Supplementary Figures

Figure S1

Figure S1. Multiple sequence alignment of fRMsrs. Sequences of *E. coli*, *S. cerevisiae* and *S. aureus* fRMsrs were aligned with BioEdit (http://www.mbio.ncsu.edu/BioEdit/bioedit.html). Catalytic Cys-102 is highlighted in red, resolving Cys-68 in blue and conserved Cys-78 in green. Secondary α-helices and β-strands determined from *S. aureus* fRMsr are indicated.

Figure S2

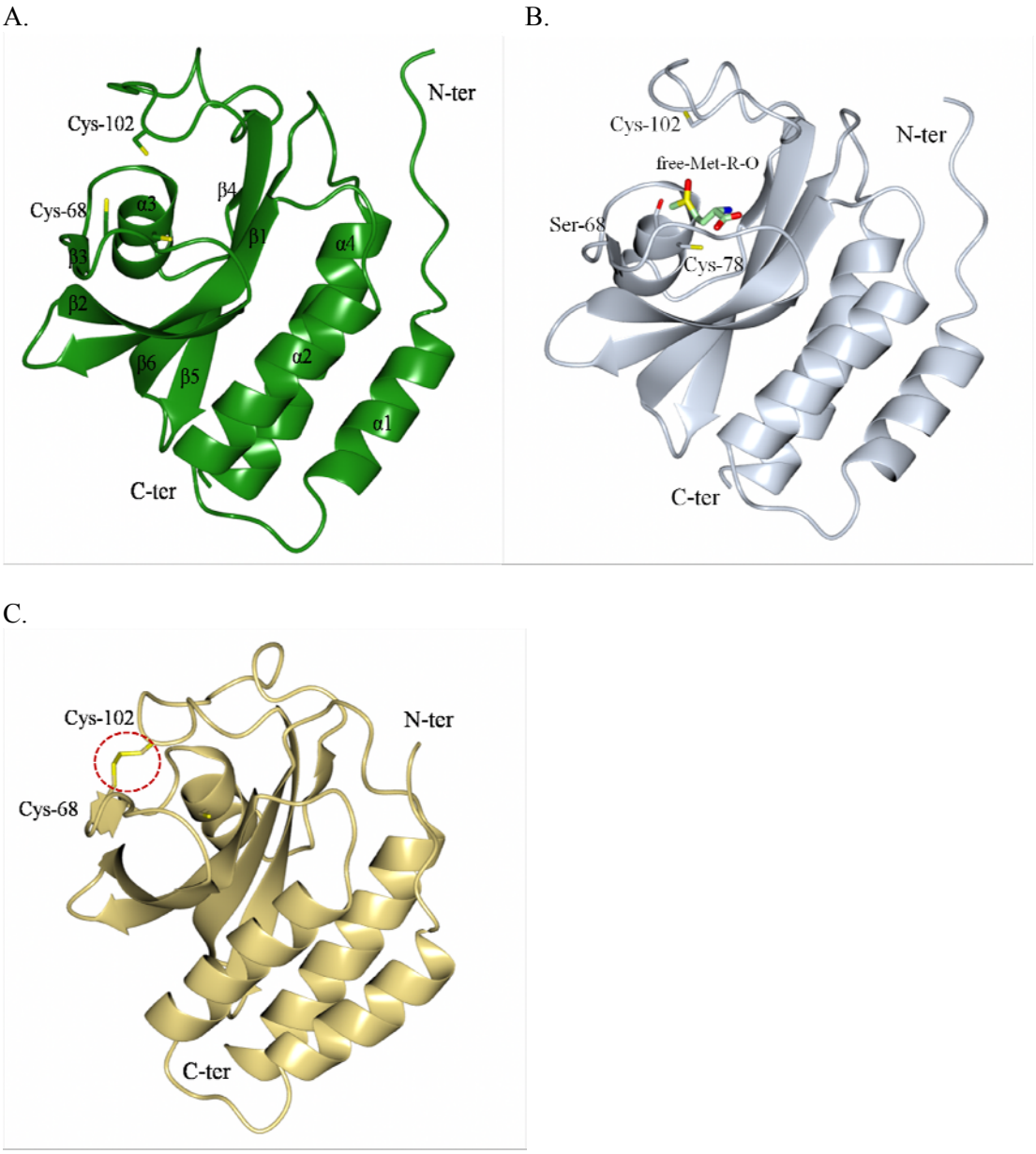
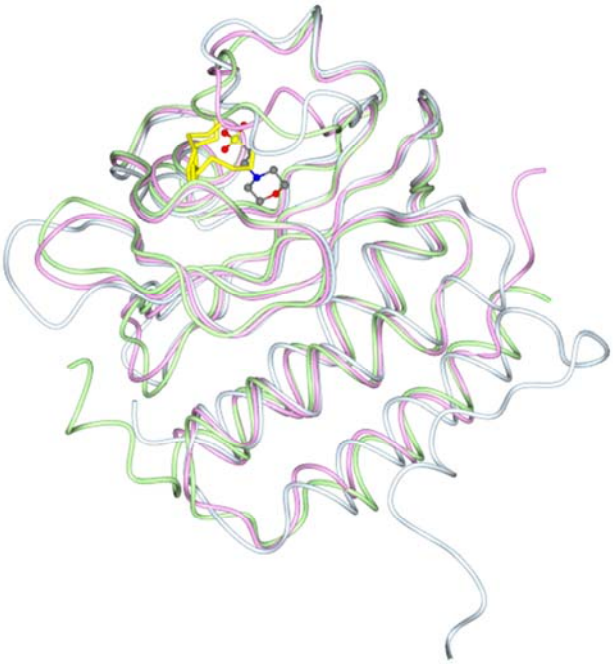


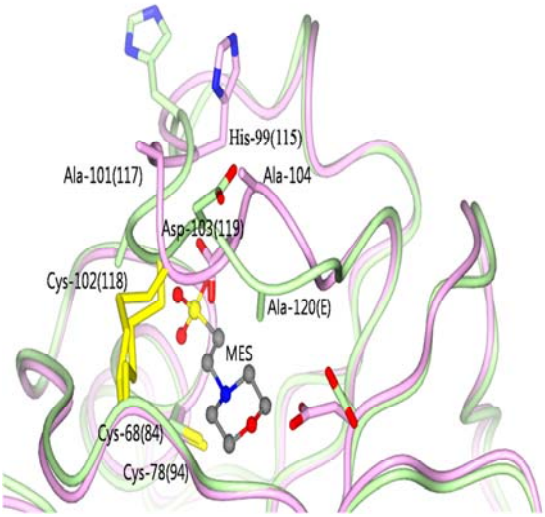
Figure S2. Structures of *S. aureus* fRMsrs. (A) Reduced form ($fRMsr_{red}$). The overall structure of $fRMsr_{red}$ is composed of six antiparallel β-strands (β1-β6) and four α-helices (α1-α4). (B) Substrate-bound form ($fRMsr_{sub}$). The substrate free Met-R-O in C68S fRMsr is indicated by a green stick model. (C) Oxidized form ($fRMsr_{ox}$). A disulfide bond formed by Cys-68 and Cys-102 is shown in red dotted circle.

Figure S3

A



B



C

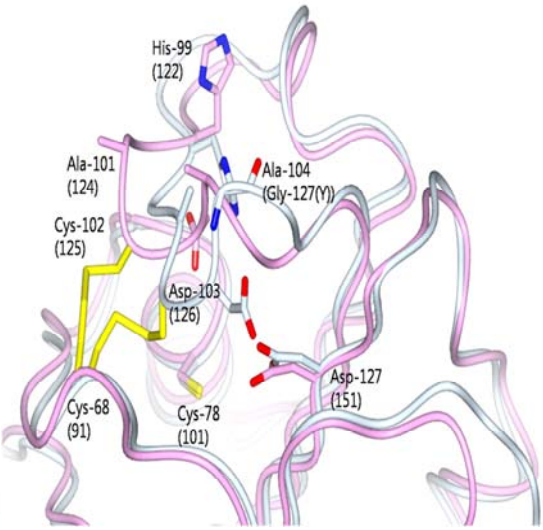


Figure S3. Structural comparison of oxidized *S. aureus* fRMsr with known fRMsrs. (A) Comparisonof overall structures. The backbone models for *S. aureus*, *E. coli*, and *S. cerevisiae* are shown in light purple, light green and light cyan, respectively. Disulfide bonds between Cys-68 and Cys-102 are represented by yellow sticks. MES in *E. coli* fRMsr is shown by a stick model. (B) Comparison of active sites between *S. aureus* (light purple) and *E. coli* (light green) fRMsrs. Disulfide bonds are represented by yellow sticks and MES in *E. coli* fRMsr is shown by a stick model. Numbers in parenthesis represents the corresponding amino acid number of *E. coli* fRMsr. Ala-120 is from *E. coli*. (C) Comparison of active sites between *S. aureus* (light purple) and *S. cerevisiae* (light cyan) fRMsrs. Disulfide bonds are represented by yellow sticks. Number in parenthesis represents the corresponding amino acid number of *S. cerevisiae* fRMsr. Gly-127 is from *S. cerevisiae*.