

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 22**

Catalog No. NR-19518

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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 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:

Each 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-19518 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 22, NR-19518."

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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Product Information Sheet for NR-19519

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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.



References:

- Gill, S. R., et al. "Insights on Evolution of Virulence and Resistance from the Complete Genome Analysis of an

Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 22 (ZSAJV)

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
4381	A01	1309	SACOL1560	2-oxoisovalerate dehydrogenase, E2 component, dihydrolipoamide acetyltransferase	YP_186401.1	6.28342246
4383	A02	1309	SACOL1682	ATPase, AAA family	YP_186522.1	6.332314744
4385	A03	1309	SACOL1777	serine protease HtrA, putative	YP_186611.1	6.30328495
4387	A04	1312	SACOL2373	conserved hypothetical protein	YP_187177.1	5.598323171
4390	A05	1312	SACOL2382	proton/sodium-glutamate symport protein	YP_187186.1	6.298780488
4391	A06	1312	SACOL2521	transporter, putative	YP_187315.1	5.292682927
4393	A07	1312	SACOL2560	hydroxymethylglutaryl-CoA reductase, degradative	YP_187352.1	5.352896341
4395	A08	1315	SACOL1362	homoserine dehydrogenase	YP_186215.1	6.40608365
4398	A09	1318	SACOL0018	adenylosuccinate synthetase	YP_184929.1	6.3323217
4400	A10	1321	SACOL0009	seryl-tRNA synthetase	YP_184920.1	6.333838002
4401	A11	1321	SACOL1281	membrane-associated zinc metalloprotease, putative	YP_186138.1	5.955336866
4404	A12	1321	SACOL1298	peptidase, M16 family	YP_186155.1	6.305071915
4409	B01	1324	SACOL1922	glutamate-1-semialdehyde-2,1-aminomutase	YP_186747.1	6.019637462
4412	B02	1327	SACOL1104	pyruvate dehydrogenase complex E2 component, dihydrolipoamide acetyltransferase	YP_185968.1	6.010550113
4415	B03	1327	SACOL1699	GTP-binding protein, GTP1/OBG family	YP_186538.1	6.441597589
4421	B04	1327	SACOL2219	preprotein translocase, SecY subunit	YP_187029.1	6.171816127
4423	B05	1330	SACOL0026	conserved hypothetical protein	YP_184937.1	6.515789474
4425	B06	1330	SACOL0553	tRNA(Ile)-lysine synthetase	YP_185441.1	6.521804511
4429	B07	1330	SACOL0699	penicillin-binding protein 4	YP_185581.1	6.407518797
4431	B08	1330	SACOL1088	conserved hypothetical protein	YP_185952.1	6.166165414
4433	B09	1330	SACOL1969	adenylosuccinate lyase	YP_186793.1	6.354135338
4435	B10	1333	SACOL1504	3-phosphoshikimate 1-carboxyvinyltransferase	YP_186348.1	6.475618905
4439	B11	1336	SACOL1410	femA protein	YP_186262.1	6.504491018
4441	B12	1336	SACOL1722	trigger factor	YP_186560.1	6.221556886
4444	C01	1336	SACOL2128	pyrimidine-nucleoside phosphorylase	YP_186943.1	6.062125749
4445	C02	1339	SACOL0842	enolase	YP_185716.1	6.575056012
4447	C03	1342	SACOL0185	peptide ABC transporter, permease protein	YP_185084.1	6.55290611
4450	C04	1342	SACOL0302	branched-chain amino acid transport system II carrier protein	YP_185195.1	6.347242921
4454	C05	1342	SACOL1211	uracil permease	YP_186074.1	6.342026826
4456	C06	1342	SACOL1229	sun protein	YP_186092.1	6.307004471
4457	C07	1342	SACOL1268	Gid protein	YP_186126.1	6.533532042
4459	C08	1342	SACOL2011	sodium transport family protein	YP_186831.1	6.275707899
4463	C09	1345	SACOL2418	IgG-binding protein SBI	YP_187220.1	6.409665428
4466	C10	1348	SACOL0316	conserved hypothetical protein	YP_185208.1	6.325667656
4467	C11	1348	SACOL1790	UDP-N-acetylmuramate--alanine ligase	YP_186623.1	5.699554896
4470	C12	1348	SACOL1951	Mur ligase family protein	YP_186776.1	6.28041543
4471	D01	1348	SACOL2319	Na ⁺ /H ⁺ antiporter family protein	YP_187126.1	6.442136499
4473	D02	1351	SACOL0946	Na ⁺ /H ⁺ antiporter family protein	YP_185815.1	5.948186529

Product Information Sheet for NR-19518

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
4475	D03	1351	SACOL0975	CoA-disulfide reductase	YP_185843.1	6.116950407
4477	D04	1351	SACOL2113	transcription termination factor Rho	YP_186928.1	5.803849001
4479	D05	1354	SACOL0926	5-nucleotidase family protein	YP_185796.1	6.360413589
4481	D06	1354	SACOL1197	cell division protein	YP_186059.1	5.921713442
4487	D07	1354	SACOL2599	conserved domain protein	YP_187390.1	6.062038405
4490	D08	1357	SACOL0640	pyridine nucleotide-disulfide oxidoreductase	YP_185525.1	6.27266028
4493	D09	1360	SACOL0487	hypothetical protein	YP_185377.1	6.495588235
4495	D10	1363	SACOL0046	metallo-beta-lactamase family protein	YP_184956.1	6.305209098
4497	D11	1366	SACOL0966	glucose-6-phosphate isomerase	YP_185835.1	6.038799414
4499	D12	1369	SACOL0021	yycH protein	YP_184932.1	6.451424397
4501	E01	1369	SACOL0064	metallo-beta-lactamase family protein	YP_184969.1	6.355003652
4503	E02	1369	SACOL0275	conserved hypothetical protein	YP_185170.1	4.877282688
4505	E03	1369	SACOL2242	xanthine/uracil permease family protein	YP_187052.1	6.368882396
4507	E04	1372	SACOL0501	sodium-dependent transporter, putative	YP_185389.1	5.397230321
4515	E07	1375	SACOL1329	glutamine synthetase FemC	YP_186184.1	5.509818182
4519	E09	1378	SACOL1443	branched-chain amino acid transport system II carrier protein	YP_186295.1	4.763425254
4530	E10	1381	SACOL1633	conserved hypothetical protein	YP_186473.1	6.086169442
4531	E11	1381	SACOL1719	glutamyl-tRNA reductase	YP_186557.1	6.332367849
4535	F01		SACOL0762	NO CLONE IS NOT AVAILABLE ¹	YP_185639.1	
4537	F02	1384	SACOL1196	UDP-N-acetylmuramoylalanine--D-glutamate ligase	YP_186058.1	4.895953757
4539	F03	1387	SACOL0122	tetracycline resistance protein, putative	YP_185026.1	5.434751262
4541	F04	1387	SACOL0543	UDP-N-acetylglucosamine pyrophosphorylase	YP_185431.1	5.044700793
4545	F05	1387	SACOL2459	para-nitrobenzyl esterase	YP_187257.1	5.248017304
4547	F06	1390	SACOL0171	branched-chain amino acid transport system II carrier protein	YP_185070.1	5.948201439
4549	F07	1390	SACOL0405	MATE efflux family protein	YP_185297.1	5.905755396
4552	F08	1390	SACOL1450	sensor histidine kinase ArlS	YP_186302.1	6.2
4553	F09	1390	SACOL1571	acetyl-CoA carboxylase, biotin carboxylase	YP_186412.1	5.103597122
4559	F10	1393	SACOL1030	sodium transport family protein	YP_185895.1	5.601579325
4561	F11	1393	SACOL1578	FtsK/SpolIIE family protein	YP_186418.1	4.677674085
4564	F12	1393	SACOL2073	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	YP_186889.1	6.137114142
4565	G01	1393	SACOL2427	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	YP_187229.1	6.262024408
4567	G02	1393	SACOL2514	gluconate transporter, permease protein	YP_187308.1	5.155061019
4569	G03	1393	SACOL2669	conserved hypothetical protein	YP_187457.1	5.065326633
4571	G04	1395	SACOL2205	conserved hypothetical protein, degenerate	N/A	5.665232975
4575	G05	1396	SACOL1094	cytochrome d ubiquinol oxidase, subunit I	YP_185958.1	5.406876791
4577	G06	1396	SACOL1661	acetyl-CoA carboxylase, biotin carboxylase, putative	YP_186501.1	5.783667622
4581	G07	1396	SACOL1957	RNA methyltransferase, TrmA family	YP_186782.1	6.196991404
4583	G08	1399	SACOL0572	DNA repair protein RadA	YP_185458.1	5.165832738
4585	G09	1402	SACOL1253	signal recognition particle protein	YP_186112.1	4.94935806
4587	G10	1405	SACOL2048	3-isopropylmalate dehydratase, large subunit	YP_186865.1	5.592882562
4591	G11	1405	SACOL2636	citrate transporter, permease protein	YP_187424.1	6.250533808
4593	G12	1408	SACOL0751	deoxyribodipyrimidine photolyase, putative	YP_185630.1	6.228693182
4595	H01	1408	SACOL1874	epidermin leader peptide processing serine protease EpiP	YP_186702.1	6.318892045
4597	H02	1408	SACOL2133	conserved hypothetical protein	YP_186948.1	5.573863636
4600	H03	1408	SACOL2359	sensor histidine kinase	YP_187164.1	5.524147727
4601	H04	1411	SACOL0261	drug transporter, putative	YP_185156.1	6.228915663
4603	H05	1411	SACOL0621	substrate--CoA ligase, putative	YP_185506.1	5.549255847

Product Information Sheet for NR-19518

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
4606	H06	1414	SACOL0200	phosphoglycerate transporter family protein	YP_185099.1	5.89533239
4607	H07	1414	SACOL0963	argininosuccinate lyase	YP_185832.1	5.445544554
4615	H08	1414	SACOL2738	tRNA modification GTPase TrmE	YP_187524.1	6.084158416
4621	H09	1417	SACOL1360	aspartate kinase	YP_186213.1	4.87791108
4623	H10	1417	SACOL2352	tcaA protein	YP_187158.1	6.141848977
4625	H11	1420	SACOL1013	magnesium transporter	YP_185881.1	6.102816901
4627	H12	1420	SACOL1908	fumarate hydratase, class II	YP_186733.1	6.068309859

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).