

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 8**

Catalog No. NR-19504

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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 cannot confirm or validate any clone not identified on the plate information table.

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-19504 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 8, NR-19504.”

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.

Disclaimers:

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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 Early Methicillin-Resistant *Staphylococcus aureus* Strain

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



Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 8 (ZSAJH)

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1489	A01	487	SACOL0059	conserved hypothetical protein	YP_184965.1	3.13963039
1491	A02	487	SACOL0631	conserved hypothetical protein	YP_185516.1	2
1493	A03	487	SACOL0755	conserved hypothetical protein	YP_185634.1	3.1724846
1495	A04	487	SACOL1565	arginine repressor	YP_186406.1	2.585215606
1497	A05	487	SACOL1688	conserved hypothetical protein TIGR00256	YP_186527.1	3.162217659
1499	A06	487	SACOL2283	urease accessory protein UreE	YP_187090.1	3.170431212
1501	A07	487	SACOL2391	conserved hypothetical protein	YP_187194.1	2.564681725
1504	A08	490	SACOL0376	prophage L54a, major tail protein, putative	YP_185268.1	2
1506	A09	490	SACOL1921	bacterioferritin comigratory protein	YP_186746.1	2
1507	A10	490	SACOL2052	peptidase, SprT family	YP_186868.1	3.165306122
1512	A11	490	SACOL2361	hypothetical protein	YP_187166.1	3.112244898
1513	A12	490	SACOL2467	lipoprotein, putative	YP_187265.1	3.187755102
1516	B01	490	SACOL2650	transcriptional regulator, putative	YP_187438.1	3.13877551
1517	B02	493	SACOL0273	hypothetical protein	YP_185168.1	3.131845842
1519	B03	493	SACOL0741	conserved hypothetical protein	YP_185620.1	2.559837728
1521	B04	493	SACOL0843	conserved hypothetical protein	YP_185717.1	2
1524	B05	493	SACOL0889	pathogenicity island protein	YP_185760.1	2.563894523
1525	B06	493	SACOL1698	ACT domain protein	YP_186537.1	3.172413793
1527	B07	493	SACOL2661	conserved hypothetical protein	YP_187449.1	3.164300203
1529	B08	496	SACOL0071	conserved hypothetical protein	YP_184976.1	3.1875
1531	B09	496	SACOL0567	transcriptional regulator CtsR	YP_185455.1	2.574596774
1533	B10	496	SACOL1126	conserved hypothetical protein	YP_185990.1	3.16733871
1535	B11	499	SACOL0847	SsrA-binding protein	YP_185721.1	3.180360721
1537	B12	499	SACOL0917	NifU domain protein	YP_185788.1	3.154308617
1539	C01	499	SACOL1572	acetyl-CoA carboxylase, biotin carboxyl carrier protein	YP_186413.1	3.160320641
1541	C02	499	SACOL1768	GAF domain protein	YP_186602.1	2.160320641
1544	C03	499	SACOL1817	6,7-dimethyl-8-ribityllumazine synthase	YP_186649.1	2.561122244
1546	C04	499	SACOL1904	transcriptional regulator, putative	YP_186729.1	3.138276553
1549	C05	499	SACOL2039	ribosomal-protein-alanine acetyltransferase, putative	YP_186856.1	3.090180361
1551	C06	499	SACOL2524	transcriptional regulator, MarR family	YP_187318.1	2.561122244
1554	C07	499	SACOL2717	hypothetical protein	YP_187503.1	3.160320641
1555	C08	502	SACOL0229	PTS system, sugar-specific IIA component	YP_185125.1	2.139442231
1557	C09	502	SACOL1284	conserved hypothetical protein	YP_186141.1	3.19123506
1560	C10	502	SACOL1380	conserved hypothetical protein	YP_186233.1	2.577689243
1561	C11	502	SACOL1386	conserved hypothetical protein TIGR00051	YP_186239.1	2.577689243
1563	C12	502	SACOL1627	conserved hypothetical protein TIGR00043	YP_186467.1	2.932270916
1565	D01	502	SACOL2402	conserved hypothetical protein	YP_187205.1	3.157370518
1569	D03	505	SACOL0592	ribosomal protein S7	YP_185478.1	3.138613861
1571	D04	505	SACOL0859	hypothetical protein	YP_185732.1	1.16039604
1573	D05	505	SACOL1064	conserved hypothetical protein	YP_185928.1	2.089108911
1577	D07	505	SACOL1827	RNA polymerase sigma-70 family protein	YP_186659.1	2.17029703
1581	D08	505	SACOL2126	autoinducer-2 production protein LuxS	YP_186941.1	2.411881188
1583	D09	507	SACOL0605	cytidine/deoxycytidylate deaminase family protein, authentic frameshift	N/A	2.585798817

Product Information Sheet for NR-19504

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1586	D10	508	SACOL0092	conserved hypothetical protein	YP_184997.1	3.153543307
1587	D11	508	SACOL0728	conserved hypothetical protein	YP_185609.1	1.580708661
1589	D12	508	SACOL0767	conserved hypothetical protein	YP_185644.1	3.161417323
1593	E02	508	SACOL1705	hypothetical protein	YP_186544.1	2.137795276
1596	E03	508	SACOL2158	conserved hypothetical protein	YP_186970.1	2.582677165
1597	E04	508	SACOL2300	conserved hypothetical protein	YP_187107.1	3.023622047
1599	E05	508	SACOL2438	endopeptidase, putative	YP_187239.1	2.356299213
1601	E06	509	SACOL2015	integrase/recombinase-related protein, authentic frameshift	N/A	2.561886051
1603	E07	511	SACOL0560	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase	YP_185448.1	2.483365949
1605	E08	511	SACOL0657	acetyltransferase, GNAT family, authentic point mutation	N/A	2.575342466
1607	E09	511	SACOL1325	glutathione peroxidase	YP_186180.1	3.170254403
1609	E10	511	SACOL1665	transcription elongation factor GreA	YP_186505.1	2.753424658
1611	E11	511	SACOL2683	peptide methionine sulfoxide reductase, putative	YP_187470.1	3.154598826
1613	E12	514	SACOL0025	conserved hypothetical protein	YP_184936.1	3.085603113
1615	F01	514	SACOL0951	Na ⁺ /H ⁺ antiporter, MnhE component	YP_185820.1	1.968871595
1618	F02	514	SACOL1461	dihydrofolate reductase	YP_186310.1	2
1619	F03	514	SACOL1841	nucleoside triphosphatase YtkD	YP_186672.1	2.426070039
1621	F04	514	SACOL2055	anti-sigma B factor	YP_186871.1	2.453307393
1623	F05	514	SACOL2064	membrane protein, putative	YP_186880.1	3.147859922
1625	F06	517	SACOL0077	hypothetical protein	YP_184982.1	2.181818182
1628	F07	517	SACOL0684	Na ⁺ /H ⁺ antiporter, MnhE component, putative	YP_185566.1	2.574468085
1629	F08	517	SACOL0756	ebsC protein	YP_185635.1	3.145067698
1633	F09	517	SACOL1120	conserved hypothetical protein	YP_185984.1	2.566731141
1635	F10	517	SACOL1134	lipopolysaccharide core biosynthesis protein	YP_185998.1	2.145067698
1637	F11	517	SACOL1845	lipoprotein, putative	YP_186676.1	3.114119923
1642	F12	520	SACOL0510	acetyltransferase, GNAT family	YP_185398.1	3.015384615
1643	G01	520	SACOL0827	acetyltransferase, putative	YP_185701.1	3.173076923
1647	G02	520	SACOL2265	molybdopterin-guanine dinucleotide biosynthesis protein B	YP_187072.1	3.167307692
1649	G03	520	SACOL2567	hypothetical protein	YP_187359.1	2.823076923
1651	G04	523	SACOL0297	conserved hypothetical protein	YP_185191.1	2.571701721
1654	G05	523	SACOL0734	conserved hypothetical protein	YP_185613.1	2
1655	G06	523	SACOL1227	polypeptide deformylase	YP_186090.1	3.143403442
1657	G07	523	SACOL2519	conserved hypothetical protein	YP_187313.1	3.135755258
1659	G08	523	SACOL2580	hypothetical protein	YP_187372.1	2.585086042
1662	G09	523	SACOL2583	acetyltransferase, GNAT family	YP_187375.1	2
1663	G10	526	SACOL0282	conserved hypothetical protein TIGR01741	YP_185177.1	2.171102662
1666	G11	526	SACOL0289	conserved hypothetical protein	YP_185183.1	2.570342205
1669	G12	526	SACOL1314	conserved hypothetical protein	YP_186170.1	3.153992395
1673	H01	526	SACOL2343	conserved hypothetical protein	YP_187149.1	2.58365019
1675	H02	526	SACOL2541	acetyltransferase, GNAT family	YP_187333.1	3.13878327
1677	H03	529	SACOL0166	conserved hypothetical protein	YP_185065.1	2.514177694
1680	H04	529	SACOL0807	conserved hypothetical protein	YP_185681.1	3.153119093
1682	H05	529	SACOL0871	acetyltransferase, putative	YP_185743.1	-
1683	H06	529	SACOL1762	thiol peroxidase, putative	YP_186596.1	3.15879017
1685	H07	529	SACOL2062	conserved hypothetical protein	YP_186878.1	2.826086957
1687	H08	529	SACOL2267	molybdenum cofactor biosynthesis protein C	YP_187074.1	1.56710775
1690	H09	530	SACOL0288	hypothetical protein, authentic frameshift	N/A	3.164150943
1691	H10	532	SACOL0172	isochorismatase	YP_185071.1	3.148496241
1693	H11	532	SACOL0710	conserved hypothetical protein	YP_185592.1	2.34962406
1695	H12	532	SACOL1048	acetyltransferase, GNAT family	YP_185913.1	3.152255639