

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 21**

Catalog No. NR-19517

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For research use only. Not for use in humans.

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 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.

Plate orientation and viability were confirmed for NR-19517.

Material Provided:

Each inoculated well of the 96-well plate contains approximately 60 µL of culture in Luria Bertani (LB) broth containing 50 µg/mL kanamycin supplemented with 15% glycerol.

Packaging/Storage:

NR-19517 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: 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 1 day.

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 21, NR-19517.”

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 \(BMBL\)](#). 6th ed. Washington, DC: U.S. Government Printing Office, 2020.

Disclaimers:

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

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

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Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 21 (ZSAJU)¹

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
4169	A01	1228	SACOL0065	conserved hypothetical protein	YP_184970.1	4.806188925
4171	A02	1228	SACOL0549	tetrapyrrole methylase family protein	YP_185437.1	5.46009772
4173	A03	1228	SACOL1066	fnt protein	YP_185930.1	4.475570033
4176	A04	1228	SACOL1837	S-adenosylmethionine synthetase	YP_186668.1	4.813517915
4177	A05	1228	SACOL2124	conserved hypothetical protein	YP_186939.1	5.258143322
4179	A06	1228	SACOL2170	transporter, putative	YP_186982.1	5.460912052
4182	A07	1228	SACOL2471	transporter, putative	YP_187268.1	4.108306189
4185	A08	1231	SACOL1900	DNA repair exonuclease family protein	YP_186726.1	5.538586515
4187	A09	1234	SACOL0392	NADH-dependent flavin oxidoreductase, Oye family	YP_185284.1	5.576985413
4190	A10	1234	SACOL1861	type I restriction-modification enzyme, S subunit, EcoA family	YP_186689.1	4.691247974
4191	A11	1234	SACOL1964	<i>Staphylococcus aureus</i> sex pheromone	YP_186788.1	5.534846029
4194	A12	1237	SACOL0107	pyridoxal-dependent decarboxylase	YP_185011.1	5.452708165
4195	B01	1237	SACOL0491	cobalamin synthesis protein, putative	YP_185381.1	5.554567502
4198	B02	1237	SACOL1497	polyA polymerase	YP_186341.1	5.444624091
4199	B03	1237	SACOL1760	acetate kinase	YP_186594.1	5.035569927
4201	B04	1237	SACOL2075	cell division protein, FtsW/RodA/SpoVE family	YP_186891.1	5.446240905
4204	B05	1237	SACOL2155	IS1181, transposase, authentic point mutation	N/A	5.423605497
4211	B08	1240	SACOL0964	argininosuccinate synthase	YP_185833.1	5.488709677
4213	B09	1240	SACOL1223	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	YP_186086.1	5.511290323
4215	B10	1240	SACOL1428	aspartokinase, alpha and beta subunits	YP_186280.1	5.467741935
4217	B11	1243	SACOL0944	NADH dehydrogenase, putative	YP_185813.1	5.2614642
4221	B12	1243	SACOL2340	sodium:glutamate symporter	YP_187146.1	5.420756235
4223	C01	1243	SACOL2350	tcaB protein	YP_187156.1	4.66773934
4226	C02	1246	SACOL0213	acyl-CoA dehydrogenase family protein	YP_185112.1	5.376404494
4229	C03	1246	SACOL1051	isochorismate synthase family protein	YP_185916.1	5.504815409
4231	C04	1246	SACOL2257	drug transporter, putative	YP_187064.1	5.128410915
4233	C05	1246	SACOL2437	bicyclomycin resistance protein	YP_187238.1	5.46388443
4236	C06	1246	SACOL2675	SecY/SecE1-alpha family protein	YP_187463.1	5.453451043
4238	C07	1249	SACOL0566	nucleoside permease NupC	YP_185454.1	5.444355484
4239	C08	1249	SACOL0936	DltB protein	YP_185806.1	5.254603683
4241	C09	1249	SACOL1408	tryptophan synthase, beta subunit	YP_186260.1	5.470776621
4243	C10	1249	SACOL2477	conserved hypothetical protein	YP_187274.1	5.496397118
4245	C11	1252	SACOL1065	transcriptional regulator, putative	YP_185929.1	5.39057508
4247	C12	1252	SACOL1941	YihY family protein	YP_186766.1	5.424920128
4250	D01	1255	SACOL0070	permease, putative	YP_184975.1	4.956175299
4251	D02	1255	SACOL0310	nucleoside permease NupC, putative	YP_185202.1	4.706772908
4253	D03	1255	SACOL0733	sugar efflux transporter, putative	YP_185612.1	5.485258964
4255	D04	1255	SACOL0885	pathogenicity island protein, integrase	YP_185756.1	5.50438247
4257	D05	1255	SACOL1658	hypothetical protein	YP_186498.1	4.827091633
4259	D06	1258	SACOL1764	thiamine biosynthesis protein ThiI	YP_186598.1	5.461844197
4262	D07	1258	SACOL1892	membrane protein, putative	YP_186718.1	5.348171701
4266	D08	1261	SACOL0806	peptidase T	YP_185680.1	4.749405234
4267	D09	1261	SACOL1122	cell division protein, FtsW/RodA/SpoVE family	YP_185986.1	5.440126883

Clone	Well Position	ORF Length	Locus ID	Description	Accession Number	Average Depth of Coverage
4269	D10	1261	SACOL2453	amino acid ABC transporter, ATP-binding protein	YP_187252.1	5.395717684
4271	D11	1264	SACOL0415	Dyp-type peroxidase family protein	YP_185307.1	5.393196203
4273	D12	1264	SACOL0701	nucleoside permease NupC, putative	YP_185583.1	5.484177215
4275	E01	1264	SACOL1659	conserved hypothetical protein	YP_186499.1	5.416139241
4277	E02	1264	SACOL1749	NADP-dependent malic enzyme, putative	YP_186585.1	5.524525316
4279	E03	1267	SACOL2334	conserved hypothetical protein	YP_187141.1	5.505919495
4281	E04	1270	SACOL2657	arginine deiminase	YP_187445.1	5.446456693
4283	E05	1273	SACOL0116	hypothetical protein	YP_185020.1	5.488609584
4286	E06	1273	SACOL0368	prophage L54a, portal protein, HK97 family	YP_185260.1	5.352710134
4287	E07	1273	SACOL1326	GTP-binding protein, putative	YP_186181.1	5.417910448
4291	E08	1273	SACOL2105	serine hydroxymethyltransferase	YP_186920.1	5.44854674
4293	E09	1273	SACOL2323	imidazolonepropionase	YP_187130.1	5.355852317
4295	E10	1273	SACOL2689	intercellular adhesion protein A	YP_187476.1	5.418695994
4299	E11	1276	SACOL0343	prophage L54a, replicative DNA helicase, putative	YP_185235.1	5.394200627
4301	E12	1276	SACOL0916	cysteine desulfurase, SufS subfamily	YP_185787.1	5.442789969
4303	F01	1276	SACOLA0003	plasmid recombination enzyme		5.45846395
4305	F02	1279	SACOL0961	glutamate dehydrogenase, NAD-specific	YP_185830.1	4.826426896
4307	F03	1279	SACOL0988	3-oxoacyl-(acyl-carrier-protein) synthase II	YP_185856.1	4.709147772
4309	F04	1279	SACOL1265	endopeptidase resistance gene	YP_186123.1	5.451915559
4311	F05	1279	SACOL1503	TPR domain protein	YP_186347.1	5.366692729
4313	F06	1279	SACOL1876	epidermin biosynthesis protein EpiC, authentic point mutation	N/A	5.388584832
4318	F07	1285	SACOL0163	drug transporter, putative	YP_185062.1	4.572762646
4319	F08	1285	SACOL1251	cell division protein FtsY, putative	YP_186110.1	5.357198444
4321	F09	1285	SACOL2031	ammonium transporter family protein	YP_186849.1	5.33229572
4323	F10	1285	SACOL2409	fmhA protein	YP_187212.1	5.339299611
4325	F11	1291	SACOL0103	drug transporter, putative	YP_185008.1	6.298993029
4327	F12	1291	SACOL1937	aminopeptidase PepS	YP_186762.1	6.336948102
4329	G01	1291	SACOL2702	histidinol dehydrogenase	YP_187488.1	6.355538342
4331	G02	1294	SACOL0232	PTS system, sorbitol-specific IIC component	YP_185128.1	6.390262751
4333	G03	1294	SACOL1411	femB protein	YP_186263.1	6.35316847
4335	G04	1294	SACOL2019	sdrH protein, putative	YP_186838.1	5.5
4337	G05	1294	SACOL2116	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 2	YP_186931.1	6.343122102
4339	G06	1294	SACOL2266	molybdopterin biosynthesis MoeA protein, putative	YP_187073.1	6.230293663
4343	G07	1297	SACOL0150	capsular polysaccharide biosynthesis protein Cap50	YP_185050.1	6.240555127
4345	G08	1297	SACOL1400	ImpB/MucB/SamB family protein	YP_186252.1	6.33461835
4347	G09	1297	SACOL1686	histidyl-tRNA synthetase	YP_186525.1	6.117193524
4349	G10	1297	SACOL1721	ATP-dependent Clp protease, ATP-binding subunit ClpX	YP_186559.1	6.064764842
4351	G11	1297	SACOL1778	tyrosyl-tRNA synthetase	YP_186612.1	6.32767926
4353	G12	1300	SACOL1297	conserved hypothetical protein	YP_186154.1	5.268461538
4355	H01	1300	SACOL1435	diaminopimelate decarboxylase	YP_186287.1	6.335384615
4357	H02	1300	SACOL2092	UDP-N-acetylglucosamine 1-carboxyvinyltransferase 1	YP_186907.1	6.28
4360	H03	1300	SACOL2253	femX protein	YP_187061.1	6.311538462
4361	H04	1303	SACOL0194	maltose ABC transporter, permease protein	YP_185093.1	6.304681504
4363	H05	1303	SACOL0459	xanthine permease	YP_185349.1	6.306983883
4365	H06	1303	SACOL1448	2-oxoglutarate dehydrogenase, E2 component, dihydroipoamide succinyltransferase	YP_186300.1	6.34228703
4368	H07	1303	SACOL1667	peptidase, U32 family	YP_186507.1	6.256331543
4369	H08	1303	SACOL1741	isocitrate dehydrogenase, NADP-dependent	YP_186578.1	6.307751343
4372	H09	1303	SACOL1805	conserved hypothetical protein TIGR00275	YP_186638.1	6.228702993
4374	H10	1303	SACOL2050	threonine dehydratase	YP_186867.1	6.253261704
4376	H11	1306	SACOL0193	maltose ABC transporter, maltose-binding protein, putative	YP_185092.1	5.797090352
4377	H12	1306	SACOL1709	folypolyglutamate synthase/dihydrofolate synthase	YP_186548.1	6.30704441

¹All information in this table was provided by the J. Craig Venter Institute at the time of deposition.