

SUPPORTING INFECTIOUS DISEASE RESEARCH

Product Information Sheet for NR-19505

Staphylococcus aureus (MRSA), Strain COL Gateway[®] Clone Set, Recombinant in Escherichia coli, Plate 9

Catalog No. NR-19505

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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 crosscontamination 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:

Each inoculated well of the 96-well plate contains approximately 60 μ L of *E. coli* culture (strain DH10B-T1) in Luria Bertani (LB) broth containing 50 μ g/mL kanamycin supplemented with 15% glycerol.

Packaging/Storage:

www.beiresources.org

NR-19505 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

<u>Incubation</u>

Temperature: *E. coli*, strain DH10B-T1 clones should be grown at 37°C.

Atmosphere: Aerobic

Propagation:

- Scrape top of frozen well with a pipette tip and streak onto again plate.
- 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 9, NR-19505."

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.

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.

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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 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 9 (ZSAJI)

Position Length					D		
1697	Clone	Well	ORF	Locus ID	Description (Gene name)	Accession	Average Depth
1703 A02 532 SACOL2706 hypothetical protein YP 187492.1 2 2 1707 A03 535 SACOL0286 conserved hypothetical protein YP 185181.1 3.145794393 1719 A04 S35 SACOL0585 fibosomal protein L10 YP 185471.1 3.14953271 1721 A05 S35 SACOL0789 GTP cyclohydrolase I family protein YP 185608.1 2.750841122 1723 A06 535 SACOL1457 PTS system, IIA component YP 185608.1 2.568224299 1725 A07 S35 SACOL1759 universal stress protein family YP 186508.1 2.2173831776 1727 A08 S35 SACOL1812 repressor of toxins YP 186508.1 2.2173831776 1729 A09 S35 SACOL1952 ferritins family protein YP 186777.1 3.145794393 1731 A10 S35 SACOL2222 ribosomal protein S5 YP 187032.1 3.154101869 1734 A11 S35 SACOL2285 staphyloxanthin biosynthesis protein, putative YP 187102.1 3.145794393 1737 A12 S35 SACOL384 acetyltransferase, GNAT family YP 187471.1 3.16635614 3.147418 B02 S38 SACOL1834 acetyltransferase, GNAT family YP 185329.1 3.863197026 1744 B02 S38 SACOL1255 S87RNA processing protein TIGR00040 YP 186026.1 3.563197026 1744 B05 S41 SACOL0669 Gonserved hypothetical protein TIGR00040 YP 186026.1 3.563197026 1749 B06 S41 SACOL0669 Conserved hypothetical protein YP 18553.1 3.34519533 1753 B08 S41 SACOL1539 conserved hypothetical protein YP 185363.1 3.347974307 1759 B10 S41 SACOL0669 conserved hypothetical protein YP 185363.1 3.34797337 1759 B10 S41 SACOL0669 conserved hypothetical protein YP 185363.1 3.34797337 1759 B10 S41 SACOL1539 conserved hypothetical protein YP 185361.1 3.147074307 1759 B10 S41 SACOL1539 conserved hypothetical protein YP 185361.1 3.147074307 1759 B10 S41 SACOL0669 conserved hypothetical protein YP 185981.1 3.14220588 1763 B08 S41 SACOL0669 conserved hypothetical protein YP 185051.1 3.24824606					-		
1707 A03 535 SACOL0286 Conserved hypothetical protein YP 185181.1 3.145794393 1719 A04 535 SACOL0885 ribosomal protein L10 YP 185647.1 3.1495327.1 1721 A05 535 SACOL0789 GTP cyclohydrolase I family protein YP 185682.1 2.730841122 1723 A06 535 SACOL1457 FTS system, IIA component YP 185682.1 2.730841122 1725 A07 535 SACOL1457 FTS system, IIA component YP 185682.1 2.730841122 1726 A07 535 SACOL1812 repressor of toxins YP 1866845.1 2 1727 A08 535 SACOL1812 repressor of toxins YP 1866845.1 2 1729 A09 535 SACOL1952 ferritins family protein YP 1866845.1 2 1731 A10 535 SACOL2222 Staphyloxanthin biosynthesis protein, putative A1734 A11 535 SACOL2229 Staphyloxanthin biosynthesis protein, putative A1734 A11 535 SACOL2229 Staphyloxanthin biosynthesis protein, putative A1734 A12 535 SACOL0488 acetyltransferase, GNAT family YP 187012.1 3.16638514 1731 A12 A12 A12 A12 A13 A14 A1							
1719							
1721							
1723 A06 535 SACOL1457 PTS system, IIA component YP 186308.1 2.588224299 1727 A07 535 SACOL1759 universal stress protein family YP 186593.1 2.173831776 1727 A08 535 SACOL1812 repressor of toxins YP 186703.1 3.15140189 1734 A10 535 SACOL2295 ferritins family protein YP 187032.1 3.151401869 1734 A11 535 SACOL2295 staphyloxanthin biosynthesis protein, putative YP 18702.1 3.151401869 1737 A12 535 SACOL284 acetyltransferase, GNAT family YP 18702.1 3.16159514 1740 B01 538 SACOL1438 single-stranded DNA-binding protein YP 186026.1 3.563197026 1741 B02 538 SACOL1631 conserved hypothetical protein RimM YP 186026.1 3.363197026 1744 B05 541 SACOL0037 conserved hypothetical protein YP 186174.1 3.13717421 1749 B06 541 SACOL0699							
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1805 D07 559 SACOL0579 conserved hypothetical protein YP_185465.1 4.254025045 1807 D08 559 SACOL0968 signal peptidase IA, inactive YP_185837.1 4.300536673 1809 D09 559 SACOL1596 shikimate kinase YP_186436.1 3.846153846	1804	D06	559	SACOL0519		YP 185407.1	3.148479428
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						YP 186436.1	
	1811	D10	559	SACOL1991	conserved hypothetical protein	YP_186815.1	4.230769231

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SUPPORTING INFECTIOUS DISEASE RESEARCH

Product Information Sheet for NR-19505

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1813	D11	559	SACOL2106	conserved hypothetical protein TIGR01440	YP 186921.1	3.837209302
1816	D12	562	SACOL0904	pathogenicity island protein	YP_185775.1	2.414590747
1818	E01	562	SACOL1210	pyrimidine operon regulatory protein	YP_186073.1	2.8113879
1819	E02	562	SACOL1654	hydrolase, HAD-superfamily, subfamily IIIA	YP_186494.1	4.304270463
1821	E03	562	SACOL1727	translation initiation factor IF-3	YP_186565.1	4.286476868
1823	E04	562	SACOL2660	immunodominant antigen B	YP_187448.1	3.256227758
1825	E05	565	SACOL0855	acetyltransferase, GNAT family	YP_185728.1	3.286725664
1827	E06	565	SACOL1032	ComK family protein	YP_185897.1	4.276106195
1829	E07	565	SACOL1703	rod shape-determining protein MreD, putative	YP_186542.1	4.309734513
1831	E08	565	SACOL1936	cytosolic long-chain acyl-CoA thioester hydrolase family protein	YP_186761.1	4.297345133
1833	E09	565	SACOL1956	conserved hypothetical protein	YP_186781.1	4.251327434
1835	E10	565	SACOL2120	DNA-directed RNA polymerase, delta subunit	YP_186935.1	3.07079646
1837	E11	565	SACOL2315	conserved hypothetical protein	YP_187122.1	3.557522124
1840	E12	568	SACOL0073	conserved hypothetical protein	YP_184978.1	4.278169014
1841	F01	568	SACOL1357	thermonuclease precursor family protein	YP_186210.1	4.105633803
1845	F03	571	SACOL0535	primase-related protein	YP_185423.1	4.250437828
1847	F04	571	SACOL0656	conserved hypothetical protein	YP_185541.1	4.257443082
1849	F05	571	SACOL2224	ribosomal protein L6	YP_187034.1	4.273204904
1851	F06	571	SACOL2400	acetyltransferase, GNAT family	YP_187203.1	4.276707531
1854	F07	571	SACOL2634	anaerobic ribonucleoside-triphosphate reductase activating protein	YP_187422.1	3.534150613
1857	F08	574	SACOL0554	hypoxanthine phosphoribosyltransferase	YP_185442.1	4.277003484
1859	F09	574	SACOL0874	nitroreductase family protein	YP_185746.1	3.132404181
1861	F10	574	SACOL1107	transcriptional regulator, Cro/CI family	YP_185971.1	4.217770035
1863	F11	574	SACOL1607	5-formyltetrahydrofolate cyclo-ligase family protein	YP_186447.1	3.534843206
1865	F12	574	SACOL1621	CBS domain protein	YP_186461.1	4.266550523
1867	G01	574	SACOL1882	hypothetical protein	YP_186709.1	4.299651568
1869	G02	574	SACOL2098	ATP synthase F1, delta subunit	YP_186913.1	3.548780488
1871	G03	574	SACOL2227	ribosomal protein L5	YP_187037.1	2.412891986
1873	G04	577	SACOL0357	prophage L54a, deoxyuridine 5-triphosphate nucleotidohydrolase	YP_185249.1	4.268630849
1875	G05	577	SACOL0739	acetyltransferase, GNAT family	YP_185618.1	4.253032929
1877	G06	577	SACOL0785	conserved hypothetical protein	YP_185659.1	4.285961872
1879	G07	577	SACOL1090	conserved hypothetical protein	YP_185954.1	4.266897747
1881	G08	577	SACOL1133	conserved hypothetical protein TIGR00095	YP_185997.1	4.251299827
1884	G09	577	SACOL1317	glycerol uptake operon antiterminator regulatory protein	YP_186173.1	2.818024263
1885	G10	577	SACOL1537	segregation and condensation protein B	YP_186379.1	3.559792028
1887	G11	577	SACOL1542	MutT/nudix family protein	YP_186384.1	3.87694974
1889	G12	577	SACOL1925	conserved hypothetical protein	YP_186750.1	4.272097054
1891	H01	580	SACOL0413	ribosomal-protein-serine acetyltransferase, putative	YP_185305.1	4.284482759
1893	H02	580	SACOL1270	heat shock protein HsIVU, ATPase subunit HsIV	YP_186128.1	4.244827586
1895	H03	580	SACOL1526	conserved hypothetical protein	YP_186369.1	4.251724138
1897	H04	582	SACOL0441	integrase, degenerate	N/A	3.235395189
1901	H05	583	SACOL0618	SIS domain protein	YP_185503.1	4.171526587
1904	H06	583	SACOL2175	conserved hypothetical protein	YP_186986.1	3.130360206
1905	H07	586	SACOL1100	polypeptide deformylase	YP_185964.1	4.271331058
1908	H08	586	SACOL1850	hypothetical protein	YP_186681.1	3.141638225
1910	H09	586	SACOL2349	transcriptional regulator, TetR family	YP_187155.1	3.109215017
1911	H10	589	SACOL1278	ribosome recycling factor	YP_186135.1	4.259762309
1913	H11	589	SACOL1885	conserved hypothetical protein	YP_186711.1	3.285229202
1915	H12	589	SACOL1954	exonuclease	YP_186779.1	4.264855688

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