

Staphylococcus aureus* Fluorescent Reporter Plasmid pSGFPS1, Recombinant in *Staphylococcus aureus

Catalog No. NR-51163

Product Description: NR-51163 is a glycerol stock of *Staphylococcus aureus* (*S. aureus*), strain RN4220 containing the green fluorescent protein (GFP) reporter plasmid pSGFPS1, a derivative of the *Escherichia coli* (*E. coli*) - staphylococcal shuttle vector pKK30.

Lot¹: 70010748

Manufacturing Date: 30NOV2017

TEST	SPECIFICATIONS	RESULTS
Phenotypic Analysis Cellular morphology Colony morphology ² Motility (wet mount) Hemolysis ³ Biochemical characterization Catalase VITEK [®] MS (MALDI-TOF)	Gram-positive cocci Report results Report results Report results Positive <i>S. aureus</i>	Gram-positive cocci Circular, convex, entire, smooth and cream (Figure 1) Non-motile β-hemolytic Positive <i>S. aureus</i> (99.9%)
Genotypic Analysis Sequencing of 16S ribosomal RNA gene (~ 730 base pairs)	≥ 99% sequence identity to <i>S. aureus</i> , strain RN4220 (GenBank: AFGU01000017.1)	100% sequence identity to <i>S. aureus</i> , strain RN4220 (GenBank: AFGU01000017.1)
Confirmation of pSGFPS1 plasmid	Report results	Consistent with pSGFPS1 plasmid description (Figure 2, Table 1) ^{4,5}
Functional Activity of Antibiotic Resistance Gene in <i>S. aureus</i> Trimethoprim ²	Growth	Growth
Purity (post-freeze)⁶	Growth consistent with expected colony morphology	Growth consistent with expected colony morphology
Viability (post-freeze)²	Growth	Growth

¹NR-51163 was produced by inoculation of the deposited material in Tryptic Soy broth containing 10 µg/mL trimethoprim and incubated for 1 day at 37°C in an aerobic atmosphere. Broth inoculum was used to inoculate Tryptic Soy agar with 10 µg/mL trimethoprim kolles, which were grown for 1 day at 37°C in an aerobic atmosphere to produce this lot.

²1 day at 37°C in an aerobic atmosphere on Tryptic Soy agar with 10 µg/mL trimethoprim

³1 day at 37°C in an aerobic atmosphere on Tryptic Soy agar with 5% defibrinated sheep blood.

⁴Illumina[®] MiSeq[®] sequence was analyzed with CLC Genomics Workbench Version 7.0.2.

⁵pSGFPS1 was sequenced and annotated at ATCC[®] for BEI Resources and is consistent with the vector described in Rodriguez, M. D., et al. "Construction of Stable Fluorescent Reporter Plasmids for Use in *Staphylococcus aureus*." *Front. Microbiol.* 8 (2017): 2491. PubMed: 29312199.

⁶Purity of this lot was assessed for 7 days at 37°C in an aerobic atmosphere with 5% CO₂ on Tryptic Soy agar with 5% defibrinated sheep blood.

Figure 1: Colony Morphology

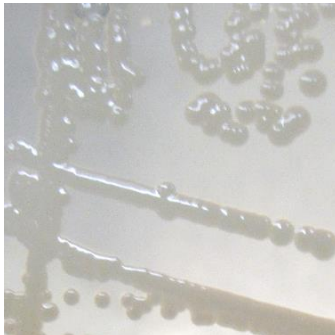


Figure 2: Fluorescent Report Plasmid pSGFPS1

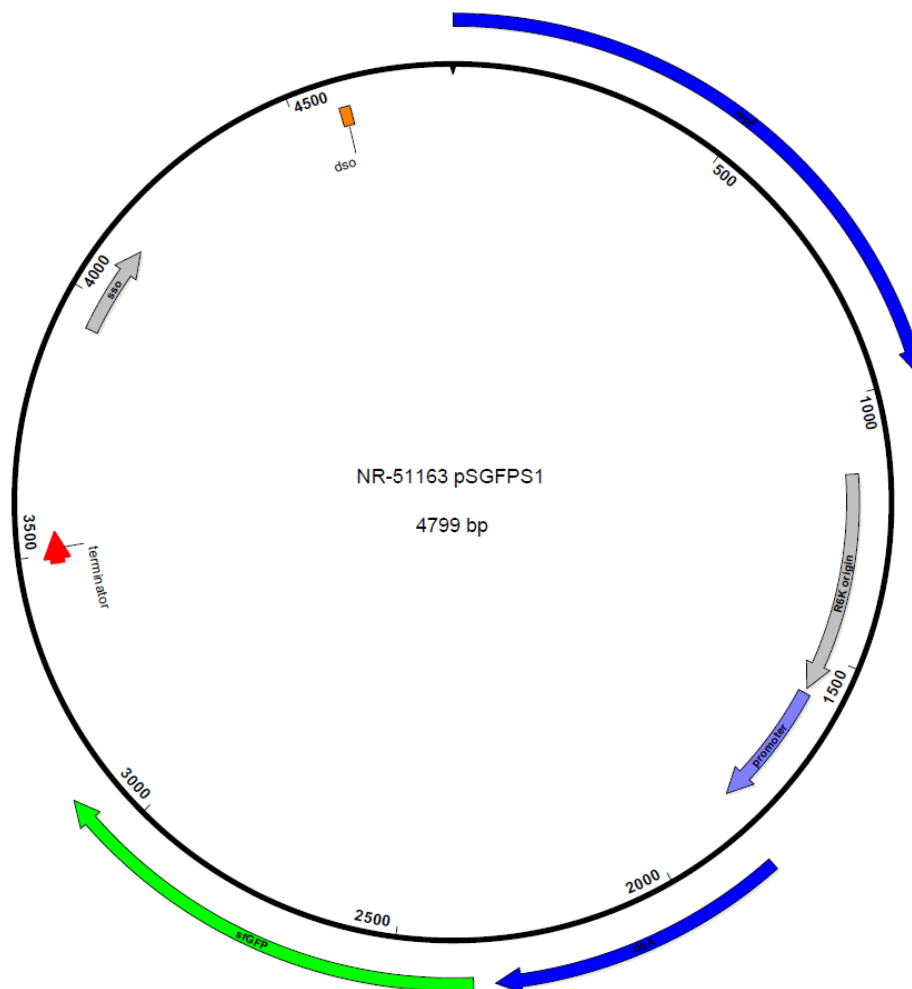


Table 1: Sequence of pSGFPS1

1	ATGCAATATA	ATACTACTAG	AAGTATAACC	GAAAATCAAG	ATAATAAAAAC	GTTAAAAGAT
61	ATGACGAAAA	GTGGGAAACA	ACGCCCATGG	AGAGAAAAGA	AAATAGATAA	TGTAAGCTAT
121	GCAGATATAC	TAGAAATTTT	AAAAATCAAA	AAGGCTTTTA	ATGTA AAAACA	ATGTGGTAAT
181	ATTTTAGAAT	TTAAGCCAAC	TGATGAAGGC	TATTTGAAGT	TACATAAGAC	ATGGTTTTGT
241	AAATCAAAAT	TATGTCCGGT	TTGTAATTGG	AGACGTGCTA	TGAAAAATAG	TTATCAAGCT
301	CAAAAAGTGA	TTGAAAAAGT	AATTAAGGAA	AAGCCAAAAG	CACGTTGGTT	GTTTTAAACT
361	CTTTCAACAA	AAAATGCGAT	AGATGGAGAT	ACTTTAGAAC	AAAGTTTGAA	GCATTTAACA
421	AAAGCATTGG	ATAGGTTGAG	TAGATATAAA	AAGGTTAAAC	AAAATCTTGT	TGGATTTATG
481	CGTTCAACAG	AAGTTACCGT	TAATAAAAAAT	GACGGTAGTT	ATAATCAGCA	CATGCATGTT
541	TTGTTATGTG	TTGAAAATGC	ATATTTTAGA	AAAAAAGAGA	ATTATATAAC	TCAAGAAGAA
601	TGGGTTAATT	TATGGCAAAG	AGCATTACAA	GTTGACTATC	GACCTGTTGC	TAATGTTAAA
661	GCGATCAAAC	CGAATAGAAA	AGGCGATAAA	GACATTGAAT	CGGCAATCAA	AGAGACCTCA
721	AAATATTCGG	TTAAATCATC	TGATTTTTTTA	ACTGATGATG	ATGAAAAAAA	TCAAGAAATT
781	GTAAGTGATT	TAGAAAAAGG	TTTGTATCGA	AAACGTATGT	TAAGTTATGG	TGGATTGCTT
841	AAACAAAAAC	ATAAAATTTT	AAACTTAGAC	GATGTCGAAG	ATGGTAATTT	GATTAATGCA
901	AGTGATGAAG	ATAAAACAAC	AGACGAAGAA	GAAAAAGCAC	ATTCAATTAC	CGCAATTTGG
961	AATTTGAAA	AGCAAAATTA	TTATTTAAGA	CATTAGTGTT	GACTAATGTC	TTTTTTGTTG
1021	ATTTTTTATA	AAAAAGTACT	GTCTTATTTT	TGTGACAAAT	GCTGTATGTA	GTGTCACAAA
1081	AATAAGACAA	ACGCAATATA	TTGTGTCACA	AAAATAAGAC	AGTACAGCTT	TGTATGATCC
1141	GTCGACGAAA	GCCTGGCCAC	GATGCGTCCG	GCGTAGAGGA	TCTGAAGATC	AGCAGTTCAA
1201	CCTGTTGATA	GTACGTACTA	AGCTCTCATG	TTTCACGTAC	TAAGCTCTCA	TGTTTAAACGT
1261	ACTAAGCTCT	CATGTTTAAAC	GAACATAACC	CTCATGGCTA	ACGTACTAAG	CTCTCATGGC
1321	TAACGTACTA	AGCTCTCATG	TTTCACGTAC	TAAGCTCTCA	TGTTTGAACA	ATAAAATTA
1381	TATAAACTAG	CAACTTAAAT	AGCCTTAAAG	GTTTTAAAGT	TTATAAGAAA	AAAAAGAATA
1441	TATAAGGCTT	TTAAAGCTTT	TAAGTTTAA	CGGTTGTGGA	CAACAAGCCA	GGGATGTAAC
1501	GCACTGAGAA	GCCCTTAGAG	CCTCTCAAAG	CAATTTTGAG	TGACACAGGA	ACACTTAACG
1561	GCTGACATGG	GAATTCGAGC	TGATATTTTT	GACTAAACCA	AATGCTAACC	CAGAAATACA
1621	ATCACTGTGT	CTAATGAATA	ATTTGTTTTA	TAAACACTTT	TTTGTTTACT	TCTCATTTTT
1681	AATTAGTTAT	AATTAACATA	ATAATAGAGC	ATTAATATA	TTTAATAAAA	CTTATTTAAT
1741	GCAAAATTAT	GAATAACATA	TCTATAATA	ATAAAGATTA	GATATCAATA	TATTATCGGG
1801	CAAATGTATC	GAGCAAGATG	CATCGGATCG	ATCCAGGAGG	TATACCATGA	CATTATCAAT
1861	AATTGTCGCT	CACGATAAAC	AAAGAGTCAT	TGGGTACCAA	AATCAATTAC	CTTGGCACTT
1921	ACCAAATGAT	TTAAAGCATA	TTAAACAAC	GACCACTGGG	AATACACTTG	TAATGGCAGC
1981	GAAAACTTTT	AATTCATAG	GGAAGCCATT	GCCAAATAGA	CGTAACGTCG	TACTCACTAA
2041	CCAAGCTTCA	TTTCGCCATG	AAGGGGTAGA	TGTTATAAAC	TCTCTTGATG	AAATTAAGA
2101	GTTATCTGGT	CATGTTTTTTA	TATTTGGAGG	ACAAACGTTA	TACGAAGCAA	TGATTGACCA
2161	GGTAGATGAT	ATGTATATCA	CAGTAATAGA	TGGAAAGTTT	CAAGGAGACA	CATTCTTTCC
2221	ACCATACACA	TTTCGAAAAC	GGGAAGTCGA	ATCTTCAGTA	GAAGGTCAAC	TAGATGAAAA
2281	AAATACTATA	CCGCATACAT	TCTTACATTT	AGTGCGTAGA	AAAGGGAAT	AGGCGCGCCT
2341	GATTAACTTT	ATAAGGAGGA	AAAACATATG	CCCGGGAGCA	AAGGAGAAGA	ACTTTTCACT
2401	GGAGTTGTCC	CAATTCCTGT	TGAATTAGAT	GGTGATGTTA	ATGGGCACAA	ATTTTCTGTG
2461	CGTGGAGAGG	GTGAAGGTGA	TGCTACAAAC	GGAAAACCTA	CCCTTAAATT	TATTTGCAC
2521	ACTGGAAAAC	TACCTGTTCC	GTGGCCAACA	CTTGCTACTA	CTCTGACCTA	TGGTGTTCAA
2581	TGCTTTTCCC	GTTATCCGGA	TCACATGAAA	CGTCATGACT	TTTTCAAGAG	TGCCATGCCT
2641	GAAGGTTATG	TACAGGAACG	CACTATATCT	TTCAAAGATG	ACGGGACCTA	CAAGACGCGT
2701	GCTGAAGTCA	AGTTTGAAGG	TGATACCCTT	GTTAATCGTA	TGCAGTTAAA	GGGTATTGAT
2761	TTTAAAGAAG	ATGGAAACAT	TCTTGGACAC	AAACTCGAGT	ACAACTTTAA	CTCACACAAT
2821	GTATACATCA	CGGCAGACAA	ACAAAAGAAT	GGAATCAAAG	CTAACTTCAA	AATTCGCCAC
2881	AACGTTGAAG	ATGGTTCCGT	TCAACTAGCA	GACCATTATC	AACAAAATAC	TCCAATTGGC
2941	GATGGCCCTG	TCCTTTTACC	AGACAACCAT	TACCTGTCTG	CACAATCTGT	CCTTTTCGAA
3001	GATCCTAACG	AAAAGCGTGA	CCACATGGTC	CTTCTTGAGT	TTGTAACCTG	TGCTGGGATT
3061	ACACATGGCA	TGGATGAGCT	CTACAAATAA	GGCGCGCCTA	TTCTAATGCA	TAATAAATAC
3121	TGATAACATC	TTATATTTTTG	TATTATATTT	TGTATTATCG	TTGACATGTA	TAATTTTGTAT

3181	ATCAAAA	ACT	GATTTT	CCCT	CTATTAT	TTTT	CGAGAT	TTT	TTAATT	CTCTTT	TAACA				
3241	AACTAGA	AAAT	ATTGTAT	ATA	CAAAAA	AATTA	TAAATA	ATAG	ATGAAT	TAATTAT	AGG				
3301	TGTTCA	TCAA	TCGAAAA	AAGC	AACGTAT	CCTT	ATTTAA	AGTG	CGTTGC	TTTT	TTCTCA	TTTA			
3361	TAAGGT	TAAA	TAATTC	TCAT	ATATCA	AAGCA	AAGTGAC	AGG	CGATGC	GGCC	GCTAGC	CTAG			
3421	GAGCTC	GGTA	CCCGGG	GATC	CGAATC	CATGA	ATTACA	AAGCA	AAAGT	AGCGG	TGATTG	TTAA			
3481	AATTGAT	GGT	AAACAAT	CAC	CGCTAT	TTTT	GCTTGT	GTAT	GTATAA	AAAAA	GGGATC	AAAG			
3541	GTCATC	CCCC	ATGATT	GATA	GTGGGG	GGGAT	GACTTT	TGAT	CCTATG	TTCA	TGTTG	CTTAT			
3601	TTAATC	GCCT	TTGATC	ACTT	TAAAAT	ACCT	TAAAAC	CCCC	GGAAT	TTCTG	GCTTTG	CCAG			
3661	ACCTAT	CATT	TTTGA	ATGAT	AGCAA	ATCT	CCTTAT	GCCT	TTACG	GAGTT	TTTAG	AGAAA			
3721	AATTA	AAAA	TCTCG	ATTTT	TGATAA	AAAAA	CGCCCT	GCAG	GAATTT	TAGAA	AAACAT	GTGG			
3781	AAGTTT	TAAA	GGATTT	TATG	CTAAT	TTTTT	ATTTGC	ATGT	AAC	TCGAGG	GAATAT	TTGA			
3841	GGGGAT	TTTTG	AAACG	AGTTT	CTTCT	TGTTT	TCACAC	TGTT	TTTTT	TATCC	TATTGG	TGTT			
3901	GTTGC	TTACT	TTTTG	TTTTT	CTATAA	AAGAT	GATGC	TTTTG	ACGAG	ATGGA	AGAAAA	ATAT			
3961	GATTAT	CATG	AAGATA	AATAA	AAAAT	AGACG	ACGCAT	TTAT	GCCG	AGAAA	TTTATT	GATG			
4021	TTGAGA	AAGAA	CCCTT	AAC	TAAC	TA	AAC	TG	CAGA	CGAAT	GTCGG	CATAG	CGTGA	GCTAT	TAAGC
4081	CGACCA	TTTCG	ACAAG	TTTTG	GGATT	GTTAA	GGGT	TCCG	AG	GCTCA	ACGTC	AATAA	AGCAA		
4141	TTGGA	AATAA	TAGTAT	CTAA	AGTA	ACCCG	ATTTA	AGATT	ACATT	GTACA	TCCT	TCGAAA			
4201	CCATAG	TAGC	TGCGAT	TCCA	GCTAG	GTTT	CTTTT	TATCC	AATTT	TAGCT	AATTTT	TTTTG			
4261	CTACG	CCCTT	TAAGT	TTTTG	GCTTT	AACAT	CTTCA	AAAA	TGCTG	TGATT	ATGTT	TCCAG			
4321	TTAAA	AGTTC	TCCAT	ATGAG	TTTAAA	ACTT	CAGAA	TAGAA	ACAGT	CACCG	CTATTT	TTGT			
4381	AGTTC	CACC	AACTG	CTCTA	GGTGA	TATG	AACTA	GTTTT	CTTTT	TATTC	TCTAT	GTCTG			
4441	TTTTT	AGTTT	TTGGA	ATCCT	TCAGG	AACAT	ATCCA	TATCG	AGATT	TGGCC	GATTTT	ATTT			
4501	GATAA	TCCTT	TTGAC	TTTTT	AGAAA	GTTTT	ATTTA	TTCAT	TGGT	TTTTC	ATTAAT	TTAT			
4561	TTAGG	TTTAG	AGGGT	CATAA	AAAGA	AGAAG	GAATA	GTTG	TTTTT	TGAAA	CGAGT	GTGAA			
4621	CGAGT	TTCTT	CTTGT	CCTGA	TACTA	TATAG	AAATA	ACTCG	ATTTT	TATATA	TATAG	CTGTA			
4681	ACTGT	TGATA	TTAC	AGTGT	TAAAC	GTTT	TTTGT	GCGTG	AAAGG	AAAAT	TTGAC	AATAA			
4741	AAAAC	CCCC	AG	TTATAT	TATT	AAGGT	GTCGA	ATCTT	AAATA	ATACT	GGGG	TCTTTT	TAT		

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