

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 14**

Catalog No. NR-19510

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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:

Every inoculated well of each 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-19510 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 14, NR-19510."

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 14 (ZSAJN)

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
2721	A01	793	SACOL1019	conserved hypothetical protein	YP_185885.1	5.296343001
2724	A02	793	SACOL1946	methionine aminopeptidase, type I	YP_186771.1	5.290037831
2725	A03	793	SACOL2697	hisF protein (cyclase)	YP_187483.1	4.287515763
2727	A04	793	SACOL2724	ABC transporter, ATP-binding protein	YP_187510.1	5.297604035
2729	A05	796	SACOL0159	ABC transporter, permease protein	YP_185058.1	5.290201005
2731	A06	796	SACOL0252	conserved hypothetical protein	YP_185148.1	5.301507538
2734	A07	796	SACOL0718	ABC transporter, ATP-binding protein	YP_185600.1	5.262562814
2735	A08	796	SACOL0798	iron compound ABC transporter, ATP-binding protein, putative	YP_185672.1	5.298994975
2737	A09	796	SACOL0808	membrane protein, putative	YP_185682.1	5.302763819
2739	A10	796	SACOL0840	triosephosphate isomerase	YP_185714.1	4.510050251
2741	A11	796	SACOL0914	FeS assembly ATPase SufC	YP_185785.1	5.293969849
2743	A12	796	SACOL1872	epidermin immunity protein F	YP_186700.1	5.311557789
2745	B01	796	SACOL2651	tributyryn esterase EstA, putative	YP_187439.1	5.300251256
2747	B02	799	SACOL0108	hypothetical protein	YP_185012.1	5.281602003
2749	B03	799	SACOL0138	capsular polysaccharide biosynthesis protein Cap5C	YP_185038.1	5.302878598
2751	B04	799	SACOL0167	acetylglutamate kinase	YP_185066.1	5.312891114
2753	B05	799	SACOL0632	membrane protein, putative	YP_185517.1	5.327909887
2757	B06	799	SACOL0757	transcriptional regulator, DeoR family	YP_185636.1	5.294117647
2759	B07	799	SACOL2255	conserved hypothetical protein	YP_187062.1	3.847309136
2761	B08	799	SACOL2317	phosphosugar-binding transcriptional regulator	YP_187124.1	5.304130163
2763	B09	799	SACOL2517	transcriptional regulator, MerR family	YP_187311.1	5.331664581
2766	B10	799	SACOL2644	ABC transporter, ATP-binding protein	YP_187432.1	5.310387985
2768	B11	802	SACOL0083	staphylococcal tandem lipoprotein	YP_184988.1	5.298004988
2769	B12	802	SACOL1261	ribonuclease HII	YP_186119.1	5.284289277
2771	C01	802	SACOL1412	hydrolase-related protein	YP_186264.1	5.296758105
2773	C02	802	SACOL2581	staphyloxanthin biosynthesis protein	YP_187373.1	5.300498753
2775	C03	802	SACOL2685	capsular polysaccharide biosynthesis protein Cap1C	YP_187472.1	5.306733167
2777	C04	802	SACOL2715	hypothetical protein	YP_187501.1	3.302992519
2780	C05	805	SACOL0079	staphylococcus tandem lipoprotein	YP_184984.1	5.275776398
2781	C06	805	SACOL0080	staphylococcus tandem lipoprotein	YP_184985.1	5.30310559
2783	C07	805	SACOL1016	enoyl-(acyl-carrier-protein) reductase	YP_185882.1	5.30931677
2785	C08	805	SACOL1279	undecaprenyl diphosphate synthase	YP_186136.1	5.283229814
2787	C09	805	SACOL1763	conserved hypothetical protein	YP_186597.1	5.298136646
2789	C10	805	SACOL1840	conserved hypothetical protein	YP_186671.1	5.31552795
2791	C11	805	SACOL2054	RNA polymerase sigma-37 factor	YP_186870.1	5.285714286
2794	C12	805	SACOL2274	acetyltransferase, GNAT family	YP_187081.1	5.272049689
2795	D01	805	SACOL2526	membrane protein, putative, authentic point mutation	N/A	5.314285714
2798	D02	808	SACOL0127	phosphonate ABC transporter, ATP-binding protein	YP_185031.1	4.727722772
2799	D03	808	SACOL0189	staphylococcus tandem lipoprotein	YP_185088.1	5.288366337
2801	D04	808	SACOL0369	prophage L54a, Clp protease, putative	YP_185261.1	4.292079208
2803	D05	808	SACOL0534	deoxyribonuclease, TatD family	YP_185422.1	5.170792079

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2806	D06	808	SACOL1272	transcriptional regulator CodY	YP_186130.1	5.301980198
2807	D07	808	SACOL1415	peptide ABC transporter, ATP-binding protein	YP_186267.1	5.27970297
2809	D08	808	SACOL1683	HesA/MoeB/ThiF family protein	YP_186523.1	5.297029703
2813	D09	811	SACOL0106	HPCH/HPAI aldolase family protein	YP_185010.1	5.302096178
2815	D10	811	SACOL0111	acetoin reductase	YP_185015.1	5.231812577
2818	D11	811	SACOL0483	staphylococcus tandem lipoprotein	YP_185373.1	4.754623921
2819	D12	811	SACOL1274	ribosomal protein S2	YP_186131.1	5.289765721
2821	E01	811	SACOL1797	metallo-beta-lactamase family protein	YP_186630.1	5.316892725
2823	E02	811	SACOL2298	N-acetylmuramoyl-L-alanine amidase, family 4	YP_187105.1	4.639950678
2826	E03	811	SACOL2461	conserved hypothetical protein TIGR00245	YP_187259.1	3.96054254
2827	E04	811	SACOL2498	staphylococcus tandem lipoprotein	YP_187293.1	5.295930949
2830	E05	812	SACOL1855	transposase, putative, degenerate	N/A	4.68226601
2831	E06	814	SACOL0931	hydrolase, haloacid dehalogenase-like family	YP_185801.1	5.245700246
2834	E07	814	SACOL1204	YlmH protein	YP_186066.1	5.272727273
2835	E08	814	SACOL2412	amino acid ABC transporter, amino acid-binding protein	YP_187215.1	5.27027027
2837	E09	817	SACOL0511	conserved hypothetical protein	YP_185399.1	5.305997552
2839	E10	817	SACOL1280	phosphatidate cytidyltransferase	YP_186137.1	5.277845777
2841	E11	817	SACOL1406	indole-3-glycerol phosphate synthase	YP_186258.1	5.29130967
2843	E12	817	SACOL2144	ABC transporter, ATP-binding protein	YP_186957.1	5.307221542
2845	F01	817	SACOL2272	molybdenum ABC transporter, molybdenum-binding protein ModA	YP_187079.1	5.279069767
2847	F02	820	SACOL0485	staphylococcus tandem lipoprotein	YP_185375.1	5.267073171
2849	F03	820	SACOL1613	ABC transporter, ATP-binding protein	YP_186453.1	5.264634146
2851	F04	820	SACOL2021	hydrolase, carbon-nitrogen family	YP_186840.1	4.954878049
2853	F05	820	SACOL2497	staphylococcus tandem lipoprotein	YP_187292.1	5.282926829
2855	F06	823	SACOL0022	yycI protein	YP_184933.1	5.260024301
2858	F07	823	SACOL0671	hydrolase, alpha/beta hydrolase fold family	YP_185555.1	4.752126367
2861	F08	826	SACOL0250	PTS system, IIA component	YP_185146.1	4.997578692
2863	F09	826	SACOL0325	prophage L54a, antirepressor, putative	YP_185217.1	4.185230024
2865	F10	826	SACOL0482	staphylococcus tandem lipoprotein	YP_185372.1	4.561743341
2867	F11	826	SACOL1200	conserved hypothetical protein TIGR00726	YP_186062.1	5.268765133
2869	F12	826	SACOL1445	CbbQ/NirQ/NorQ/GpvN family protein	YP_186297.1	4.998789346
2871	G01	826	SACOL1799	conserved hypothetical protein	YP_186632.1	5.279661017
2877	G02	829	SACOL0694	tagH protein, teichoic acid ABC transporter protein, putative	YP_185576.1	5.240048251
2881	G03	829	SACOL2493	staphylococcus tandem lipoprotein	YP_187288.1	5.294330519
2883	G04	829	SACOL2722	N-acetyltransferase family protein	YP_187508.1	5.265379976
2885	G05	832	SACOL0704	iron compound ABC transporter, ATP-binding protein	YP_185586.1	5.263221154
2887	G06	832	SACOL0723	LysM domain protein	YP_185604.1	5.272836538
2889	G07	832	SACOL1109	spermidine/putrescine ABC transporter, permease protein	YP_185973.1	5.271634615
2891	G08	832	SACOL1207	glyoxalase family protein	YP_186069.1	5.268028846
2893	G09	832	SACOL1307	conserved hypothetical protein TIGR00282	YP_186164.1	5.180288462
2895	G10	832	SACOL2273	formate dehydrogenase accessory protein FdhD	YP_187080.1	5.283653846
2897	G11	832	SACOL2303	inositol monophosphatase family protein	YP_187110.1	5.304086538
2899	G12	835	SACOL0023	metallo-beta-lactamase family protein YycJ	YP_184934.1	5.295808383
2901	H01	835	SACOL0126	phosphonate ABC transporter, permease protein	YP_185030.1	5.241916168
2903	H02	835	SACOL0314	conserved hypothetical protein	YP_185206.1	5.2
2905	H03	835	SACOL0341	conserved hypothetical protein	YP_185233.1	5.279041916
2908	H04	835	SACOL0396	conserved domain protein	YP_185288.1	5.286227545
2910	H05	835	SACOL0481	staphylococcus tandem lipoprotein	YP_185371.1	3.725748503
2911	H06	835	SACOL0668	hydrolase, alpha/beta hydrolase fold family	YP_185552.1	5.256287425
2913	H07	835	SACOL1161	glutamate racemase	YP_186024.1	4.936526946

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Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
2915	H08	835	SACOL2536	hydrolase, haloacid dehalogenase-like family	YP_187329.1	4.241916168
2917	H09	838	SACOL0527	conserved hypothetical protein	YP_185415.1	4.186157518
2921	H10	838	SACOL1026	conserved hypothetical protein	YP_185892.1	4.708830549
2923	H11	838	SACOL1053	hydrolase, alpha/beta hydrolase fold family	YP_185918.1	5.257756563
2925	H12	838	SACOL1365	hydrolase, haloacid dehalogenase-like family	YP_186218.1	4.933174224