

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 10**

**Catalog No. NR-19506**

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-19506 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 10, NR-19506."

**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/bmbl5/index.htm](http://www.cdc.gov/biosafety/publications/bmbl5/index.htm).

**Disclaimers:**

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

Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at [www.beiresources.org](http://www.beiresources.org).

While BEI Resources uses reasonable efforts to include accurate and up-to-date information on this product sheet, neither ATCC® nor the U.S. Government makes any warranties or representations as to its accuracy. Citations from scientific literature and patents are provided for informational purposes only. Neither ATCC® nor the U.S. Government warrants that such information has been confirmed to be accurate.

This product is sent with the condition that you are responsible for its safe storage, handling, use and disposal. ATCC® and the U.S. Government are not liable for any damages or injuries arising from receipt and/or use of this product. While reasonable effort is made to ensure authenticity and reliability of materials on deposit, the U.S. Government, ATCC®, their suppliers and contributors to BEI Resources are not liable for damages arising from the misidentification or misrepresentation of products.

**Use Restrictions:**

This material is distributed for internal research, non-commercial purposes only. This material, its product or its derivatives may not be distributed to third parties. Except as performed under a U.S. Government contract, individuals contemplating commercial use of the material, its products or its derivatives must contact the contributor to determine if a license is required. U.S. Government contractors may need a license before first commercial sale.

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

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



**Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 10 (ZSAJJ)**

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1917	A01	589	SACOL2275	BioY family protein	YP_187082.1	3.263157895
1920	A02	589	SACOL2709	conserved hypothetical protein	YP_187495.1	3.132427844
1921	A03	592	SACOL0148	capsular polysaccharide biosynthesis galactosyltransferase Cap5M	YP_185048.1	3.136824324
1924	A04	592	SACOL0908	hypothetical protein	YP_185779.1	3.527027027
1925	A05	592	SACOL1136	conserved hypothetical protein	YP_186000.1	3.565878378
1927	A06	592	SACOL1587	translation elongation factor P	YP_186427.1	4.297297297
1929	A07	592	SACOL1896	conserved hypothetical protein	YP_186722.1	3.518581081
1931	A08	592	SACOL1990	conserved hypothetical protein	YP_186814.1	3.22972973
1933	A09	592	SACOL2593	transcriptional regulator, TetR family	YP_187384.1	4.22972973
1938	A10	595	SACOL0678	integrase/recombinase, phage integrase family	YP_185561.1	2.416806723
1939	A11	595	SACOL1711	DNA-3-methyladenine glycosylase	YP_186550.1	4.275630252
1942	A12	595	SACOL1858	hypothetical protein	YP_186686.1	2.803361345
1943	B01	595	SACOL1981	isochorismatase family protein	YP_186805.1	4.151260504
1945	B02	595	SACOL2066	K <sup>+</sup> -transporting ATPase, C subunit	YP_186882.1	4.240336134
1947	B03	595	SACOL2667	isochorismatase family protein	YP_187455.1	4.282352941
1949	B04	595	SACOL2688	intercellular adhesion regulator	YP_187475.1	3.537815126
1951	B05	598	SACOL1202	YlmF protein	YP_186064.1	4.284280936
1953	B06	598	SACOL1485	conserved hypothetical protein	YP_186330.1	3.242474916
1955	B07	598	SACOL1811	conserved hypothetical protein	YP_186644.1	3.558528428
1957	B08	598	SACOL1992	conserved hypothetical protein	YP_186816.1	3.52173913
1959	B09	598	SACOL2630	conserved hypothetical protein	YP_187419.1	3.254180602
1961	B10	601	SACOL0410	FMN reductase-related protein	YP_185302.1	2.803660566
1963	B11	601	SACOL0568	conserved hypothetical protein	YP_185456.1	4.25124792
1965	B12	601	SACOL0607	azoreductase	YP_185492.1	2.108153078
1969	C02	601	SACOL1081	phosphoribosylglycinamide formyltransferase	YP_185945.1	3.269550749
1971	C03	601	SACOL1404	anthranilate synthase, glutamine amidotransferase, component II	YP_186256.1	4.254575707
1974	C04	601	SACOL1870	hypothetical protein	YP_186698.1	3.845257903
1975	C05	604	SACOL0452	alkyl hydroperoxide reductase, C subunit	YP_185342.1	4.286423841
1977	C06	604	SACOL0580	conserved hypothetical protein	YP_185466.1	3.533112583
1979	C07	604	SACOL0864	conserved domain protein	YP_185737.1	4.23013245
1981	C08	604	SACOL0906	phage terminase family protein	YP_185777.1	3.544701987
1983	C09	604	SACOL1650	nicotinate (nicotinamide) nucleotide adenyltransferase	YP_186490.1	4.248344371
1985	C10	604	SACOL2023	accessory gene regulator protein B	YP_186842.1	3.561258278
1987	C11	604	SACOL2320	conserved hypothetical protein	YP_187127.1	3.627483444
1989	C12	604	SACOL2732	transcriptional regulator, putative	YP_187518.1	3.541390728
1991	D01	607	SACOL0199	conserved hypothetical protein	YP_185098.1	3.507413509
1993	D02	607	SACOL0444	lipoprotein, putative	YP_185334.1	3.504118616

## Product Information Sheet for NR-19506

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1995	D03	607	SACOL0546	peptidyl-tRNA hydrolase	YP_185434.1	3.850082372
1997	D04	607	SACOL0815	ribosomal subunit interface protein	YP_185689.1	3.532125206
1999	D05	607	SACOL1242	conserved hypothetical protein	YP_186102.1	4.196046129
2001	D06	607	SACOL1512	conserved hypothetical protein	YP_186356.1	2.718286656
2003	D07	607	SACOL2049	3-isopropylmalate dehydratase, small subunit	YP_186866.1	3.538714992
2005	D08	610	SACOL0967	conserved hypothetical protein	YP_185836.1	4.249180328
2007	D09	610	SACOL1086	conserved hypothetical protein	YP_185950.1	3.532786885
2009	D10	610	SACOL1502	conserved hypothetical protein	YP_186346.1	3.109836066
2011	D11	610	SACOL2720	hypothetical protein	YP_187506.1	3.875409836
2014	D12	613	SACOL0191	M23/M37 peptidase domain protein	YP_185090.1	3.518760196
2015	E01	613	SACOL0458	xanthine phosphoribosyltransferase	YP_185348.1	3.525285481
2017	E02	613	SACOL0902	pathogenicity island protein	YP_185773.1	3.543230016
2019	E03	613	SACOL1302	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	YP_186159.1	3.08319739
2021	E04	613	SACOL2699	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit	YP_187485.1	4.254486134
2023	E05	613	SACOL2700	imidazoleglycerol-phosphate dehydratase	YP_187486.1	3.831973899
2025	E06	616	SACOL0447	phosphoglycerate mutase family protein	YP_185337.1	3.868506494
2027	E07	616	SACOL1589	lipoprotein, putative	YP_186429.1	3.13474026
2029	E08	619	SACOL0708	DAK2 domain protein	YP_185590.1	3.844911147
2031	E09	619	SACOL0769	conserved hypothetical protein	YP_185646.1	3.523424879
2034	E10	619	SACOL0969	signal peptidase IB	YP_185838.1	3.127625202
2036	E11	619	SACOL1649	conserved hypothetical protein TIGR00488	YP_186489.1	3.11631664
2037	E12	622	SACOL0269	conserved hypothetical protein	YP_185164.1	2.813504823
2039	F01	622	SACOL0833	ATP-dependent Clp protease, proteolytic subunit ClpP	YP_185707.1	3.834405145
2041	F02	622	SACOL1162	HAM1 protein	YP_186025.1	4.263665595
2044	F03	622	SACOL1501	conserved hypothetical protein	YP_186345.1	3.122186495
2045	F04	622	SACOL2610	transcriptional regulator, TetR family, putative	YP_187400.1	3.136655949
2048	F05	625	SACOL0869	phosphoglycerate mutase family protein	YP_185741.1	3.528
2049	F06	625	SACOL1359	conserved hypothetical protein	YP_186212.1	4.256
2051	F07	625	SACOL1575	hypothetical protein	YP_186415.1	3.5056
2053	F08	625	SACOL1720	GTP-binding protein, putative	YP_186558.1	3.5152
2055	F09	625	SACOL2014	phage terminase family protein	YP_186834.1	3.4416
2057	F10	625	SACOL2393	respiratory nitrate reductase, delta subunit	YP_187196.1	4.0096
2059	F11	628	SACOL0773	para-aminobenzoate synthase, glutamine amidotransferase, component II	YP_185650.1	3.522292994
2061	F12	628	SACOL0957	peptidyl-prolyl cis-trans isomerase, cyclophilin-type	YP_185826.1	3.52388535
2063	G01	628	SACOL1008	conserved hypothetical protein	YP_185876.1	3.845541401
2065	G02	628	SACOL2529	phospholipase/carboxylesterase family protein	YP_187322.1	3.863057325
2067	G03	631	SACOL0082	staphylococcus tandem lipoprotein	YP_184987.1	3.849445325
2069	G04	631	SACOL0522	recombination protein RecR	YP_185410.1	3.507131537
2071	G05	631	SACOL1792	conserved hypothetical protein	YP_186625.1	4.228209192
2073	G06	634	SACOL0118	superoxide dismutase	YP_185022.1	3.829652997
2075	G07	634	SACOL1610	superoxide dismutase	YP_186450.1	3.835962145
2077	G08	634	SACOL1912	glucosamine-6-phosphate isomerase, putative	YP_186737.1	3.544164038
2079	G09	634	SACOL2111	thymidine kinase	YP_186926.1	3.501577287
2081	G10	634	SACOL2201	conserved domain protein, putative	YP_187012.1	2.823343849
2083	G11	634	SACOL2262	molybdopterin-guanine dinucleotide biosynthesis protein A	YP_187069.1	3.110410095
2085	G12	634	SACOL2407	lipoprotein, putative	YP_187210.1	3.522082019
2087	H01	634	SACOL2456	conserved hypothetical protein	YP_187254.1	2.520504732
2089	H02	634	SACOL2570	galactoside O-acetyltransferase	YP_187362.1	3.548895899
2091	H03	637	SACOL0075	hypothetical protein	YP_184980.1	4.263736264

## Product Information Sheet for NR-19506

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
2093	H04	637	SACOL1036	protease, putative	YP_185901.1	3.516483516
2095	H05	637	SACOL1355	DNA-binding response regulator, LuxR family	YP_186207.1	4.20722135
2097	H06	637	SACOL1697	Holliday junction DNA helicase RuvA	YP_186536.1	4.241758242
2099	H07	637	SACOL1769	ribosomal protein S4	YP_186603.1	4.233908948
2101	H08	637	SACOL1973	conserved hypothetical protein	YP_186797.1	3.551020408
2103	H09	637	SACOL2587	conserved hypothetical protein	YP_187378.1	3.535321821
2105	H10	640	SACOL1068	cytochrome aa3 quinol oxidase, subunit III	YP_185932.1	3.7953125
2108	H11	640	SACOL2270	molybdenum ABC transporter, ATP-binding protein ModC	YP_187077.1	3.8375
2109	H12	640	SACOL2638	siroheme synthase, putative	YP_187426.1	4.2359375