

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 18**

Catalog No. NR-19514

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For research use only. Not for use in humans.

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 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-19514.

Material Provided:

Each inoculated well of the 96-well plate contains approximately 60 µL of culture in Luria Bertani (LB) broth containing 50 µg/mL kanamycin supplemented with 15% glycerol.

Packaging/Storage:

NR-19514 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: 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 1 day.

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 18, NR-19514.”

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 \(BMBL\)](#). 6th ed. Washington, DC: U.S. Government Printing Office, 2020.

Disclaimers:

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license is required. U.S. Government contractors may need a license before first commercial sale.

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 and a Biofilm-Producing Methicillin-Resistant

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Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 18 (ZSAJR)^{1,2}

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
3541	A01	1003	SACOL1746	6-phosphofructokinase	YP_186582.1	4.985044865
3547	A02	1003	SACOL2530	conserved hypothetical protein	YP_187323.1	4.957128614
3549	A03	1003	SACOL2549	esterase, putative	YP_187341.1	4.740777667
3551	A04	1006	SACOL0113	NAD-dependent epimerase/dehydratase family protein	YP_185017.1	4.688866799
3554	A05	1006	SACOL0793	ribonucleoside-diphosphate reductase 2, beta subunit	YP_185667.1	4.505964215
3557	A07	1006	SACOL1291	riboflavin biosynthesis protein RibF	YP_186148.1	4.997017893
3563	A09	1009	SACOL1601	competence protein comGA, putative	YP_186441.1	5.008919723
3565	A10	1009	SACOL1643	DNA polymerase III, delta subunit	YP_186483.1	5.019821606
3567	A11	1009	SACOL1715	delta-aminolevulinic acid dehydratase	YP_186553.1	4.445986125
3570	A12	1012	SACOL0781	osmoprotectant ABC transporter, ATP-binding protein, putative	YP_185656.1	5.08201581
3571	B01	1012	SACOL1103	pyruvate dehydrogenase complex E1 component, beta subunit	YP_185967.1	4.945652174
3574	B02	1012	SACOL1371	GMP reductase	YP_186224.1	5.08201581
3575	B03	1012	SACOL1639	heat-inducible transcription repressor HrcA	YP_186479.1	4.867588933
3577	B04	1012	SACOL1927	conserved hypothetical protein	YP_186752.1	4.893280632
3579	B05	1012	SACOL2396	uroporphyrinogen III methylase SirB, putative	YP_187199.1	4.954545455
3584	B07	1015	SACOL0998	oligopeptide ABC transporter, ATP-binding protein	YP_185866.1	5.078817734
3586	B08	1015	SACOL1557	conserved hypothetical protein	YP_186398.1	5.079802956
3589	B09	1015	SACOL2183	tagatose 1,6-diphosphate aldolase	YP_186994.1	4.95270936
3591	B10	1018	SACOL0637	mevalonate diphosphate decarboxylase	YP_185522.1	4.933202358
3593	B11	1018	SACOL0764	glycosyl transferase, group 2 family protein	YP_185641.1	4.927308448
3595	B12	1018	SACOL1398	transcriptional regulator, putative	YP_186250.1	4.044204322
3597	C01	1018	SACOL1424	phosphate ABC transporter, phosphate-binding protein	YP_186276.1	4.784872299
3599	C02	1018	SACOL1561	2-oxoisovalerate dehydrogenase, E1 component, beta subunit	YP_186402.1	4.847740668
3603	C04	1018	SACOL2167	iron compound ABC transporter, iron compound-binding protein	YP_186979.1	4.919449902
3605	C05	1021	SACOL0034	methicillin-resistance MecR1 regulatory protein	YP_184945.1	4.916748286
3607	C06	1021	SACOL0078	1-phosphatidylinositol phosphodiesterase	YP_184983.1	4.953966699
3609	C07	1021	SACOL0634	phosphate acetyltransferase	YP_185519.1	4.8374143
3611	C08	1021	SACOL0997	oligopeptide ABC transporter, ATP-binding protein	YP_185865.1	4.921645446
3613	C09	1021	SACOL1004	competence protein, putative	YP_185872.1	4.916748286
3615	C10	1021	SACOL1034	lipote-protein ligase A family protein	YP_185899.1	4.941234084
3618	C11	1021	SACOL1243	fatty acid/phospholipid synthesis protein PlsX	YP_186103.1	5.100881489
3619	C12	1021	SACOL1417	peptide ABC transporter, permease protein	YP_186269.1	4.377081293
3621	D01	1021	SACOL1520	pyridine nucleotide-disulfide oxidoreductase	YP_186363.1	4.861900098
3623	D02	1021	SACOL1604	glucokinase	YP_186444.1	4.860920666
3625	D03	1021	SACOL1947	conserved hypothetical protein	YP_186772.1	4.806072478
3628	D04	1024	SACOL0012	homoserine O-acetyltransferase, putative	YP_184923.1	5.063476563
3629	D05	1024	SACOL1001	tryptophanyl-tRNA synthetase	YP_185869.1	4.876953125
3631	D06	1024	SACOL1429	aspartate-semialdehyde dehydrogenase	YP_186281.1	4.884765625
3633	D07	1024	SACOL1630	conserved hypothetical protein	YP_186470.1	4.870117188
3635	D08	1024	SACOL1786	catabolite control protein A	YP_186619.1	3.827148438
3637	D09	1027	SACOL0099	iron compound ABC transporter, iron compound-binding protein SirA	YP_185004.1	4.934761441
3639	D10	1027	SACOL0262	Cchloylglycine hydrolase family protein	YP_185157.1	4.102239533

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
3641	D11	1027	SACOL1562	2-oxoisovalerate dehydrogenase, E1 component, alpha subunit	YP_186403.1	4.911392405
3643	D12	1027	SACOL2003	phospholipase C	YP_186826.1	3.808179163
3645	E01	1027	SACOL2535	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_187328.1	4.842259007
3647	E02	1030	SACOL0098	iron compound ABC transporter, permease protein SirB	YP_185003.1	3.987378641
3650	E03	1030	SACOL0411	membrane protein, putative	YP_185303.1	5.028155534
3651	E04	1030	SACOL0831	conserved hypothetical protein	YP_185705.1	4.894174757
3653	E05	1030	SACOL1847	conserved domain protein, putative	YP_186678.1	4.906796117
3655	E06	1033	SACOL0097	iron compound ABC transporter, permease protein SirC	YP_185002.1	3.818005808
3657	E07	1033	SACOL0101	ornithine cyclodeaminase, putative	YP_185006.1	4.918683446
3659	E08	1033	SACOL0257	ribose operon repressor, putative	YP_185152.1	4.907066796
3661	E09	1033	SACOL1405	anthranilate phosphoribosyltransferase	YP_186257.1	4.878025169
3663	E10	1033	SACOL1514	glycerol-3-phosphate dehydrogenase, NAD-dependent	YP_186358.1	4.896418199
3665	E11	1033	SACOL2574	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_187366.1	4.869312682
3667	E12	1036	SACOL0394	conserved hypothetical protein	YP_185286.1	4.834942085
3669	F01	1036	SACOL1181	ornithine carbamoyltransferase	YP_186044.1	4.857142857
3673	F02	1036	SACOL1843	o-succinylbenzoic acid (OSB) synthetase, putative	YP_186674.1	4.923745174
3675	F03	1036	SACOL2057	sigma factor B regulator protein	YP_186873.1	4.894787645
3679	F04	1036	SACOL2178	alcohol dehydrogenase, zinc-containing	YP_186989.1	4.907335907
3681	F05	1039	SACOL0507	LysM domain protein	YP_185395.1	5.602502406
3683	F06	1039	SACOL0705	iron compound ABC transporter, permease protein	YP_185587.1	5.518768046
3685	F07	1039	SACOL0777	urea amidolyase-related protein	YP_185652.1	5.948026949
3687	F08	1039	SACOL1696	Holliday junction DNA helicase RuvB	YP_186535.1	5.963426372
3689	F09	1039	SACOL2045	ketol-acid reductoisomerase	YP_186862.1	5.980750722
3692	F10	1039	SACOL2269	molybdopterin biosynthesis MoeB protein, putative	YP_187076.1	5.856592878
3693	F11	1039	SACOL2367	quinone oxidoreductase, YhdH/YhfP family	YP_187172.1	5.235803657
3695	F12	1042	SACOL0569	ATP:guanido phosphotransferase family protein	YP_185457.1	5.850287908
3697	G01	1042	SACOL0722	phosphate transporter family protein	YP_185603.1	5.780230326
3699	G02	1042	SACOL2426	biotin synthetase	YP_187228.1	4.025911708
3701	G03	1045	SACOL0660	alcohol dehydrogenase, zinc-containing	YP_185544.1	5.213397129
3704	G04	1045	SACOL0838	glyceraldehyde 3-phosphate dehydrogenase	YP_185712.1	5.849760766
3705	G05	1045	SACOL1057	V8 Protease	YP_185922.1	5.988516746
3707	G06	1045	SACOL1059	conserved hypothetical protein	YP_185924.1	5.954066986
3710	G07	1045	SACOL1663	urea amidolyase-related protein	YP_186503.1	5.745454545
3711	G08	1045	SACOL2596	conserved hypothetical protein	YP_187387.1	6.004784689
3713	G09	1045	SACOL2656	ornithine carbamoyltransferase	YP_187444.1	5.523444976
3715	G10	1048	SACOL0837	gap transcriptional regulator	YP_185711.1	5.915076336
3717	G11	1048	SACOL1678	bacterial luciferase family protein	YP_186518.1	5.458015267
3719	G12	1048	SACOL2701	histidinol-phosphate aminotransferase, putative	YP_187487.1	5.088740458
3721	H01	1051	SACOL0706	iron compound ABC transporter, permease protein	YP_185588.1	5.893434824
3723	H02	1054	SACOL1095	cytochrome d ubiquinol oxidase, subunit II	YP_185959.1	5.509487666
3725	H03	1054	SACOL1112	conserved hypothetical protein	YP_185976.1	5.95256167
3728	H04	1054	SACOL1552	maltose operon repressor	YP_186393.1	5.714421252
3729	H05	1054	SACOL2332	aldose 1-epimerase	YP_187139.1	5.95256167
3732	H06	1055	SACOL1573	integrase/recombinase, core domain family, authentic frameshift	N/A	5.545023697
3733	H07	1057	SACOL0398	lipoate-protein ligase A family protein	YP_185290.1	5.947019868
3736	H08	1057	SACOL0858	secretory extracellular matrix and plasma binding protein	YP_185731.1	5.750236518
3739	H09	1060	SACOL0162	formate dehydrogenase, NAD-dependent	YP_185061.1	5.967924528
3741	H10	1060	SACOL0237	alcohol dehydrogenase, zinc-containing	YP_185133.1	5.900943396
3743	H11	1060	SACOL0241	alcohol dehydrogenase, zinc-containing	YP_185137.1	5.833018868
3745	H12	1060	SACOL0399	oxidoreductase, putative	YP_185291.1	5.128301887

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

²25 clones in the *Staphylococcus aureus* (MRSA), Strain COL Gateway® 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).