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SUPPORTING INFECTIOUS DISEASE RESEARCH

# Staphylococcus aureus (MRSA), Strain COL Gateway<sup>®</sup> Clone Set, Recombinant in Escherichia coli, Plate 7

## Catalog No. NR-19503

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 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<sup>®</sup> 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 <u>pDONR<sup>TM</sup>221</u> (<u>Invitrogen<sup>TM</sup></u>) 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<sup>®</sup> Clones can be obtained from <u>Invitrogen</u><sup>™</sup>. Recombination was facilitated through an *att*B substrate (*att*B-PCR product or a linearized *att*B expression clone) with an *att*P substrate (pDONR<sup>™</sup>221) to create an *att*L-containing entry clone. The entry clone contains recombinational cloning sites, *att*L1 and *att*L2 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<sup>™</sup> Gateway<sup>®</sup> Technology Manual for additional details.

#### Material Provided:

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

### Packaging/Storage:

NR-19503 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<sup>®</sup> Clone Set, Recombinant in *Escherichia coli*, Plate 7, NR-19503."

## 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. <u>Biosafety in Microbiological and Biomedical Laboratories</u>. 5th ed. Washington, DC: U.S. Government Printing Office, 2009; see www.cdc.gov/biosafety/publications/bmbl5/index.htm.

#### Disclaimers:

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## **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." <u>J. Bacteriol.</u> 187 (2005): 2426-2438. PubMed: 15774886.

ATCC<sup>®</sup> is a trademark of the American Type Culture Collection.



## Table 1: Staphylococcus aureus, Strain COL Gateway® Clones, Plate 7 (ZSAJG)

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1287	A01	439	SACOL0254	ribose transport protein	YP 185150.1	2.587699317
1289	A02	439	SACOL0260	IS1272-related, transposase, degenerate	N/A	3.182232346
1291	A03	439	SACOL0347	conserved hypothetical protein	YP_185239.1	2.574031891
1293	A04	439	SACOL0577	conserved hypothetical protein	YP 185463.1	3.182232346
1295	A05	439	SACOL1625	cytidine deaminase	YP 186465.1	3.177676538
1299	A06	442	SACOL0109	hypothetical protein	YP 185013.1	3.156108597
1302	A07	442	SACOL0457	conserved hypothetical protein	YP 185347.1	3.171945701
1306	A09	445	SACOL2281	urease, beta subunit	YP 187088.1	2.573033708
1307	A10	445	SACOL2551	conserved hypothetical protein TIGR00051	YP_187343.1	3.188764045
1309	A11	448	SACOL0591	ribosomal protein S12	YP 185477.1	3.142857143
1311	A12	448	SACOL1753	universal stress protein family	YP_186589.1	3.171875
1313	B01	448	SACOL1948	hypothetical protein	YP 186773.1	3.178571429
1315	B02	448	SACOL2132	conserved hypothetical protein	YP 186947.1	2.185267857
1317	B03	451	SACOL2193	transcriptional regulator, MerR family	YP 187004.1	3.175166297
1319	B04	451	SACOL2621	hypothetical protein	YP_187410.1	3.179600887
1321	B05	454	SACOL0339	prophage L54a, single-stranded DNA binding protein	YP_185231.1	3.174008811
1323	B06	454	SACOL0404	transcriptional regulator, MarR family	YP 185296.1	3.162995595
1325	B07	454	SACOL0771	6-pyruvoyl tetrahydrobiopterin synthase, putative	YP 185648.1	3.178414097
1327	B08	454	SACOL1060	transcriptional regulator, MarR family	YP 185925.1	3.171806167
1329	B09	454	SACOL1113	conserved hypothetical protein	YP 185977.1	3.18722467
1331	B10	454	SACOL2107	phosphotyrosine protein phosphatase	YP 186922.1	3.191629956
1335	B11	454	SACOL2344	hypothetical protein	YP_187150.1	3.174008811
1337	B12	454	SACOL2485	hypothetical protein	YP 187281.1	3.176211454
1341	C01	457	SACOL0753	conserved hypothetical protein	YP 185632.1	3.159737418
1343	C02	457	SACOL0872	OsmC/Ohr family protein	YP 185744.1	3.15536105
1345	C03	457	SACOL1681	Rrf2 family protein	YP 186521.1	3.168490153
1347	C04	457	SACOL1802	conserved hypothetical protein	YP 186635.1	3.166301969
1349	C05	457	SACOL1894	HIT family protein	YP 186720.1	3.177242888
1351	C06	457	SACOL2294	conserved hypothetical protein	YP 187101.1	3.164113786
1353	C07	457	SACOL2379	conserved hypothetical protein	YP 187183.1	3.177242888
1355	C08	457	SACOL2484	alkylhydroperoxidase, AhpD family	YP 187280.1	2.177242888
1357	C09	457	SACOL2487	conserved hypothetical protein	YP 187283.1	3.161925602
1360	C10	460	SACOL0346	prophage L54a, N-6-adenine-methyltransferase	YP 185238.1	3.176086957
1362	C11	460	SACOL0680	Na+/H+ antiporter, MnhB component, putative	YP 185563.1	3.152173913
1363	C12	460	SACOL0726	staphylococcal accessory protein X	YP 185607.1	3.191304348
1365	D01	460	SACOL1339	conserved hypothetical protein	YP 186193.1	3.180434783
1367	D01	460	SACOL2197	surface protein, putative	YP 187008.1	2.173913043
1369	D02	463	SACOL0032	MaoC domain protein	YP 184943.1	3.172786177
1371	D00	463	SACOL0662	conserved hypothetical protein	YP 185546.1	3.177105832
1373	D04	463	SACOL0002	hypothetical protein	YP 185595.1	3.174946004
1375	D05	463	SACOL0713	Na+/H+ antiporter, MnhB component	YP_185823.1	3.172786177
1377	D00	463	SACOL1671	conserved hypothetical protein TIGR00250	YP_186511.1	3.168466523
1379	D07	463	SACOL1071 SACOL2186	galactose-6-phosphate isomerase, LacA subunit	YP 186997.1	3.183585313
13/3	000	463	SACOL2186 SACOL2385	heat shock protein, Hsp20 family	YP 187189.1	3.146868251

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# **Product Information Sheet for NR-19503**

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Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
1383	D10	463	SACOL2679	hypothetical protein	N/A	3.149028078
1385	D11	466	SACOL0583	ribosomal protein L11	YP 185469.1	3.130901288
1388	D12	466	SACOL0888	pathogenicity island, lipoprotein, putative	YP 185759.1	2.587982833
1389	E01	466	SACOL1191	mraZ protein	YP_186053.1	3.173819742
1391	E02	466	SACOL1645	comE operon protein 2	YP_186485.1	3.180257511
1393	E03	466	SACOL2371	conserved hypothetical protein	YP 187175.1	2.587982833
1395	E04	466	SACOL2557	conserved domain protein	YP 187350.1	2.165236052
1398	E05	469	SACOL0930	conserved hypothetical protein	YP 185800.1	1.976545842
1400	E06	469	SACOL0985	surface protein, putative	YP_185853.1	3.153518124
1402	E07	469	SACOL1063	acetyltransferase, GNAT family	YP_185927.1	3.153518124
1403	E08	469	SACOL1129	conserved hypothetical protein	YP 185993.1	3.176972281
1405	E09	469	SACOL2041	conserved hypothetical protein TIGR00150	YP 186858.1	3.172707889
1407	E10	469	SACOL2148	PTS system, mannitol-specific IIA component	YP 186961.1	3.187633262
1409	E11	469	SACOL2232	ribosomal protein L16	YP 187042.1	3.162046908
1411	E12	469	SACOL2531	transcriptional regulator, MarR family	YP 187324.1	3.18336887
1413	F01	472	SACOL0364	prophage L54a, transcriptional regulator, RinA family	YP_185256.1	3.150423729
1415	F02	472	SACOL0686	Na+/H+ antiporter, MnhG component, putative	YP 185568.1	3.167372881
1417	F03	472	SACOL1464	conserved hypothetical protein	YP_186312.1	3.156779661
1420	F04	472	SACOL1558	conserved hypothetical protein	YP_186399.1	2
1421	F05	472	SACOL2013	hypothetical protein	YP_186833.1	3.167372881
1423	F06	472	SACOL2207	ribosomal protein L13	YP_187017.1	2.593220339
1426	F07	475	SACOL0287	conserved hypothetical protein	YP_185182.2	2
1429	F08	475	SACOL0406	hypothetical protein	YP 185298.1	3.181052632
1433	F10	475	SACOL0768	lipoprotein, putative	YP 185645.1	2.591578947
1435	F11	475	SACOL1189	acetyltransferase, GNAT family	YP 186051.1	3.168421053
1437	F12	475	SACOL2090	ywpF protein	YP 186905.1	3.166315789
1439	G01	475	SACOL2091	beta-hydroxyacyl-(acyl-carrier-protein) dehydratase FabZ	YP_186906.1	2.591578947
1441	G02	475	SACOL2220	ribosomal protein L15	YP 187030.1	3.141052632
1443	G03	475	SACOL2256	transcriptional regulator, MarR family	YP_187063.1	3.166315789
1445	G04	478	SACOL0247	holin-like protein LrgA	YP_185143.1	2.569037657
1447	G05	478	SACOL0402	PTS system, IIA component	YP 185294.1	3.158995816
1450	G06	478	SACOL0736	acetyltransferase, GNAT family	YP 185615.1	2.575313808
1451	G07	478	SACOL0746	transcriptional regulator, MarR family	YP 185625.1	3.179916318
1453	G08	478	SACOL1828	conserved hypothetical protein	YP_186660.1	3.165271967
1455	G09	478	SACOL1829	conserved hypothetical protein	YP_186661.1	3.150627615
1457	G10	478	SACOL1832	crcB protein	YP 186664.1	2.569037657
1459	G11	478	SACOL2012	acetyltransferase, GNAT family	YP 186832.1	2.587866109
1463	G12	478	SACOL2360	response regulator-related protein	YP_187165.1	3.133891213
1465	H01	478	SACOL2625	conserved hypothetical protein	YP_187414.1	2.587866109
1467	H02	481	SACOL0015	ribosomal protein L9	YP_184926.1	2.56964657
1469	H03	481	SACOL1598	ComG operon competence protein, putative	YP_186438.1	2.584199584
1471	H04	481	SACOL1771	OsmC/Ohr family protein	YP_186605.1	3.130977131
1473	H05	481	SACOL1919	transcriptional regulator, Fur family	YP_186744.1	2.584199584
1475	H06	481	SACOL2264	molybdenum cofactor biosynthesis protein E	YP_187071.1	3.17047817
1478	H07	481	SACOL2384	staphylococcal accessory protein Z	YP_187188.1	3.180873181
1479	H08	484	SACOL1509	nucleoside diphosphate kinase	YP_186353.1	3.146694215
1481	H09	484	SACOL1541	transcriptional regulator, Fur family	YP_186383.1	3.188016529
1483	H10	484	SACOL1662	acetyl-CoA carboxylase, biotin carboxyl carrier protein, putative	YP_186502.1	2.588842975
1485	H11	484	SACOL2609	conserved hypothetical protein	YP_187399.1	3.181818182
1487	H12	484	SACOL2658	transcriptional regulator, ArgR family	YP_187446.1	3.175619835

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