

TABLE S1. Primers used in this study

Primer name	Sequence (5'-3')	Description
<i>For construction of mutants</i>		
srtG-A	GGAGAATTGCCATCAAC AGG	Amplification of upstream region of <i>srtG</i> and fused fragment of upstream and downstream regions of <i>srtG</i>
srtG-B	TCTCTTCTGATCACGATC AGGTACAGGCTG	Amplification of upstream region of <i>srtG</i>
srtG-C	CAGCCTGTACCTGATCGT GATCAGAAGAGA	Amplification of downstream region of <i>srtG</i>
srtG-D	CCTTATAAGGCAGGTAG AGT	Amplification of downstream region of <i>srtG</i> and fused fragment of upstream and downstream regions of <i>srtG</i>
sgp1-A	GCAAGCGGTGAGACAGA TAG	Amplification of upstream region of <i>sgp1</i> and fused fragment of upstream and downstream regions of <i>sgp1</i>
sgp1-B	TAGGTATGTTCCCATACG TGCATTCATTCC	Amplification of upstream region of <i>sgp1</i>
sgp1-C	GGAATGAATGCACGTAT GGGAACATACCTA	Amplification of downstream region of <i>sgp1</i>
sgp1-D	CTAGAATCCCCTCACGT AAG	Amplification of downstream region of <i>sgp1</i> and fused fragment of upstream and downstream regions of <i>sgp1</i>
sgp2-A	TACCGAAACGAATCGGT CAG	Amplification of upstream region of <i>sgp2</i> and fused fragment of upstream and downstream regions of <i>sgp2</i>
sgp2-B	ACCATACCCACCTGTAA CCAAGGAGCCATC	Amplification of upstream region of <i>sgp2</i>
sgp2-C	GATGGCTCCTTGGTTACA GGTGGGTATGGT	Amplification of downstream region of <i>sgp2</i>
sgp2-D	ACTTTTGATGCTTTGGCT TG	Amplification of downstream region of <i>sgp2</i> and fused fragment of upstream and downstream regions of <i>sgp2</i>
cps2B-F	AGTGTTGACTGCGGGGT TGGC	Amplification of a internal region of <i>cps2B</i>
cps2B-R	CGTTGCTACTTGTGTCAA TACATC	Amplification of a internal region of <i>cps2B</i>
<i>For construction of complemented mutants</i>		
srtG-CF	AGAAGGATCCAACAAGT ATGGAGGGAAGGC <sup>a</sup>	Complementation of <i>srtG</i>
srtG-CR	GCATGAATTCGGTACAA ATGACTCAATAGA <sup>b</sup>	Complementation of <i>srtG</i>
sgp1-CF	ACATGGATCCGAGAAGA GAAAGCAGATTGC <sup>a</sup>	Complementation of <i>sgp1</i>
sgp1-CR	TAGAGAATTC AACGCCT TCCCTCCATACTT <sup>b</sup>	Complementation of <i>sgp1</i>

TABLE S1. (continued)

Primer name	Sequence (5'-3')	Description
sgp2-CF	TGTGCCATGGTACCAAA AGATTCTTTGCTA <sup>c</sup>	Complementation of <i>sgp2</i>
sgp2-CR	CTTTCCATGGTTAAGCAA TCTGCTTTCTCT <sup>c</sup>	Complementation of <i>sgp2</i>
<i>For construction of His-tagged recombinant proteins</i>		
rSgp1-F	TACCCTTTATCATATGGG TGAAGGTGTATA <sup>d</sup>	Generation of His-tagged recombinant Sgp1 (50th-453rd)
rSgp1-R	TCAAGGATCCAACCAAC TTGTGTGCTATCC <sup>a</sup>	Generation of His-tagged recombinant Sgp1 (50th-453rd)
rSgp2-F	TATGCGTTAGAGCATAT GAGTGAGTCAACA <sup>d</sup>	Generation of His-tagged recombinant Sgp2 (34th-457th)
rSgp2-R	AGATGGATCCGATAGAG TTCATGCGTATCT <sup>a</sup>	Generation of His-tagged recombinant Sgp2 (34th-457th)

<sup>a</sup> BamHI restriction site is underlined.

<sup>b</sup> EcoRI restriction site is underlined.

<sup>c</sup> NcoI restriction site is underlined.

<sup>d</sup> NdeI restriction site is underlined.

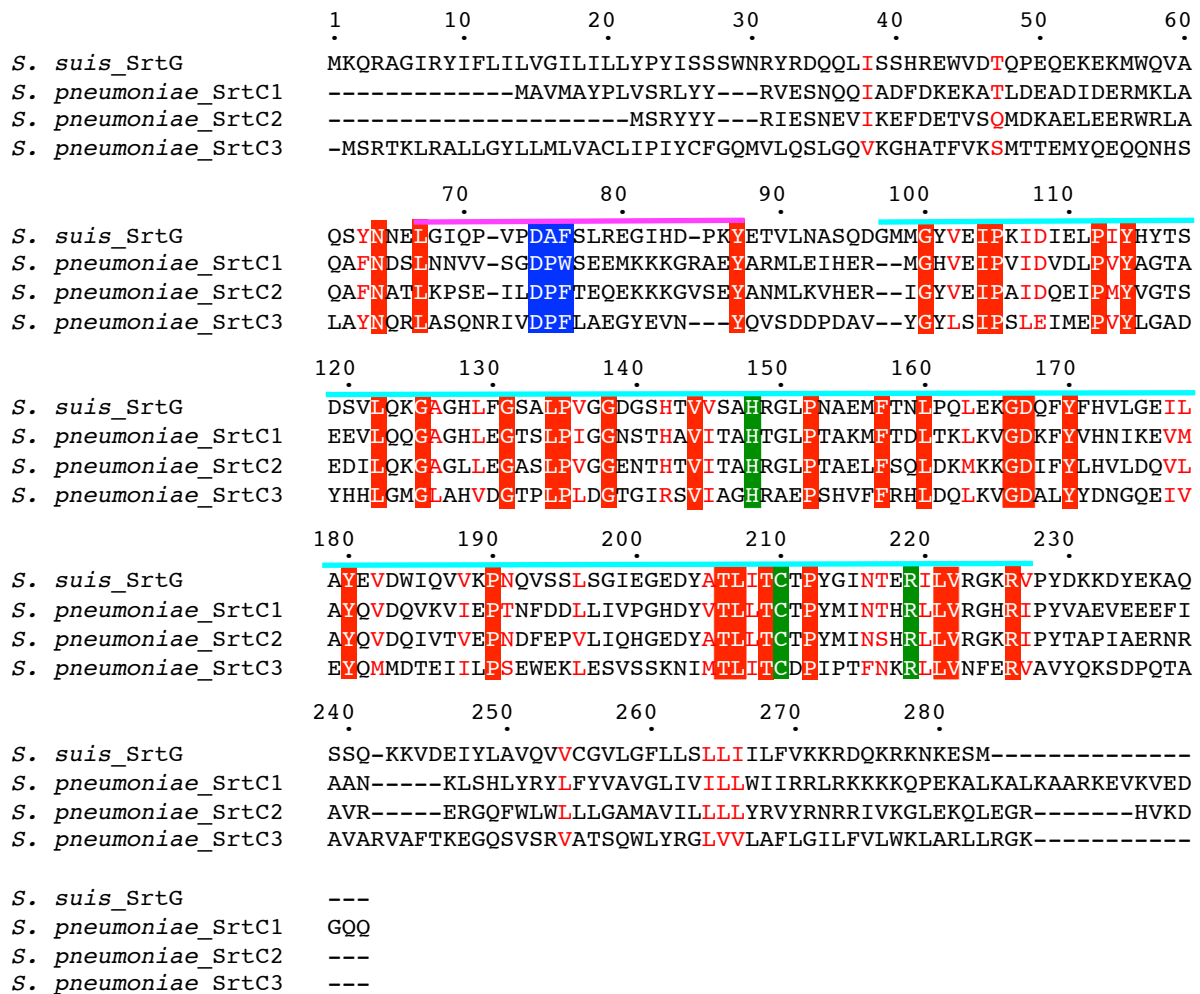


FIG. S1. Amino acid sequence alignment of the SrtG and the three class C sortases in the pneumococcal *rlrA* pilus islet (SrtC1, SrtC2, and SrtC3). Identical residues are shown with a red background, whereas similar residues are shown in red. The class C sortase domain regions are shown in cyan line, and the catalytic active site are highlighted in green. The lid regions of *S. pneumoniae* are shown in magenta line, and the lid anchor residues are highlighted in blue. The GenBank accession numbers of the listed proteins are follows: SrtC1, AAK74626; SrtC2, AAK74627; SrtC3, AAK74628.

Fig.S1