

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 23**

Catalog No. NR-19519

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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-19519.

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-19519 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 23, NR-19519.”

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 23 (ZSAJW)^{1,2}

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
4629	A01	1423	SACOL0086	drug transporter, putative	YP_184991.1	5.988756149
4631	A02	1423	SACOL0454	sodium:dicarboxylate symporter family protein	YP_185344.1	5.495432186
4635	A03	1426	SACOL1622	glycyl-tRNA synthetase	YP_186462.1	5.00911641
4637	A04	1432	SACOL0091	transcriptional regulator, GntR family/aminotransferase, class I	YP_184996.1	6.122905028
4639	A05	1432	SACOL0918	FeS assembly protein SufB	YP_185789.1	6.166201117
4643	A06	1435	SACOL0016	replicative DNA helicase	YP_184927.1	5.72543554
4645	A07	1435	SACOL0576	cysteinyI-tRNA synthetase	YP_185462.1	6.059930314
4647	A08	1435	SACOL0620	osmoprotectant proline transporter	YP_185505.1	5.821602787
4653	A09	1435	SACOL1887	protoporphyrinogen oxidase	YP_186713.1	5.505226481
4656	A10	1435	SACOL2292	Na ⁺ /H ⁺ antiporter NhaC	YP_187099.1	5.958885017
4657	A11	1435	SACOL2449	drug transporter, putative	YP_187248.1	5.530313589
4662	A12	1441	SACOL1105	pyruvate dehydrogenase complex E3 component, lipoamide dehydrogenase	YP_185969.1	5.879944483
4663	B01	1441	SACOL1403	anthranilate synthase component I	YP_186255.1	6.131158917
4665	B02	1441	SACOL1554	6-phosphogluconate dehydrogenase, decarboxylating	YP_186395.1	6.097154754
4667	B03	1444	SACOL0643	conserved hypothetical protein	YP_185528.1	6.186980609
4669	B04	1444	SACOL1801	peptidase, M20/M25/M40 family	YP_186634.1	6.051939058
4673	B05	1447	SACOL1198	cell division protein FtsA	YP_186060.1	6.111955771
4675	B06	1447	SACOL2095	ATP synthase F1, beta subunit	YP_186910.1	6.089149965
4678	B07	1447	SACOL2180	6-phospho-beta-galactosidase	YP_186991.1	6.00138217
4681	B08	1456	SACOL1368	catalase	YP_186221.1	6.150412088
4683	B09	1456	SACOL1563	2-oxoisovalerate dehydrogenase, E3 component, lipoamide dehydrogenase	YP_186404.1	5.500686813
4688	B10	1462	SACOL0516	PTS system, IIBC components	YP_185404.1	5.924076607
4698	B11	1471	SACOL0251	6-phospho-beta-glucosidase	YP_185147.1	5.90278722
4699	B12	1474	SACOL0828	TPR domain protein	YP_185702.1	5.844640434
4702	C01	1477	SACOL2157	drug resistance transporter, EmrB/QacA subfamily	YP_186969.1	5.86662153
4703	C02	1477	SACOL2376	PTS system, sucrose-specific IIBC components, putative	YP_187180.1	5.72647258
4706	C03	1483	SACOL2619	amino acid permease	YP_187408.1	5.788941335
4707	C04	1489	SACOL0178	PTS system, IIBC components	YP_185077.1	4.934184016
4709	C05	1489	SACOL0389	prophage L54a, amidase, putative	YP_185281.1	5.860980524
4711	C06	1489	SACOL0574	glutamyl-tRNA synthetase	YP_185460.1	5.702484889
4713	C07	1489	SACOL1367	amino acid permease	YP_186220.1	5.77904634
4715	C08	1492	SACOL0897	conserved hypothetical protein	YP_185768.1	4.606568365
4717	C09	1492	SACOL0935	D-alanine-activating enzyme/D-alanine-D-alanyl carrier protein ligase	YP_185805.1	5.787533512
4719	C10	1492	SACOL1916	amino acid ABC transporter, permease/substrate-binding protein	YP_186741.1	5.237935657
4721	C11	1492	SACOL1961	glutamyl-tRNA(Gln) amidotransferase, A subunit	YP_186785.1	5.693699732
4723	C12	1495	SACOL1522	elastin binding protein, putative	YP_186365.1	5.711036789
4727	D01	1498	SACOL1606	rhomboïd family protein	YP_186446.1	5.283044059
4732	D02	1501	SACOL0460	inosine-5-monophosphate dehydrogenase	YP_185350.1	5.818121253
4735	D03	1504	SACOL1975	conserved hypothetical protein	YP_186799.1	5.658244681
4739	D04	1507	SACOL1593	glycine cleavage system P protein, subunit 2	YP_186433.1	5.583941606

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
4747	D05	1513	SACOL1082	phosphoribosylaminoimidazolecarboxamide formyltransferase/IMP cyclohydrolase	YP_185946.1	4.962987442
4749	D06	1513	SACOL1844	O-succinylbenzoic acid--CoA ligase, putative	YP_186675.1	5.776602776
4751	D07	1513	SACOL2362	malate:quinone oxidoreductase	YP_187167.1	5.710508923
4757	D08	1516	SACOL1351	cardiolipin synthetase	YP_186204.1	5.413588391
4759	D09	1519	SACOL0494	NADH dehydrogenase I, F subunit	YP_185382.1	5.60236998
4763	D10	1519	SACOL1079	amidophosphoribosyltransferase	YP_185943.1	5.191573404
4765	D11	1519	SACOL1549	glucose-6-phosphate 1-dehydrogenase	YP_186390.1	5.725477288
4768	D12	1519	SACOL2029	sucrose-6-phosphate hydrolase	YP_186847.1	5.949967084
4771	E01	1522	SACOL0154	aldehyde dehydrogenase	YP_185054.1	5.681997372
4773	E02	1522	SACOL0562	lysyl-tRNA synthetase	YP_185450.1	5.720105125
4775	E03	1522	SACOL1738	hypothetical protein	YP_186575.1	5.229303548
4781	E04	1525	SACOL2628	betaine aldehyde dehydrogenase	YP_187417.1	5.771147541
4783	E05	1528	SACOL1728	amino acid permease	YP_186566.1	5.797120419
4785	E06	1528	SACOL2579	phytoene dehydrogenase	YP_187371.1	5.293848168
4788	E07	1531	SACOL0682	Na ⁺ /H ⁺ antiporter, MnhD component, putative	YP_185565.1	6.024167211
4789	E08	1531	SACOL0952	Na ⁺ /H ⁺ antiporter, MnhD component	YP_185821.1	5.580666231
4794	E09	1531	SACOL2445	fntA-like protein	YP_187245.1	6.112998041
4795	E10	1531	SACOL2623	malate:quinone oxidoreductase	YP_187412.1	5.841933377
4797	E11	1537	SACOL1821	conserved hypothetical protein	YP_186653.1	5.895901106
4800	E12	1540	SACOL0214	long-chain-fatty-acid--CoA ligase, putative	YP_185113.1	7.028571429
4802	F01	1540	SACOL0788	proton-dependent oligopeptide transporter family protein	YP_185661.1	6.528571429
4803	F02	1543	SACOL0479	surface protein, putative	YP_185369.1	6.766040181
4807	F03	1543	SACOL2576	dehydrosqualene desaturase	YP_187368.1	6.255994815
4809	F04	1543	SACOL2670	glycosyl transferase, group 1 family protein	YP_187458.1	6.771872975
4811	F05	1546	SACOL0052	glycosyl transferase, group 1 family protein	YP_184962.1	6.678525226
4814	F06	1546	SACOL1031	5 nucleotidase family protein	YP_185896.1	6.045278137
4817	F07	1549	SACOL0783	osmoprotectant ABC transporter, permease protein	YP_185657.1	6.757908328
4819	F08	1552	SACOL0841	phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent	YP_185715.1	6.716494845
4823	F09	1552	SACOL1929	ABC transporter, ATP-binding protein, putative	YP_186754.1	6.121778351
4825	F10	1555	SACOL2072	ATP-dependent RNA helicase, DEAD/DEAH box family	YP_186888.1	4.594855305
4831	F11	1558	SACOL0451	alkyl hydroperoxide reductase, subunit F	YP_185341.1	6.532092426
4834	F12	1561	SACOL0095	immunoglobulin G binding protein A precursor	YP_185000.1	4.420243434
4835	G01	1561	SACOL0548	polysaccharide biosynthesis protein	YP_185436.1	6.67648943
4837	G02		SACOL0857	CLONE IS NOT AVAILABLE ¹	YP_185730.1	
4839	G03	1564	SACOL0224	PTS system, IIBC components	YP_185122.1	6.46483376
4841	G04	1564	SACOL2046	2-isopropylmalate synthase	YP_186863.1	6.650895141
4843	G05	1564	SACOL2659	zinc metalloproteinase aureolysin	YP_187447.1	6.672634271
4846	G06	1567	SACOL0311	sodium:solute symporter family protein	YP_185203.1	7.09444799
4853	G07	1573	SACOL2483	transporter, putative	YP_187279.1	6.552447552
4856	G08	1576	SACOL0461	GMP synthase	YP_185351.1	6.860406091
4857	G09	1579	SACOL0129	conserved hypothetical protein	YP_185033.1	6.73780874
4859	G10	1579	SACOL1312	tRNA-i(6)A37 modification enzyme MiaB	YP_186168.1	6.694110196
4861	G11	1579	SACOL2569	delta-1-pyrroline-5-carboxylate dehydrogenase, putative	YP_187361.1	6.724509183
4863	G12	1585	SACOL2403	ABC transporter, substrate-binding protein	YP_187206.1	6.641009464
4865	H01	1588	SACOL0750	anion transporter family protein	YP_185629.1	6.698992443
4867	H02	1588	SACOL2515	gluconokinase	YP_187309.1	6.632871537
4870	H03	1588	SACOL2674	accessory secretory protein Asp1	YP_187462.1	5.921284635
4871	H04	1591	SACOL0202	sensor histidine kinase family protein	YP_185101.1	6.548082967
4879	H06	1594	SACOL1305	HD/HDIG/KH domain protein	YP_186162.1	6.624843162
4883	H07	1597	SACOL1025	peptide chain release factor 3	YP_185891.1	6.629304947
4887	H08	1597	SACOL2176	osmoprotectant transporter, BCCT family	YP_186987.1	6.658108954
4890	H09	1603	SACOL1018	sodium:alanine symporter family protein	YP_185884.1	6.874610106
4891	H10	1603	SACOL2673	accessory secretory protein Asp2	YP_187461.1	6.613225203
4893	H11	1606	SACOL0215	propionate CoA-transferase, putative	YP_185114.1	6.653175592
4895	H12	1606	SACOL1294	metallo-beta-lactamase family protein	YP_186151.1	5.97011208

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).