Electronic Supplementary Material (ESI) for RSC Advances.

Supporting Information

Functional disruption of Staphylococcal Accessory Regulator A from *Staphylococcus aureus* by Silver Ions

Xiangwen Liao[a*], Guijuan Jiang[a], Jing Wang[a], Jintao Wang[a]

[a] School of Pharmacy, Jiangxi Science & Technology Normal University, Nanchang, 330013, China

*Correspondence author.

Tel/Fax: +86 791 8380-2393;

E-mail address: liao492008522@163.com (Liao X)

Table S1 Strains, plasmids and primers used in this study

Strain, plasmids or primers	Application	
***E.coli* strains**		
XL1-Blue	Plasmid maintenance	
BL21(DE_3)	Protein expression	
***Staphylococcus aureus* strains**		
Newman	Wide-type strain	
Plasmids		
pET47b		
pET47b-*sarA*	SarA protein expression	
pET47b-$sarA^{C9S}$	$SarA^{C9S}$ protein expression	
Primers for SarA		
	Forward Primer	Reverse Primer
SarA	TAGCTCATATGGCAATTACAAAAATCAATGATTGCTTTGAGTTGTTATCAAT	TATGGATCCTTATAGTTCAATTTCGTTGTTTGCTTCAGTGATTCG
Primers for qRT-PCR		
16s RNA	CCATAAAGTTGTTCTCAGTT	CATGTCGATCTACGATTACT
hla	ACAATTTTAGAGAGCCCAACTGAT	TCCCCAATTTTGATTCACCAT
hld	AAGAATTTTTATCTTAATTAAGGAAGGAGTG	TTAGTGAATTTGTTCACTGTGTCGA
fnbA	ACAAGTTGAAGTGGCACAGCC	CCGCTACATCTGCTGATCTTGTC

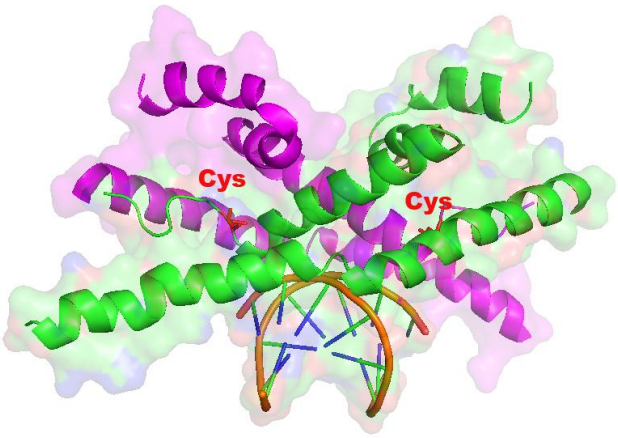

Figure S1 The crystal structure of the SarA (PDB:1fzp) from *Staphylococcus aureus*

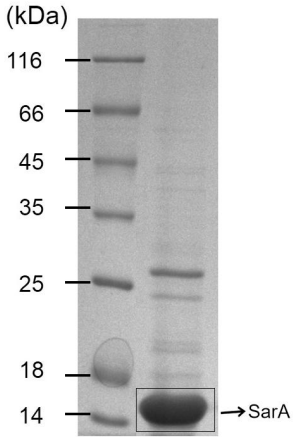

Figure S2 SDS-PAGE analysis of the purified SarA

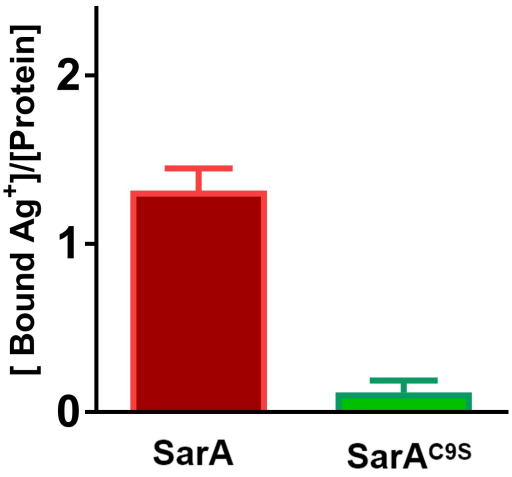

Figure S3 Ag^+-binding capability of $SarA^{C9S}$ determined by ICP-MS; $SarA^{C9S}$ were treated with 3 molar equivalents of Ag^+. Excess amounts of Ag^+ were removed by a desalting column. The bound Ag^+ contents were determined by ICP-MS and protein concentrations were measured by BCA assay.

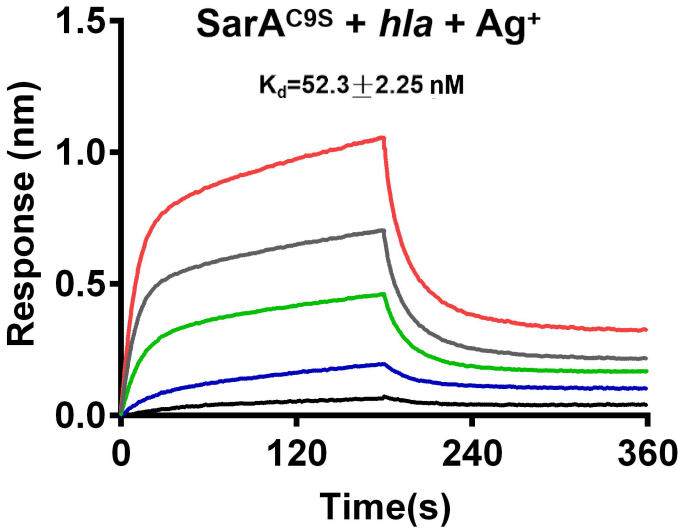

Figure S4 The DNA binding capabilities of $SarA^{C9S}$ with Ag^{+} were measured by BioLayer Interferometry(BLI). Biotinylated hla (300 nM) were captured on pre-immobilized streptavidin Dip and Read sensor heads for 3 min. Association occurred from 0 to 180 s and dissociation was monitored thereafter up to 360 s. The K_d values are presented as the mean ± s.e.m. derived from a global fitting of all binding curves.