

Product Information Sheet for NR-19514

***Staphylococcus aureus* (MRSA), Strain COL Gateway® Clone Set, Recombinant in *Escherichia coli*, Plate 18**

Catalog No. NR-19514

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-19514 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 18, NR-19514."

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.

Use of this product is subject to the terms and conditions of the BEI Resources Material Transfer Agreement (MTA). The MTA is available on our Web site at www.beiresources.org.

While BEI Resources uses reasonable efforts to include accurate and up-to-date information on this product sheet, neither ATCC® nor the U.S. Government makes any warranties or representations as to its accuracy. Citations from scientific literature and patents are provided for informational purposes only. Neither ATCC® nor the U.S. Government warrants that such information has been confirmed to be accurate.

This product is sent with the condition that you are responsible for its safe storage, handling, use and disposal. ATCC® and the U.S. Government are not liable for any damages or injuries arising from receipt and/or use of this product. While reasonable effort is made to ensure authenticity and reliability of materials on deposit, the U.S. Government, ATCC®, their suppliers and contributors to BEI Resources are not liable for damages arising from the misidentification or misrepresentation of products.

Use Restrictions:

This material is distributed for internal research, non-commercial purposes only. This material, its product or its derivatives may not be distributed to third parties. Except as performed under a U.S. Government contract, individuals

Product Information Sheet for NR-19514

contemplating commercial use of the material, its products or its derivatives must contact the contributor to determine if a license is required. U.S. Government contractors may need a license before first commercial sale.

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:

1. 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

Table 1: *Staphylococcus aureus*, Strain COL Gateway® Clones, Plate 18 (ZSAJR)¹

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
3541	A01	1003	SACOL1746	6-phosphofructokinase	YP_186582.1	4.985044865
3547	A02	1003	SACOL2530	conserved hypothetical protein	YP_187323.1	4.957128614
3549	A03	1003	SACOL2549	esterase, putative	YP_187341.1	4.740777667
3551	A04	1006	SACOL0113	NAD-dependent epimerase/dehydratase family protein	YP_185017.1	4.688866799
3554	A05	1006	SACOL0793	ribonucleoside-diphosphate reductase 2, beta subunit	YP_185667.1	4.505964215
3557	A07	1006	SACOL1291	riboflavin biosynthesis protein RibF	YP_186148.1	4.997017893
3563	A09	1009	SACOL1601	competence protein comGA, putative	YP_186441.1	5.008919723
3565	A10	1009	SACOL1643	DNA polymerase III, delta subunit	YP_186483.1	5.019821606
3567	A11	1009	SACOL1715	delta-aminolevulinic acid dehydratase	YP_186553.1	4.445986125
3570	A12	1012	SACOL0781	osmoprotectant ABC transporter, ATP-binding protein, putative	YP_185656.1	5.08201581
3571	B01	1012	SACOL1103	pyruvate dehydrogenase complex E1 component, beta subunit	YP_185967.1	4.945652174
3574	B02	1012	SACOL1371	GMP reductase	YP_186224.1	5.08201581
3575	B03	1012	SACOL1639	heat-inducible transcription repressor HrcA	YP_186479.1	4.867588933
3577	B04	1012	SACOL1927	conserved hypothetical protein	YP_186752.1	4.893280632
3579	B05	1012	SACOL2396	uroporphyrinogen III methylase SirB, putative	YP_187199.1	4.954545455
3584	B07	1015	SACOL0998	oligopeptide ABC transporter, ATP-binding protein	YP_185866.1	5.078817734
3586	B08	1015	SACOL1557	conserved hypothetical protein	YP_186398.1	5.079802956
3589	B09	1015	SACOL2183	tagatose 1,6-diphosphate aldolase	YP_186994.1	4.95270936
3591	B10	1018	SACOL0637	mevalonate diphosphate decarboxylase	YP_185522.1	4.933202358
3593	B11	1018	SACOL0764	glycosyl transferase, group 2 family protein	YP_185641.1	4.927308448
3595	B12	1018	SACOL1398	transcriptional regulator, putative	YP_186250.1	4.044204322
3597	C01	1018	SACOL1424	phosphate ABC transporter, phosphate-binding protein	YP_186276.1	4.784872299
3599	C02	1018	SACOL1561	2-oxoisovalerate dehydrogenase, E1 component, beta subunit	YP_186402.1	4.847740668
3603	C04	1018	SACOL2167	iron compound ABC transporter, iron compound-binding protein	YP_186979.1	4.919449902
3605	C05	1021	SACOL0034	methicillin-resistance MecR1 regulatory protein	YP_184945.1	4.916748286
3607	C06	1021	SACOL0078	1-phosphatidylinositol phosphodiesterase	YP_184983.1	4.953966699
3609	C07	1021	SACOL0634	phosphate acetyltransferase	YP_185519.1	4.8374143
3611	C08	1021	SACOL0997	oligopeptide ABC transporter, ATP-binding protein	YP_185865.1	4.921645446
3613	C09	1021	SACOL1004	competence protein, putative	YP_185872.1	4.916748286
3615	C10	1021	SACOL1034	lipoate-protein ligase A family protein	YP_185899.1	4.941234084
3618	C11	1021	SACOL1243	fatty acid/phospholipid synthesis protein PlsX	YP_186103.1	5.100881489
3619	C12	1021	SACOL1417	peptide ABC transporter, permease protein	YP_186269.1	4.377081293
3621	D01	1021	SACOL1520	pyridine nucleotide-disulfide oxidoreductase	YP_186363.1	4.861900098
3623	D02	1021	SACOL1604	glucokinase	YP_186444.1	4.860920666

Product Information Sheet for NR-19514

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
3625	D03	1021	SACOL1947	conserved hypothetical protein	YP_186772.1	4.806072478
3628	D04	1024	SACOL0012	homoserine O-acetyltransferase, putative	YP_184923.1	5.063476563
3629	D05	1024	SACOL1001	tryptophanyl-tRNA synthetase	YP_185869.1	4.876953125
3631	D06	1024	SACOL1429	aspartate-semialdehyde dehydrogenase	YP_186281.1	4.884765625
3633	D07	1024	SACOL1630	conserved hypothetical protein	YP_186470.1	4.870117188
3635	D08	1024	SACOL1786	catabolite control protein A	YP_186619.1	3.827148438
3637	D09	1027	SACOL0099	iron compound ABC transporter, iron compound-binding protein SirA	YP_185004.1	4.934761441
3639	D10	1027	SACOL0262	Cchologylglycine hydrolase family protein	YP_185157.1	4.102239533
3641	D11	1027	SACOL1562	2-oxoisovalerate dehydrogenase, E1 component, alpha subunit	YP_186403.1	4.911392405
3643	D12	1027	SACOL2003	phospholipase C	YP_186826.1	3.808179163
3645	E01	1027	SACOL2535	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_187328.1	4.842259007
3647	E02	1030	SACOL0098	iron compound ABC transporter, permease protein SirB	YP_185003.1	3.987378641
3650	E03	1030	SACOL0411	membrane protein, putative	YP_185303.1	5.02815534
3651	E04	1030	SACOL0831	conserved hypothetical protein	YP_185705.1	4.894174757
3653	E05	1030	SACOL1847	conserved domain protein, putative	YP_186678.1	4.906796117
3655	E06	1033	SACOL0097	iron compound ABC transporter, permease protein SirC	YP_185002.1	3.818005808
3657	E07	1033	SACOL0101	ornithine cyclodeaminase, putative	YP_185006.1	4.918683446
3659	E08	1033	SACOL0257	ribose operon repressor, putative	YP_185152.1	4.907066796
3661	E09	1033	SACOL1405	anthranilate phosphoribosyltransferase	YP_186257.1	4.878025169
3663	E10	1033	SACOL1514	glycerol-3-phosphate dehydrogenase, NAD-dependent	YP_186358.1	4.896418199
3665	E11	1033	SACOL2574	D-isomer specific 2-hydroxyacid dehydrogenase family protein	YP_187366.1	4.869312682
3667	E12	1036	SACOL0394	conserved hypothetical protein	YP_185286.1	4.834942085
3669	F01	1036	SACOL1181	ornithine carbamoyltransferase	YP_186044.1	4.857142857
3673	F02	1036	SACOL1843	o-succinylbenzoic acid (OSB) synthetase, putative	YP_186674.1	4.923745174
3675	F03	1036	SACOL2057	sigma factor B regulator protein	YP_186873.1	4.894787645
3679	F04	1036	SACOL2178	alcohol dehydrogenase, zinc-containing	YP_186989.1	4.907335907
3681	F05	1039	SACOL0507	LysM domain protein	YP_185395.1	5.602502406
3683	F06	1039	SACOL0705	iron compound ABC transporter, permease protein	YP_185587.1	5.518768046
3685	F07	1039	SACOL0777	urea amidolyase-related protein	YP_185652.1	5.948026949
3687	F08	1039	SACOL1696	Holliday junction DNA helicase RuvB	YP_186535.1	5.963426372
3689	F09	1039	SACOL2045	ketol-acid reductoisomerase	YP_186862.1	5.980750722
3692	F10	1039	SACOL2269	molybdopterin biosynthesis MoeB protein, putative	YP_187076.1	5.856592878
3693	F11	1039	SACOL2367	quinone oxidoreductase, YhdH/YhfP family	YP_187172.1	5.235803657
3695	F12	1042	SACOL0569	ATP:guanido phosphotransferase family protein	YP_185457.1	5.850287908
3697	G01	1042	SACOL0722	phosphate transporter family protein	YP_185603.1	5.780230326
3699	G02	1042	SACOL2426	biotin synthetase	YP_187228.1	4.025911708
3701	G03	1045	SACOL0660	alcohol dehydrogenase, zinc-containing	YP_185544.1	5.213397129
3704	G04	1045	SACOL0838	glyceraldehyde 3-phosphate dehydrogenase	YP_185712.1	5.849760766
3705	G05	1045	SACOL1057	V8 Protease	YP_185922.1	5.988516746
3707	G06	1045	SACOL1059	conserved hypothetical protein	YP_185924.1	5.954066986
3710	G07	1045	SACOL1663	urea amidolyase-related protein	YP_186503.1	5.745454545
3711	G08	1045	SACOL2596	conserved hypothetical protein	YP_187387.1	6.004784689
3713	G09	1045	SACOL2656	ornithine carbamoyltransferase	YP_187444.1	5.523444976

Product Information Sheet for NR-19514

Clone	Well Position	ORF Length	Locus ID	Description (Gene name)	Accession Number	Average Depth of Coverage
3715	G10	1048	SACOL0837	gap transcriptional regulator	YP_185711.1	5.915076336
3717	G11	1048	SACOL1678	bacterial luciferase family protein	YP_186518.1	5.458015267
3719	G12	1048	SACOL2701	histidinol-phosphate aminotransferase, putative	YP_187487.1	5.088740458
3721	H01	1051	SACOL0706	iron compound ABC transporter, permease protein	YP_185588.1	5.893434824
3723	H02	1054	SACOL1095	cytochrome d ubiquinol oxidase, subunit II	YP_185959.1	5.509487666
3725	H03	1054	SACOL1112	conserved hypothetical protein	YP_185976.1	5.95256167
3728	H04	1054	SACOL1552	maltose operon repressor	YP_186393.1	5.714421252
3729	H05	1054	SACOL2332	aldose 1-epimerase	YP_187139.1	5.95256167
3732	H06	1055	SACOL1573	integrase/recombinase, core domain family, authentic frameshift	N/A	5.545023697
3733	H07	1057	SACOL0398	lipoate-protein ligase A family protein	YP_185290.1	5.947019868
3736	H08	1057	SACOL0858	secretory extracellular matrix and plasma binding protein	YP_185731.1	5.750236518
3739	H09	1060	SACOL0162	formate dehydrogenase, NAD-dependent	YP_185061.1	5.967924528
3741	H10	1060	SACOL0237	alcohol dehydrogenase, zinc-containing	YP_185133.1	5.900943396
3743	H11	1060	SACOL0241	alcohol dehydrogenase, zinc-containing	YP_185137.1	5.833018868
3745	H12	1060	SACOL0399	oxidoreductase, putative	YP_185291.1	5.128301887

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).