D02	304	SACOL1292	ribosomal protein S15	YP_186149.1	3.276315789
753	D04	304	SACOL1439	acylphosphatase	YP_186291.1	3.253289474

## Product Information Sheet for NR-19500

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
755	D05	304	SACOL1656	hypothetical protein	YP_186496.1	3.259868421
757	D06	307	SACOL0464	transposase, IS3 family	YP_185354.1	3.247557003
759	D07	307	SACOL0892	pathogenicity island protein	YP_185763.1	3.263843648
761	D08	307	SACOL1513	DNA-binding protein HU	YP_186357.1	3.283387622
763	D09	310	SACOL1106	conserved hypothetical protein	YP_185970.1	3.264516129
766	D10	310	SACOL1121	conserved hypothetical protein	YP_185985.1	3.232258065
767	D11	310	SACOL1254	ribosomal protein S16	YP_186113.1	2.232258065
769	D12	310	SACOL1940	conserved hypothetical protein	YP_186765.1	3.25483871
771	E01	310	SACOL2237	ribosomal protein L23	YP_187047.1	3.270967742
774	E02	310	SACOL2607	hypothetical protein	YP_187397.1	3.251612903
775	E03	313	SACOL0230	PTS system, sorbitol-specific IIB component	YP_185126.1	3.28115016
777	E04	313	SACOL0371	prophage L54a, DNA packaging protein, putative	YP_185263.1	2.658146965
779	E05	313	SACOL0437	ribosomal protein S6	YP_185328.2	3.284345048
781	E06	313	SACOL1067	cytochrome aa3 quinol oxidase, subunit IV	YP_185931.1	3.236421725
785	E07	313	SACOL2235	ribosomal protein S19	YP_187045.1	3.249201278
787	E08	313	SACOL2603	hypothetical protein	YP_187394.1	2.619808307
789	E09	316	SACOL0848	lipoprotein, putative	YP_185722.1	3.262658228
791	E10	319	SACOL0401	conserved hypothetical protein	YP_185293.1	2.282131661
793	E11	319	SACOL0863	conserved hypothetical protein	YP_185736.1	3.253918495
796	E12	319	SACOL0899	pathogenicity island protein	YP_185770.1	2.253918495
797	F01	319	SACOL1286	conserved hypothetical protein	YP_186143.1	3.106583072
800	F02	319	SACOL1586	hypothetical protein	YP_186426.1	2.605015674
802	F03	319	SACOL1700	ribosomal protein L27	YP_186539.1	3.269592476
803	F04	319	SACOL1706	hypothetical protein	YP_186545.1	3.206896552
805	F05	319	SACOL2017	chaperonin, 10 kDa	YP_186836.1	3.235109718
808	F06	319	SACOL2532	acetyltransferase, GNAT family	YP_187325.1	3.235109718
811	F08	322	SACOL1042	hypothetical protein	YP_185907.1	3.248447205
813	F09	322	SACOL2494	hypothetical protein	YP_187289.1	3.242236025
815	F10	325	SACOL0382	hypothetical protein	YP_185274.1	3.28
817	F11	325	SACOL1041	hypothetical protein	YP_185906.1	3.218461538
819	F12	325	SACOL1047	conserved domain protein	YP_185912.1	3.246153846
822	G01	325	SACOL1203	YlmG protein	YP_186065.1	3.227692308
823	G02	325	SACOL1345	hypothetical protein	YP_186198.1	3.255384615
825	G03	325	SACOL1651	conserved hypothetical protein TIGR00253	YP_186491.1	3.270769231
827	G04	328	SACOL0271	conserved hypothetical protein	YP_185166.1	3.243902439
829	G05	328	SACOL0450	hypothetical protein	YP_185340.1	2.618902439
831	G06	328	SACOL0950	Na <sup>+</sup> /H <sup>+</sup> antiporter, MnhF component	YP_185819.1	3.265243902
833	G07	328	SACOL1310	conserved hypothetical protein	YP_186167.1	3.286585366
836	G08	328	SACOL2078	conserved hypothetical protein	YP_186894.1	2.625
837	G09	331	SACOL0044	conserved hypothetical protein	YP_184954.1	3.253776435
839	G10	331	SACOL0069	conserved hypothetical protein	YP_184974.1	3.223564955
841	G11	331	SACOL0412	conserved hypothetical protein	YP_185304.1	2.622356495
843	G12	331	SACOL0881	thioredoxin, putative	YP_185752.1	3.241691843
845	H01	331	SACOL1387	conserved hypothetical protein	YP_186240.1	3.250755287
847	H02	331	SACOL1425	IS1272-related, transposase, truncation	YP_186277.1	2.616314199
849	H03	331	SACOL2601	conserved hypothetical protein	YP_187392.1	3.250755287
851	H04	334	SACOL0387	conserved hypothetical protein	YP_185279.1	3.200598802
853	H05	334	SACOL0738	conserved hypothetical protein	YP_185617.1	3.230538922
858	H06	337	SACOL0388	prophage L54a, holin, SPP1 family	YP_185280.1	3.225519288
859	H07	337	SACOL0541	spoVG protein	YP_185429.1	3.216617211
863	H08	337	SACOL1584	hypothetical protein	YP_186424.1	3.231454006
865	H09	337	SACOL1962	glutamyl-tRNA(Gln) amidotransferase, C subunit	YP_186786.1	3.258160237

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
867	H10	337	SACOL1968	conserved hypothetical protein	YP_186792.1	3.201780415
663	H10	286	SACOL0332	conserved hypothetical protein	YP_185224.1	2
869	H11	337	SACOL2280	urease, gamma subunit	YP_187087.1	2.643916914
665	H11	286	SACOL0446	conserved hypothetical protein	YP_185336.1	2
871	H12	337	SACOL2680	hypothetical protein	YP_187467.1	3.240356083
667	H12	286	SACOL1024	conserved hypothetical protein	YP_185890.1	2

<sup>1</sup>25 clones in the *Staphylococcus aureus* (MRSA), Strain COL Gateway<sup>®</sup> Clone Set (Plates 1-25), Recombinant in *Escherichia coli*, have been physically removed from the clone set due to international distribution limitations set by U.S. Department of Commerce restrictions (Commerce Control List).