

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 9**

**Catalog No. NR-19505**

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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:**

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-19505 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 9, NR-19505.”

**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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Early Methicillin-Resistant *Staphylococcus aureus* Strain and a Biofilm-Producing Methicillin-Resistant *Staphylococcus epidermidis* Strain." *J. Bacteriol.* 187 (2005): 2426-2438. PubMed: 15774886.

**References:**

- Gill, S. R., et al. "Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an

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**Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 9 (ZSAJ1)**

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1697	A01	532	SACOL1168	fibrinogen-binding protein	YP_186031.1	3.152255639
1703	A02	532	SACOL2706	hypothetical protein	YP_187492.1	2
1707	A03	535	SACOL0286	conserved hypothetical protein	YP_185181.1	3.145794393
1719	A04	535	SACOL0585	ribosomal protein L10	YP_185471.1	3.14953271
1721	A05	535	SACOL0789	GTP cyclohydrolase I family protein	YP_185662.1	2.730841122
1723	A06	535	SACOL1457	PTS system, IIA component	YP_186308.1	2.568224299
1725	A07	535	SACOL1759	universal stress protein family	YP_186593.1	2.173831776
1727	A08	535	SACOL1812	repressor of toxins	YP_186645.1	2
1729	A09	535	SACOL1952	ferritins family protein	YP_186777.1	3.145794393
1731	A10	535	SACOL2222	ribosomal protein S5	YP_187032.1	3.151401869
1734	A11	535	SACOL2295	staphyloxanthin biosynthesis protein, putative	YP_187102.1	3.145794393
1737	A12	535	SACOL2684	acetyltransferase, GNAT family	YP_187471.1	3.16635514
1740	B01	538	SACOL0438	single-stranded DNA-binding protein	YP_185329.1	3.851301115
1741	B02	538	SACOL1163	conserved hypothetical protein TIGR00040	YP_186026.1	3.563197026
1743	B03	538	SACOL1255	16S rRNA processing protein RimM	YP_186114.1	3.146840149
1746	B04	538	SACOL1891	RNAIII-activating protein TRAP	YP_186717.1	3.537174721
1747	B05	541	SACOL0037	conserved hypothetical protein	YP_184948.1	4.303142329
1749	B06	541	SACOL0669	conserved hypothetical protein	YP_185553.1	3.534195933
1753	B08	541	SACOL1167	hypothetical protein	YP_186030.1	2.850277264
1755	B09	541	SACOL1539	conserved hypothetical protein	YP_186381.1	3.147874307
1759	B10	541	SACOL2318	conserved hypothetical protein	YP_187125.1	4.329020333
1761	B11	544	SACOL1020	conserved hypothetical protein	YP_185886.1	3.145220588
1763	B12	544	SACOL1397	peptide methionine sulfoxide reductase	YP_186249.1	3.876838235
1765	C01	544	SACOL2173	alkaline shock protein 23	YP_186984.1	2.411764706
1769	C02	547	SACOL0157	conserved hypothetical protein	YP_185057.1	3.548446069
1771	C03	547	SACOL2723	conserved hypothetical protein	YP_187509.1	4.294332724
1773	C04	550	SACOL0984	conserved hypothetical protein TIGR00481	YP_185852.1	2.425454545
1775	C05	550	SACOL1933	ThiJ/Pfpl family protein	YP_186758.1	2.401818182
1777	C06	550	SACOL2162	conserved hypothetical protein	YP_186974.1	3.872727273
1779	C07	550	SACOL2185	galactose-6-phosphate isomerase, LacB subunit	YP_186996.1	2.152727273
1781	C08	550	SACOL2366	acetyltransferase, GNAT family	YP_187171.1	3.138181818
1783	C09	550	SACOL2711	conserved hypothetical protein	YP_187497.1	3.14
1785	C10	553	SACOL0802	conserved hypothetical protein	YP_185676.1	4.305605787
1789	C11	553	SACOL1875	epidermin biosynthesis protein EpiD	YP_186703.1	4.323688969
1791	C12	556	SACOL0659	conserved hypothetical protein	YP_185543.1	3.014388489
1793	D01	556	SACOL0854	hypothetical protein	YP_185727.1	4.248201439
1796	D02	556	SACOL1152	colicin V production protein, putative	YP_186015.1	3.115107914
1797	D03	556	SACOL2099	ATP synthase F0, B subunit	YP_186914.1	4.275179856
1800	D04	556	SACOL2118	conserved hypothetical protein	YP_186933.1	2.838129496
1801	D05	556	SACOL2562	methylated-DNA--protein-cysteine methyltransferase	YP_187354.1	3.570143885
1804	D06	559	SACOL0519	acetyltransferase, GNAT family	YP_185407.1	3.148479428
1805	D07	559	SACOL0579	conserved hypothetical protein	YP_185465.1	4.254025045
1807	D08	559	SACOL0968	signal peptidase IA, inactive	YP_185837.1	4.300536673
1809	D09	559	SACOL1596	shikimate kinase	YP_186436.1	3.846153846
1811	D10	559	SACOL1991	conserved hypothetical protein	YP_186815.1	4.230769231

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1813	D11	559	SACOL2106	conserved hypothetical protein TIGR01440	YP_186921.1	3.837209302
1816	D12	562	SACOL0904	pathogenicity island protein	YP_185775.1	2.414590747
1818	E01	562	SACOL1210	pyrimidine operon regulatory protein	YP_186073.1	2.8113879
1819	E02	562	SACOL1654	hydrolase, HAD-superfamily, subfamily IIIA	YP_186494.1	4.304270463
1821	E03	562	SACOL1727	translation initiation factor IF-3	YP_186565.1	4.286476868
1823	E04	562	SACOL2660	immunodominant antigen B	YP_187448.1	3.256227758
1825	E05	565	SACOL0855	acetyltransferase, GNAT family	YP_185728.1	3.286725664
1827	E06	565	SACOL1032	ComK family protein	YP_185897.1	4.276106195
1829	E07	565	SACOL1703	rod shape-determining protein MreD, putative	YP_186542.1	4.309734513
1831	E08	565	SACOL1936	cytosolic long-chain acyl-CoA thioester hydrolase family protein	YP_186761.1	4.297345133
1833	E09	565	SACOL1956	conserved hypothetical protein	YP_186781.1	4.251327434
1835	E10	565	SACOL2120	DNA-directed RNA polymerase, delta subunit	YP_186935.1	3.07079646
1837	E11	565	SACOL2315	conserved hypothetical protein	YP_187122.1	3.557522124
1840	E12	568	SACOL0073	conserved hypothetical protein	YP_184978.1	4.278169014
1841	F01	568	SACOL1357	thermonuclease precursor family protein	YP_186210.1	4.105633803
1845	F03	571	SACOL0535	primase-related protein	YP_185423.1	4.250437828
1847	F04	571	SACOL0656	conserved hypothetical protein	YP_185541.1	4.257443082
1849	F05	571	SACOL2224	ribosomal protein L6	YP_187034.1	4.273204904
1851	F06	571	SACOL2400	acetyltransferase, GNAT family	YP_187203.1	4.276707531
1854	F07	571	SACOL2634	anaerobic ribonucleoside-triphosphate reductase activating protein	YP_187422.1	3.534150613
1857	F08	574	SACOL0554	hypoxanthine phosphoribosyltransferase	YP_185442.1	4.277003484
1859	F09	574	SACOL0874	nitroreductase family protein	YP_185746.1	3.132404181
1861	F10	574	SACOL1107	transcriptional regulator, Cro/Ci family	YP_185971.1	4.217770035
1863	F11	574	SACOL1607	5-formyltetrahydrofolate cyclo-ligase family protein	YP_186447.1	3.534843206
1865	F12	574	SACOL1621	CBS domain protein	YP_186461.1	4.266550523
1867	G01	574	SACOL1882	hypothetical protein	YP_186709.1	4.299651568
1869	G02	574	SACOL2098	ATP synthase F1, delta subunit	YP_186913.1	3.548780488
1871	G03	574	SACOL2227	ribosomal protein L5	YP_187037.1	2.412891986
1873	G04	577	SACOL0357	prophage L54a, deoxyuridine 5-triphosphate nucleotidohydrolase	YP_185249.1	4.268630849
1875	G05	577	SACOL0739	acetyltransferase, GNAT family	YP_185618.1	4.253032929
1877	G06	577	SACOL0785	conserved hypothetical protein	YP_185659.1	4.285961872
1879	G07	577	SACOL1090	conserved hypothetical protein	YP_185954.1	4.266897747
1881	G08	577	SACOL1133	conserved hypothetical protein TIGR00095	YP_185997.1	4.251299827
1884	G09	577	SACOL1317	glycerol uptake operon antiterminator regulatory protein	YP_186173.1	2.818024263
1885	G10	577	SACOL1537	segregation and condensation protein B	YP_186379.1	3.559792028
1887	G11	577	SACOL1542	MutT/nudix family protein	YP_186384.1	3.87694974
1889	G12	577	SACOL1925	conserved hypothetical protein	YP_186750.1	4.272097054
1891	H01	580	SACOL0413	ribosomal-protein-serine acetyltransferase, putative	YP_185305.1	4.284482759
1893	H02	580	SACOL1270	heat shock protein HslIV, ATPase subunit HslV	YP_186128.1	4.244827586
1895	H03	580	SACOL1526	conserved hypothetical protein	YP_186369.1	4.251724138
1897	H04	582	SACOL0441	integrase, degenerate	N/A	3.235395189
1901	H05	583	SACOL0618	SIS domain protein	YP_185503.1	4.171526587
1904	H06	583	SACOL2175	conserved hypothetical protein	YP_186986.1	3.130360206
1905	H07	586	SACOL1100	polypeptide deformylase	YP_185964.1	4.271331058
1908	H08	586	SACOL1850	hypothetical protein	YP_186681.1	3.141638225
1910	H09	586	SACOL2349	transcriptional regulator, TetR family	YP_187155.1	3.109215017
1911	H10	589	SACOL1278	ribosome recycling factor	YP_186135.1	4.259762309
1913	H11	589	SACOL1885	conserved hypothetical protein	YP_186711.1	3.285229202
1915	H12	589	SACOL1954	exonuclease	YP_186779.1	4.264855688