

Product Information Sheet for NR-19515

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 19**

Catalog No. NR-19515

This reagent is the tangible property of the U.S. Government.

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:

Every 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-19515 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 19, NR-19515."

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:

You are authorized to use this product for research use only. It is not intended for human use.

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Staphylococcus epidermidis Strain." J. Bacteriol. 187 (2005): 2426-2438. PubMed: 15774886.

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



References:

1. 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

Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 19 (ZSAJS)¹

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
3747	A01	1060	SACOL0504	ABC transporter, ATP-binding protein	YP_185392.1	5.947169811
3749	A02	1060	SACOL0882	ABC transporter, ATP-binding protein	YP_185753.1	5.971698113
3752	A03	1060	SACOL1349	conserved hypothetical protein	YP_186202.1	5.399056604
3753	A04	1060	SACOL1695	S-adenosylmethionine:tRNA ribosyltransferase-isomerase	YP_186534.1	5.967924528
3755	A05	1060	SACOL1734	glyceraldehyde 3-phosphate dehydrogenase	YP_186571.1	5.987735849
3757	A06	1060	SACOL2038	metalloendopeptidase, putative, glycoprotease family	YP_186855.1	5.933962264
3759	A07	1063	SACOL0140	capsular polysaccharide biosynthesis protein Cap5E	YP_185040.1	5.952963311
3761	A08	1063	SACOL0799	transferrin receptor	YP_185673.1	5.466603951
3763	A09	1063	SACOL1080	phosphoribosylformylglycinamide cyclo-ligase	YP_185944.1	5.939793039
3765	A10	1063	SACOL1985	conserved hypothetical protein	YP_186809.1	5.898400753
3767	A11	1066	SACOL0160	conserved hypothetical protein	YP_185059.1	5.85272045
3769	A12	1066	SACOL0169	N-acetyl-gamma-glutamyl-phosphate reductase	YP_185068.1	5.045028143
3772	B01	1066	SACOL0307	perfringolysin O regulator protein	YP_185199.1	4.695121951
3773	B02	1066	SACOL1402	glutamyl aminopeptidase, putative	YP_186254.1	5.948405253
3775	B03	1066	SACOL2166	iron compound ABC transporter, permease protein	YP_186978.1	5.785178236
3779	B04	1069	SACOL2390	sensory box histidine kinase, putative	YP_187193.1	4.882132834
3781	B05	1072	SACOL1889	uroporphyrinogen decarboxylase	YP_186715.1	5.259328358
3783	B06	1072	SACOL1926	A/G-specific adenine glycosylase	YP_186751.1	5.844216418
3785	B07	1075	SACOL0197	oxidoreductase, Gfo/Idh/MocA family	YP_185096.1	5.909767442
3787	B08	1075	SACOL0717	sensor histidine kinase	YP_185599.1	5.92372093
3789	B09	1075	SACOL0921	CBS domain protein	YP_185792.1	5.586046512
3791	B10	1075	SACOL1477	threonine dehydratase, catabolic	YP_186322.1	5.83627907
3793	B11	1075	SACOL1988	acyl-coenzyme A:6-aminopenicillanic acid acyl-transferase	YP_186812.1	5.844651163
3795	B12	1078	SACOL0235	hexitol dehydrogenase	YP_185131.1	5.866419295
3797	C01	1078	SACOL0712	lipase/esterase	YP_185594.1	5.882189239
3799	C02	1078	SACOL1304	recA protein	YP_186161.1	5.634508349
3801	C03	1078	SACOL1820	riboflavin biosynthesis protein RibD	YP_186652.1	5.907235622
3804	C04	1078	SACOL1943	sensor histidine kinase VraS	YP_186768.1	4.32096475
3805	C05	1078	SACOL2546	perfringolysin O regulator protein, putative	YP_187338.1	5.653988868
3807	C06	1081	SACOL1576	traG protein, putative	YP_186416.1	5.882516189
3809	C07	1081	SACOL2047	3-isopropylmalate dehydrogenase	YP_186864.1	5.452358927
3811	C08	1084	SACOL0305	ABC transporter, permease protein	YP_185197.1	5.885608856
3813	C09	1084	SACOL2341	isopentenyl diphosphate isomerase	YP_187147.1	5.857933579
3815	C10	1086	SACOL2692	intercellular adhesion protein C, authentic frameshift	N/A	5.821362799
3817	C11	1087	SACOL1140	LPXTG cell wall surface anchor protein	YP_186003.1	5.785648574
3819	C12	1087	SACOL2721	high-affinity nickel-transport protein	YP_187507.1	5.833486661
3821	D01	1090	SACOL0176	conserved hypothetical protein	YP_185075.1	5.851376147

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3824	D02	1090	SACOL0233	sorbitol dehydrogenase	YP_185129.1	5.277981651
3825	D03	1090	SACOL0765	sensor histidine kinase SaeS	YP_185642.1	5.634862385
3827	D04	1090	SACOL0810	glycosyl transferase, group 4 family protein	YP_185684.1	4.008256881
3829	D05	1090	SACOL1582	conserved hypothetical protein	YP_186422.1	4.070642202
3831	D06	1090	SACOL1756	proline dipeptidase	YP_186590.1	4.799082569
3835	D08	1090	SACOL2108	Sua5/YciO/YrdC/YwIC family protein	YP_186923.1	5.85412844
3837	D09	1090	SACOL2357	ABC transporter, permease protein	YP_187162.1	5.811926606
3839	D10	1090	SACOL2585	regulatory protein, putative	YP_187377.1	5.040366972
3845	D12	1093	SACOL1148	phenylalanyl-tRNA synthetase, alpha subunit	YP_186011.1	5.628545288
3848	E01	1096	SACOL0409	conserved hypothetical protein	YP_185301.1	5.76459854
3849	E02	1096	SACOL0697	teichoic acid biosynthesis protein X	YP_185579.1	5.823905109
3853	E03	1096	SACOL1588	proline dipeptidase	YP_186428.1	5.011861314
3855	E04	1096	SACOL1917	PTS system, IIC component	YP_186742.1	5.864051095
3858	E05	1099	SACOL1505	3-dehydroquinate synthase	YP_186349.1	5.403093722
3859	E06	1099	SACOL2156	ATP-binding protein, Mrp/Nbp35 family	YP_186968.1	4.98544131
3861	E07	1099	SACOL2606	dihydroorotate dehydrogenase	YP_187396.1	5.761601456
3863	E08	1100	SACOL0941	NADH dehydrogenase, putative, authentic frameshift	N/A	4.879090909
3867	E09	1102	SACOL0063	conserved hypothetical protein	YP_184968.1	5.831215971
3870	E10	1102	SACOL0711	conserved hypothetical protein	YP_185593.1	5.323049002
3871	E11	1102	SACOL0922	conserved hypothetical protein	YP_185793.1	5.863883848
3873	E12	1105	SACOL0809	GGDEF domain protein	YP_185683.1	5.865158371
3877	F01	1105	SACOL1124	cytochrome oxidase assembly protein	YP_185988.1	5.012669683
3879	F02	1105	SACOL1453	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	YP_186305.1	5.721266968
3881	F03	1105	SACOL1600	competence protein ComGB, putative	YP_186440.1	5.833484163
3884	F04	1105	SACOL1955	DNA-damage-inducible protein P	YP_186780.1	4.847963801
3885	F05	1105	SACOL2074	D-alanine--D-alanine ligase	YP_186890.1	5.752941176
3887	F06	1105	SACOL2168	conserved hypothetical protein	YP_186980.1	5.753846154
3892	F07	1108	SACOL0573	PIN/TRAM domain protein	YP_185459.1	5.767148014
3894	F08	1108	SACOL1111	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein	YP_185975.1	5.315884477
3895	F09	1108	SACOL1712	abrB protein abrB protein, putative	YP_186551.1	5.873646209
3897	F10	1111	SACOL0196	oxidoreductase, Gfo/Idh/MocA family	YP_185095.1	5.832583258
3899	F11	1111	SACOL0600	branched-chain amino acid aminotransferase	YP_185486.1	5.02520252
3901	F12	1111	SACOL0638	phosphomevalonate kinase	YP_185523.1	5.891989199
3903	G01	1111	SACOL1142	hypothetical protein	YP_186005.1	4.99909991
3907	G02	1111	SACOL1976	nitric-oxide synthase, oxygenase subunit	YP_186800.1	5.815481548
3909	G03	1111	SACOL2110	peptide chain release factor 1	YP_186925.1	5.767776778
3911	G04	1111	SACOL2463	glutamyl-aminopeptidase	YP_187261.1	5.760576058
3913	G05	1114	SACOL2034	conserved hypothetical protein	YP_186851.1	5.831238779
3915	G06	1114	SACOL2528	conserved hypothetical protein	YP_187321.1	5.828545781
3917	G07	1117	SACOL0813	comf operon protein 1, putative	YP_185687.1	5.607878245
3920	G08	1117	SACOL0993	oligopeptide ABC transporter, ATP-binding protein	YP_185861.1	5.794091316
3923	G10	1120	SACOL1017	conserved hypothetical protein	YP_185883.1	5.56875
3925	G11	1120	SACOL1434	alanine racemase family protein	YP_186286.1	5.591964286
3929	G12	1126	SACOL1401	prephenate dehydrogenase	YP_186253.1	5.826820604
3931	H01	1126	SACOL1583	replication initiation factor family protein	YP_186423.1	3.846358792
3934	H02	1126	SACOL1595	glycine cleavage system T protein	YP_186435.1	5.703374778
3935	H03	1126	SACOL1787	chorismate mutase/phospho-2-dehydro-3-deoxyheptonate aldolase	YP_186620.1	5.726465364
3937	H04	1129	SACOL1108	spermidine/putrescine ABC transporter, ATP-binding protein	YP_185972.1	5.748449956

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3939	H05	1129	SACOL1230	conserved hypothetical protein TIGR00048	YP_186093.1	5.469441984
3941	H06	1129	SACOL1923	conserved hypothetical protein	YP_186748.1	5.8255093
3943	H07	1132	SACOL0192	maltose ABC transporter, ATP-binding protein, putative	YP_185091.1	4.786219081
3945	H08	1132	SACOL0435	conserved hypothetical protein TIGR00092	YP_185326.1	5.787985866
3947	H09	1132	SACOL1980	conserved hypothetical protein	YP_186804.1	4.465547703
3949	H10	1135	SACOL1070	cytochrome aa3 quinol oxidase, subunit II	YP_185934.1	5.47753304
3951	H11	1135	SACOL1214	carbamoyl-phosphate synthase, small subunit	YP_186077.1	4.727753304
3953	H12	1135	SACOL1616	conserved hypothetical protein TIGR00486	YP_186456.1	4.873127753

¹25 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).