

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 25**

**Catalog No. NR-19521**

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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-19521 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 25, NR-19521."

**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](http://www.cdc.gov/biosafety/publications/bmbl5/index.htm).

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# Product Information Sheet for NR-19521

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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.

**References:**

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

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**Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 25 (ZSAJY)**

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
5141	A01	1969	SACOL0005	DNA gyrase, B subunit	YP_184916.1	6.171152869
5143	A02	1969	SACOL0317	lipase precursor, interruption-N	YP_185209.1	5.269680041
5145	A03	1972	SACOL1138	LPXTG cell wall surface anchor protein	YP_186002.1	5.929513185
5147	A04	1972	SACOL1729	threonyl-tRNA synthetase	YP_186567.1	6.116125761
5150	A05	1975	SACOL0778	sulfatase family protein	YP_185653.1	6.143797468
5152	A06	1987	SACOL2663	PTS system, fructose-specific IIABC components	YP_187451.1	6.186713639
5154	A07	1990	SACOL0403	transcriptional antiterminator, BglG family	YP_185295.1	6.142211055
5156	A08	1990	SACOL2290	transcriptional regulator, AraC family	YP_187097.1	6.179396985
5157	A09	1992	SACOL0759	PTS system, fructose-specific IIABC component, authentic frameshift	N/A	6.175702811
5160	A10	1999	SACOL1038	membrane protein	YP_185903.1	5.793896948
5162	A11	1999	SACOL2527	fructose-1,6-bisphosphatase, putative	YP_187320.1	5.804902451
5163	A12	2002	SACOL0014	DHH subfamily 1 protein	YP_184925.1	5.198801199
5165	B01	2008	SACOL0533	methionyl-tRNA synthetase	YP_185421.1	5.883964143
5167	B02	2011	SACOL2171	aerobactin biosynthesis protein, lucA/lucC family	YP_186983.1	5.711586275
5169	B03	2023	SACOL1069	quinol oxidase, subunit I	YP_185933.1	5.685121107
5172	B04	2023	SACOL1377	transketolase	YP_186230.1	6.152249135
5173	B05	2026	SACOL0823	excinuclease ABC, B subunit	YP_185697.1	6.023198421
5177	B06	2029	SACOL2564	ferrous iron transport protein B	YP_187356.1	6.075406604
5179	B07	2032	SACOL1389	DNA topoisomerase IV, B subunit	YP_186242.1	6.082185039
5181	B08	2035	SACOL2643	ABC transporter, permease protein	YP_187431.1	6.230958231
5183	B09	2038	SACOL1965	DNA ligase, NAD-dependent	YP_186789.1	6.390088322
5185	B10	2041	SACOL0033	penicillin-binding protein 2	YP_184944.1	6.9377756
5187	B11	2041	SACOL0188	gamma-glutamyltranspeptidase	YP_185087.1	6.947574718
5189	B12	2044	SACOL1316	DNA mismatch repair protein HexB	YP_186172.1	6.851761252
5193	C01	2077	SACOL0687	Na <sup>+</sup> /H <sup>+</sup> antiporter, putative	YP_185569.1	6.586422725
5195	C02	2077	SACOL2694	lipase	YP_187480.1	6.602311026
5197	C03	2080	SACOL0175	PTS system, IIABC components	YP_185074.1	6.745192308
5201	C04	2090	SACOL2002	map protein, programmed frameshift	YP_186825.1	6.149282297
5203	C05	2095	SACOL1241	ATP-dependent DNA helicase RecG	YP_186101.1	6.811455847
5205	C06	2101	SACOL2552	PTS system, IIABC components	YP_187344.1	6.855782961
5207	C07	2104	SACOL1267	DNA topoisomerase I	YP_186125.1	6.397813688
5211	C08	2113	SACOL2442	Na <sup>+</sup> /H <sup>+</sup> antiporter, putative	YP_187243.1	6.877898722
5213	C09	2116	SACOL0593	translation elongation factor G	YP_185479.1	6.823251418
5215	C10	2128	SACOL0555	cell division protein FtsH, putative	YP_185443.1	6.45018797
5220	C11	2131	SACOL1293	polyribonucleotide nucleotidyltransferase	YP_186150.1	7.392773346
5221	C12	2140	SACOL0792	ribonucleoside-diphosphate reductase, alpha subunit	YP_185666.1	6.828037383
5227	D03	2152	SACOL1288	translation initiation factor IF-2	YP_186145.1	6.281598513
5231	D04	2170	SACOL2243	DNA topoisomerase III	YP_187053.1	5.9
5234	D05	2182	SACOL1644	competence protein ComEC/Rec2, putative	YP_186484.1	7.334555454
5239	D06	2197	SACOL1532	hypothetical protein	YP_186374.1	6.816112881
5241	D07	2218	SACOL1490	penicillin-binding protein 2	YP_186334.1	6.77141569
5243	D08	2224	SACOL1078	phosphoribosylformylglycinamide synthase II	YP_185942.1	6.208183453
5245	D09	2224	SACOL1689	GTP pyrophosphokinase	YP_186528.1	6.68705036

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Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
5247	D10	2227	SACOL1966	ATP-dependent DNA helicase PcrA	YP_186790.1	6.961832061
5250	D11	2233	SACOL0084	transcriptional regulator, AraC family	YP_184989.1	6.426332288
5252	D12	2263	SACOL0428	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase	YP_185319.1	7.155103844
5254	E01	2269	SACOL1194	penicillin-binding protein 1	YP_186056.1	7.135301895
5255	E02	2284	SACOL0204	formate acetyltransferase	YP_185103.1	6.356830123
5257	E03	2296	SACOL0212	3-hydroxyacyl-CoA dehydrogenase protein	YP_185111.1	7.632404181
5260	E04	2308	SACOL1691	single-stranded-DNA-specific exonuclease RecJ	YP_186530.1	7.808925477
5264	E05	2344	SACOL1028	serine protease	YP_185894.1	7.663822526
5268	E06	2383	SACOL1154	DNA mismatch repair MutS2 family protein	YP_186017.1	7.582039446
5271	E07	2413	SACOL1295	FtsK/SpolIIE family protein	YP_186152.1	6.934521343
5273	E08	2425	SACOL2671	secA family protein	YP_187459.1	6.952164948
5276	E09	2437	SACOL0679	Na <sup>+</sup> /H <sup>+</sup> antiporter, MnhA component, putative	YP_185562.1	7.463274518
5277	E10	2437	SACOL1149	phenylalanyl-tRNA synthetase, beta subunit	YP_186012.1	6.96512105
5280	E11	2437	SACOL1390	DNA topoisomerase IV, A subunit	YP_186243.1	7.490356996
5282	E12	2440	SACOL0955	Na <sup>+</sup> /H <sup>+</sup> antiporter, MnhA component	YP_185824.1	7.674180328
5285	F01	2443	SACOL1224	primosomal protein N'	YP_186087.1	7.396234138
5287	F02	2443	SACOL2572	copper-translocating P-type ATPase	YP_187364.1	7.312320917
5289	F03	2452	SACOL1808	leucyl-tRNA synthetase	YP_186641.1	7.356035889
5291	F04	2458	SACOL2194	hyaluronate lyase	YP_187005.1	6.239218877
5295	F05	2512	SACOL1674	helicase, putative, RecD/TraA family	YP_186514.1	5.503582803
5297	F06	2524	SACOL2566	MmpL efflux pump, putative	YP_187358.1	6.69770206
5299	F07	2530	SACOL1579	conserved hypothetical protein	YP_186419.1	6.759683794
5301	F08	2557	SACOL1396	fmtC protein	YP_186248.1	6.926867423
5305	F09	2641	SACOL1259	conserved hypothetical protein	YP_186117.1	7.037864445
5307	F10	2644	SACOL0135	alcohol dehydrogenase, iron-containing	YP_185035.1	7.067322239
5309	F11	2644	SACOL0979	ATP-dependent Clp protease, ATP-binding subunit ClpB	YP_185847.1	7.09720121
5313	F12	2665	SACOL1673	alanyl-tRNA synthetase	YP_186513.1	6.637523452
5317	G01	2665	SACOL1737	DNA polymerase I	YP_186574.1	7.012007505
5319	G02	2692	SACOL2070	sensor histidine kinase KdpD	YP_186886.1	7.001485884
5321	G03	2698	SACOL0006	DNA gyrase, A subunit	YP_184917.1	7.055967383
5325	G04	2728	SACOL1495	DNA polymerase III, epsilon subunit/ATP-dependent helicase DinG	YP_186339.1	6.890395894
5328	G05	2740	SACOL0495	conserved hypothetical protein	YP_185383.1	5.398175182
5329	G06	2740	SACOL1385	aconitate hydratase	YP_186238.1	6.718978102
5334	G07	2788	SACOL1206	isoleucyl-tRNA synthetase	YP_186068.1	7.175394548
5342	G08	2857	SACOL2509	fibronectin binding protein B	YP_187304.1	6.949947497
5343	G09	2878	SACOL0608	sdrC protein	YP_185493.1	6.550034746
5345	G10	2881	SACOL0824	excinuclease ABC, A subunit	YP_185698.1	6.804928844
5349	G11	2971	SACOL1899	conserved hypothetical protein	YP_186725.1	6.587680916
5353	G12	3016	SACOL2665	phage infection protein, putative	YP_187453.1	5.959880637
5355	H01	3028	SACOL1877	epidermin biosynthesis protein EpiB	YP_186704.1	6.552840159
5358	H02	3064	SACOL0272	hypothetical protein	YP_185167.1	7.157963446
5360	H03	3064	SACOL1382	exonuclease SbcC	YP_186235.1	7.166775457
5361	H04	3085	SACOL1859	hypothetical protein	YP_186687.1	6.645380875
5363	H05	3091	SACOL2511	fibronectin-binding protein A	YP_187306.1	6.730507926
5366	H06	3187	SACOL0076	hypothetical protein	YP_184981.1	6.858487606
5370	H07	3208	SACOL1215	carbamoyl-phosphate synthase, large subunit	YP_186078.1	6.424875312
5371	H08	3232	SACOL1750	DNA polymerase III, alpha subunit	YP_186586.1	7.275680693
5387	H09	3658	SACOL0589	DNA-directed RNA polymerase, beta subunit	YP_185475.1	7.937124112
5397	H10	3859	SACOL1791	FtsK/SpolIIE family protein	YP_186624.1	6.455558435
5406	H11	4534	SACOL0514	glutamate synthase, large subunit	YP_185402.1	6.973312748
5410	H12	6235	SACOL0379	prophage L54a, tail tape measurement protein, TP901 family	YP_185271.1	7.194707298