

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 16**

**Catalog No. NR-19512**

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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:**

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-19512 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 16, NR-19512.”

**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](http://www.cdc.gov/biosafety/publications/bmb15/index.htm).

**Disclaimers:**

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## Product Information Sheet for NR-19512

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*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 Early Methicillin-Resistant *Staphylococcus aureus* Strain and a Biofilm-Producing Methicillin-Resistant

**Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 16 (ZSAJP)<sup>1</sup>**

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
3137	A01	898	SACOL2246	sugar transporter, putative	YP_187055.1	5.178173719
3139	A02	898	SACOL2577	dehydrosqualene synthase	YP_187369.1	4.638084633
3141	A03	901	SACOL0731	transcriptional regulator, LysR family	YP_185611.1	5.116537181
3143	A04	901	SACOL0790	integral membrane domain protein	YP_185663.1	5.095449501
3145	A05	901	SACOL0812	degV family protein	YP_185686.1	5.187569367
3147	A06	901	SACOL1309	pyruvate ferredoxin oxidoreductase, beta subunit	YP_186166.1	4.166481687
3149	A07	901	SACOL2096	ATP synthase F1, gamma subunit	YP_186911.1	4.680355161
3151	A08	901	SACOL2416	cation efflux family protein	YP_187219.1	4.639289678
3154	A09	901	SACOL2508	UTP-glucose-1-phosphate uridylyltransferase	YP_187303.1	4.690344062
3155	A10	904	SACOL0606	hydrolase, haloacid dehalogenase-like family	YP_185491.1	4.828539823
3158	A11	904	SACOL0896	pathogenicity island protein	YP_185767.1	5.201327434
3159	A12	904	SACOL0980	transcriptional regulator, LysR family	YP_185848.1	5.202433628
3161	B01	904	SACOL2143	conserved hypothetical protein	YP_186956.1	5.186946903
3164	B02	904	SACOL2179	conserved hypothetical protein	YP_186990.1	4.655973451
3165	B03	904	SACOL2474	peptide ABC transporter, permease protein	YP_187271.1	5.138274336
3167	B04	907	SACOL0090	integral membrane domain protein	YP_184995.1	5.065049614
3169	B05	907	SACOL1266	DNA processing protein DprA, putative	YP_186124.1	5.106945976
3171	B06	907	SACOL1736	formamidopyrimidine-DNA glycosylase	YP_186573.1	5.184123484
3177	B08	907	SACOL2082	lipoprotein, putative	YP_186898.1	3.600882029
3179	B09	907	SACOL2308	phosphosugar-binding transcriptional regulator, RpiR family	YP_187115.1	4.861080485
3181	B10	910	SACOL0179	phosphosugar-binding transcriptional regulator, RpiR family	YP_185078.1	4.004395604
3184	B11	910	SACOL0743	bacitracin resistance protein	YP_185622.1	4.363736264
3185	B12	910	SACOL1234	conserved hypothetical protein TIGR00157	YP_186095.1	5.185714286
3187	C01	910	SACOL1687	N-acetylmuramoyl-L-alanine amidase, family 3	YP_186526.1	4.693406593
3189	C02	913	SACOL0597	conserved hypothetical protein	YP_185483.1	5.040525739
3191	C03	913	SACOL0613	conserved hypothetical protein TIGR00294	YP_185498.1	5.076670318
3194	C04	913	SACOL0803	lipoprotein, putative	YP_185677.1	4.657174151
3195	C05	913	SACOL0879	conserved hypothetical protein	YP_185750.1	4.242059146
3197	C06	913	SACOL1143	iron compound ABC transporter, iron compound-binding protein, putative	YP_186006.1	5.13253012
3199	C07	913	SACOL1479	5-3 exonuclease, putative	YP_186324.1	5.209200438
3201	C08	913	SACOL2691	intercellular adhesion protein B	YP_187478.1	5.127053669
3204	C09	916	SACOL0255	membrane protein, putative	YP_185151.1	5.240174672
3205	C10	916	SACOL0312	N-acetylneuraminase lyase	YP_185204.1	5.159388646
3207	C11	916	SACOL0433	conserved hypothetical protein	YP_185324.1	5.147379913
3209	C12	916	SACOL0556	chaperonin, 33 kDa	YP_185444.1	5.148471616
3211	D01	916	SACOL1000	oligopeptide ABC transporter, permease protein	YP_185868.1	5.128820961
3213	D02	916	SACOL1212	aspartate carbamoyltransferase	YP_186075.1	5.081877729
3215	D03	916	SACOL1276	translation elongation factor Ts	YP_186133.1	4.887554585
3217	D04	916	SACOL1566	geranyltranstransferase	YP_186407.1	5.052401747
3219	D05	916	SACOL2321	oxidoreductase, short chain dehydrogenase/reductase family	YP_187128.1	5.135371179

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
3221	D06	919	SACOL0513	transcriptional regulatory protein GltC	YP_185401.1	5.168661589
3223	D07	919	SACOL1260	GTP-binding protein, putative	YP_186118.1	4.903155604
3225	D08	919	SACOL2325	transcriptional regulator, LysR family	YP_187132.1	4.253536453
3228	D09	919	SACOL2555	transcriptional regulator, LysR family, putative	YP_187348.1	5.258977149
3229	D10	922	SACOL0149	capsular polysaccharide biosynthesis protein Cap5N	YP_185049.1	5.15835141
3231	D11	922	SACOL0564	pyridoxine biosynthesis protein	YP_185452.1	5.145336226
3233	D12	922	SACOL0665	iron compound ABC transporter, iron compound-binding protein, putative	YP_185549.1	5.112798265
3237	E01	922	SACOL1540	tyrosine recombinase XerD	YP_186382.1	4.527114967
3239	E02	922	SACOL2245	acetyltransferase, GNAT family	YP_187054.1	5.032537961
3241	E03	922	SACOL2645	sensor histidine kinase, putative	YP_187433.1	4.581344902
3245	E04	925	SACOL1614	endonuclease IV	YP_186454.1	3.256216216
3247	E05	925	SACOL2598	cobalamin synthesis protein, putative	YP_187389.1	4.984864865
3251	E07	928	SACOL0132	replication initiation protein, degenerate	N/A	4.810344828
3253	E08	928	SACOL0270	staphyloxanthin biosynthesis protein, putative	YP_185165.1	4.327586207
3255	E09	928	SACOL0536	dimethyladenosine transferase	YP_185424.1	5.11637931
3261	E11	931	SACOL1269	tyrosine recombinase XerC	YP_186127.1	5.056928034
3263	E12	931	SACOL1996	ABC transporter, ATP-binding protein	YP_186820.1	4.899033298
3265	F01	934	SACOL0177	glucokinase regulator-related protein	YP_185076.1	5.025695931
3268	F02	934	SACOL1128	conserved hypothetical protein	YP_185992.1	5.177730193
3269	F03	934	SACOL1624	GTP-binding protein Era	YP_186464.1	5.132762313
3271	F04	934	SACOL2335	ABC transporter, ATP-binding protein	YP_187142.1	5.128479657
3274	F05	934	SACOL2544	L-serine dehydratase, iron-sulfur-dependent, alpha subunit	YP_187336.1	4.644539615
3275	F06	937	SACOL0834	conserved hypothetical protein TIGR01777	YP_185708.1	5.101387407
3277	F07	937	SACOL0973	fumarylacetoacetate hydrolase family protein	YP_185841.1	5.140875133
3280	F08	937	SACOL1426	conserved hypothetical protein	YP_186278.1	5.178228388
3281	F09	937	SACOL2345	esterase, putative	YP_187151.1	5.071504803
3283	F10	940	SACOL1779	transglycosylase domain protein	YP_186613.1	5.077659574
3286	F11	940	SACOL2279	urea transporter	YP_187086.1	5.172340426
3288	F12	943	SACOL0748	oxidoreductase, aldo/keto reductase family	YP_185627.1	5.152704136
3289	G01	943	SACOL1263	succinyl-CoA synthase, alpha subunit	YP_186121.1	3.890774125
3291	G02	943	SACOL1352	ABC transporter, ATP-binding protein	YP_186205.1	5.098621421
3293	G03	943	SACOL1543	oxidoreductase, aldo/keto reductase family	YP_186385.1	5.138918346
3295	G04	943	SACOL1836	conserved hypothetical protein	YP_186667.1	5.114528102
3297	G05	943	SACOL2154	arginase	YP_186967.1	5.159066808
3299	G06	943	SACOL2248	conserved hypothetical protein	YP_187057.1	3.895015907
3301	G07	943	SACOL2277	iron compound ABC transporter, iron compound-binding protein	YP_187084.1	5.054082715
3303	G08	943	SACOL2719	rarD protein	YP_187505.1	4.688229056
3307	G09	946	SACOL1125	protoheme IX farnesyltransferase	YP_185989.1	5.069767442
3311	G10	949	SACOL0253	ribokinase	YP_185149.1	4.971548999
3313	G11	949	SACOL0502	cysteine synthase/cystathionine beta-synthase family protein	YP_185390.1	5.073761855
3317	G12	949	SACOL1364	homoserine kinase	YP_186217.1	4.798735511
3319	H01	949	SACOL1528	lipoprotein, putative	YP_186370.1	5.126448894
3322	H02	949	SACOL2387	conserved hypothetical protein, authentic point mutation	N/A	5.220231823
3323	H03	952	SACOL0787	conserved hypothetical protein TIGR00147	YP_185660.1	5.102941176
3325	H04	952	SACOL0927	lipoate synthase	YP_185797.1	5.071428571
3327	H05	952	SACOL1209	ribosomal large subunit pseudouridine synthases, RluD subfamily	YP_186070.1	4.133403361
3331	H07	952	SACOL1422	phosphate ABC transporter, permease protein	YP_186274.1	5.033613445
3333	H08	952	SACOL1531	lipoprotein, putative	YP_186373.1	4.930672269

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
3335	H09	952	SACOL2314	sodium/bile acid symporter family protein	YP_187121.1	4.969537815
3337	H10	955	SACOL0265	hypothetical protein	YP_185160.1	4.203141361
3339	H11	955	SACOL0636	mevalonate kinase	YP_185521.1	4.22408377
3341	H12	955	SACOL0758	1-phosphofructokinase	YP_185637.1	4.120418848

<sup>1</sup>25 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).