

Product Information Sheet for NR-19511

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 15**

Catalog No. NR-19511

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 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-19511 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 15, NR-19511."

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.

Disclaimers:

You are authorized to use this product for research use only. It is not intended for human use.

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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:

1. 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 15 (ZSAJO)

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
2928	A01	838	SACOL2122	pantothenate kinase, putative	YP_186937.1	5.260143198
2929	A02	838	SACOL2208	tRNA pseudouridine synthase A	YP_187018.1	4.737470167
2932	A03	838	SACOL2291	staphyloxanthin biosynthesis protein	YP_187098.1	4.730310263
2933	A04	841	SACOL1006	conserved hypothetical protein	YP_185874.1	5.292508918
2935	A05	841	SACOL1084	cobalt transport family protein	YP_185948.1	5.22235434
2937	A06	841	SACOL1652	shikimate 5-dehydrogenase	YP_186492.1	4.401902497
2939	A07	841	SACOL2209	cobalt transport family protein	YP_187019.1	5.312722949
2941	A08	841	SACOL2440	conserved hypothetical protein	YP_187241.1	5.262782402
2943	A09	841	SACOL2533	glyoxalase family protein	YP_187326.1	5.221165279
2946	A10	844	SACOL1011	conserved hypothetical protein	YP_185879.1	5.302132701
2947	A11	844	SACOL1110	spermidine/putrescine ABC transporter, permease protein	YP_185974.1	5.273696682
2950	A12	844	SACOL1447	conserved hypothetical protein	YP_186299.1	4.71563981
2951	B01	844	SACOL1932	transglycosylase domain protein	YP_186757.1	4.646919431
2953	B02	844	SACOL2153	conserved hypothetical protein TIGR00159	YP_186966.1	5.238151659
2956	B03	844	SACOL2211	ABC transporter, ATP-binding protein	YP_187021.1	5.254739336
2957	B04	844	SACOL2605	conserved hypothetical protein	YP_187395.1	5.16943128
2959	B05	847	SACOL0695	tagG protein, teichoic acid ABC transporter protein, putative	YP_185577.1	5.26918536
2961	B06	850	SACOL0125	phosphonate ABC transporter, permease protein	YP_185029.1	3.281176471
2963	B07	850	SACOL0484	Staphylococcus tandem lipoprotein	YP_185374.1	5.268235294
2965	B08	850	SACOL0486	staphylococcus tandem lipoprotein	YP_185376.1	5.276470588
2967	B09	850	SACOL1160	succinate dehydrogenase, iron-sulfur protein	YP_186023.1	5.275294118
2969	B10	850	SACOL1546	pyrroline-5-carboxylate reductase	YP_186388.1	5.311764706
2971	B11	850	SACOL1718	hemX protein	YP_186556.1	5.212941176
2973	B12	850	SACOL2196	conserved hypothetical protein	YP_187007.1	5.202352941
2975	C01	850	SACOL2473	peptide ABC transporter, ATP-binding protein	YP_187270.1	4.601176471
2977	C02	853	SACOL1319	glycerol uptake facilitator protein	YP_186174.1	4.64126612
2979	C03	853	SACOL1620	conserved hypothetical protein	YP_186460.1	5.223915592
2981	C04	853	SACOL1931	FAD-binding RecX family protein	YP_186756.1	5.264947245
2983	C05	853	SACOL2478	conserved hypothetical protein	YP_187275.1	4.409144197
2985	C06	853	SACOL2482	3-oxoacyl-(acyl carrier protein) reductase, authentic point mutation	N/A	4.177022274
2987	C07	853	SACOL2615	3-methyl-2-oxobutanoate hydroxymethyltransferase	YP_187404.1	4.822977726
2989	C08	853	SACOL2704	conserved hypothetical protein	YP_187490.1	5.254396249
2992	C09	856	SACOL0884	ABC transporter, substrate-binding protein	YP_185755.1	4.178738318
2993	C10	856	SACOL1054	naphthoate synthase	YP_185919.1	5.23364486
2995	C11	856	SACOL1907	ribosomal large subunit pseudouridine synthase, RluD subfamily	YP_186732.1	4.142523364
2998	C12	856	SACOL1974	NH(3)-dependent NAD ⁺ synthetase	YP_186798.1	5.25817757
2999	D01	856	SACOL2479	conserved hypothetical protein	YP_187276.1	5.162383178
3001	D02	856	SACOL2591	actVA 4 protein	YP_187382.1	5.186915888
3005	D03	859	SACOL0539	pur operon repressor	YP_185427.1	4.279394645
3009	D04	859	SACOL2401	formate/nitrite transporter family protein	YP_187204.1	5.256111758

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Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
3011	D05	862	SACOL0391	hypothetical protein	YP_185283.1	4.938515081
3015	D06	862	SACOL1116	inositol monophosphatase family protein	YP_185980.1	4.393271462
3017	D07	862	SACOL1300	ACT domain protein	YP_186157.1	5.257540603
3019	D08	862	SACOL1814	lysophospholipase, putative	YP_186646.1	5.220417633
3021	D09	865	SACOL0626	phosphomethylpyrimidine kinase	YP_185511.1	5.147976879
3023	D10	865	SACOL1416	peptide ABC transporter, permease protein, putative	YP_186268.1	5.169942197
3025	D11	865	SACOL1591	lipoate-protein ligase A family protein	YP_186431.1	5.16416185
3027	D12	865	SACOL2085	phosphomethylpyrimidine kinase	YP_186901.1	5.167630058
3029	E01	865	SACOL2597	hydrolase, alpha/beta hydrolase fold family	YP_187388.1	4.652023121
3032	E02	868	SACOL0703	conserved hypothetical protein	YP_185585.1	4.700460829
3033	E03	868	SACOL1835	oxidoreductase, aldo/keto reductase family	YP_186666.1	5.232718894
3035	E04	868	SACOL2236	ribosomal protein L2	YP_187046.1	5.123271889
3037	E05	868	SACOL2707	cobalt transport family protein	YP_187493.1	4.466589862
3039	E06	871	SACOL0635	lipoate-protein ligase A family protein	YP_185520.1	5.167623421
3041	E07	871	SACOL0689	ABC transporter, permease protein	YP_185571.1	5.213547646
3043	E08	871	SACOL1928	conserved hypothetical protein	YP_186753.1	4.638346728
3046	E09	871	SACOL2109	modification methylase, HemK family	YP_186924.1	4.715269805
3047	E10	871	SACOL2286	urease accessory protein UreD	YP_187093.1	4.34902411
3049	E11	874	SACOL0195	maltose ABC transporter, permease protein	YP_185094.1	5.145308924
3052	E12	874	SACOL0531	tetrapyrrole methylase family protein	YP_185419.1	4.709382151
3053	F01	874	SACOL0763	oxidoreductase, aldo/keto reductase family	YP_185640.1	5.156750572
3056	F02	874	SACOL0820	LysM domain protein	YP_185694.1	5.223112128
3057	F03	874	SACOL0826	prolipoprotein diacylglycerol transferase	YP_185700.1	5.180778032
3059	F04	874	SACOL1460	degV family protein	YP_186309.1	4.639588101
3061	F05	874	SACOL2735	chromosome partitioning protein, ParB family	YP_187521.1	5.171624714
3064	F06	877	SACOL0181	conserved domain protein	YP_185080.1	5.269099202
3065	F07	877	SACOL0422	ABC transporter, ATP-binding protein	YP_185314.1	5.13340935
3067	F08	877	SACOL0506	ABC transporter, substrate-binding protein	YP_185394.1	4.59977195
3071	F09	877	SACOL1989	conserved hypothetical protein	YP_186813.1	4.238312429
3075	F10	880	SACOL0432	spoOJ protein	YP_185323.1	5.181818182
3077	F11	880	SACOL0467	conserved hypothetical protein	YP_185357.1	4.497727273
3079	F12	880	SACOL2009	tetracenomycin polyketide synthesis O-methyltransferase TcmP, putative	YP_186829.1	4.646590909
3081	G01	883	SACOL0538	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	YP_185426.1	5.201585504
3083	G02	883	SACOL0924	conserved hypothetical protein	YP_185794.1	5.194790487
3085	G03	883	SACOL0991	oligopeptide ABC transporter, permease protein	YP_185859.1	4.662514156
3087	G04	883	SACOL1800	D-alanine aminotransferase	YP_186633.1	5.193657984
3089	G05	883	SACOL2192	oxidoreductase, aldo/keto reductase family	YP_187003.1	5.204983012
3091	G06	883	SACOL2710	conserved hypothetical protein	YP_187496.1	4.874292186
3093	G07	886	SACOL0913	conserved hypothetical protein	YP_185784.1	4.600451467
3097	G08	886	SACOL1421	phosphate ABC transporter, ATP-binding protein	YP_186273.1	5.14221219
3099	G09	886	SACOL2446	epimerase/dehydratase, putative	YP_187246.1	4.639954853
3101	G10	886	SACOL2614	pantoate--beta-alanine ligase	YP_187403.1	5.22234763
3104	G11	889	SACOL0414	lipoprotein, putative	YP_185306.1	4.721034871
3105	G12	889	SACOL1012	ribosomal large subunit pseudouridine synthases, RluD subfamily	YP_185880.1	5.193475816
3107	H01	889	SACOL1358	conserved hypothetical protein	YP_186211.1	4.143982002
3109	H02	889	SACOL1825	N-acetylmuramoyl-L-alanine amidase, family 4	YP_186657.1	5.187851519
3111	H03	889	SACOL2195	M23/M37 peptidase domain protein	YP_187006.1	4.12935883
3113	H04	892	SACOL1748	acetyl-CoA carboxylase, carboxyl transferase, beta subunit	YP_186584.1	5.161434978
3115	H05	892	SACOL1793	conserved hypothetical protein	YP_186626.1	5.184977578
3120	H06	895	SACOL0313	ROK family protein	YP_185205.1	4.736312849
3121	H07	895	SACOL0408	glyoxalase family protein	YP_185300.1	5.204469274

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3123	H08	895	SACOL1072	methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase	YP_185936.1	4.896089385
3125	H09	895	SACOL2117	fructose-bisphosphate aldolase, class II	YP_186932.1	4.193296089
3127	H10	895	SACOL2121	acetyltransferase, GNAT family	YP_186936.1	4.875977654
3129	H11	895	SACOL2210	ABC transporter, ATP-binding protein	YP_187020.1	5.204469274
3135	H12	898	SACOL1612	ABC transporter, permease protein	YP_186452.1	5.165924276