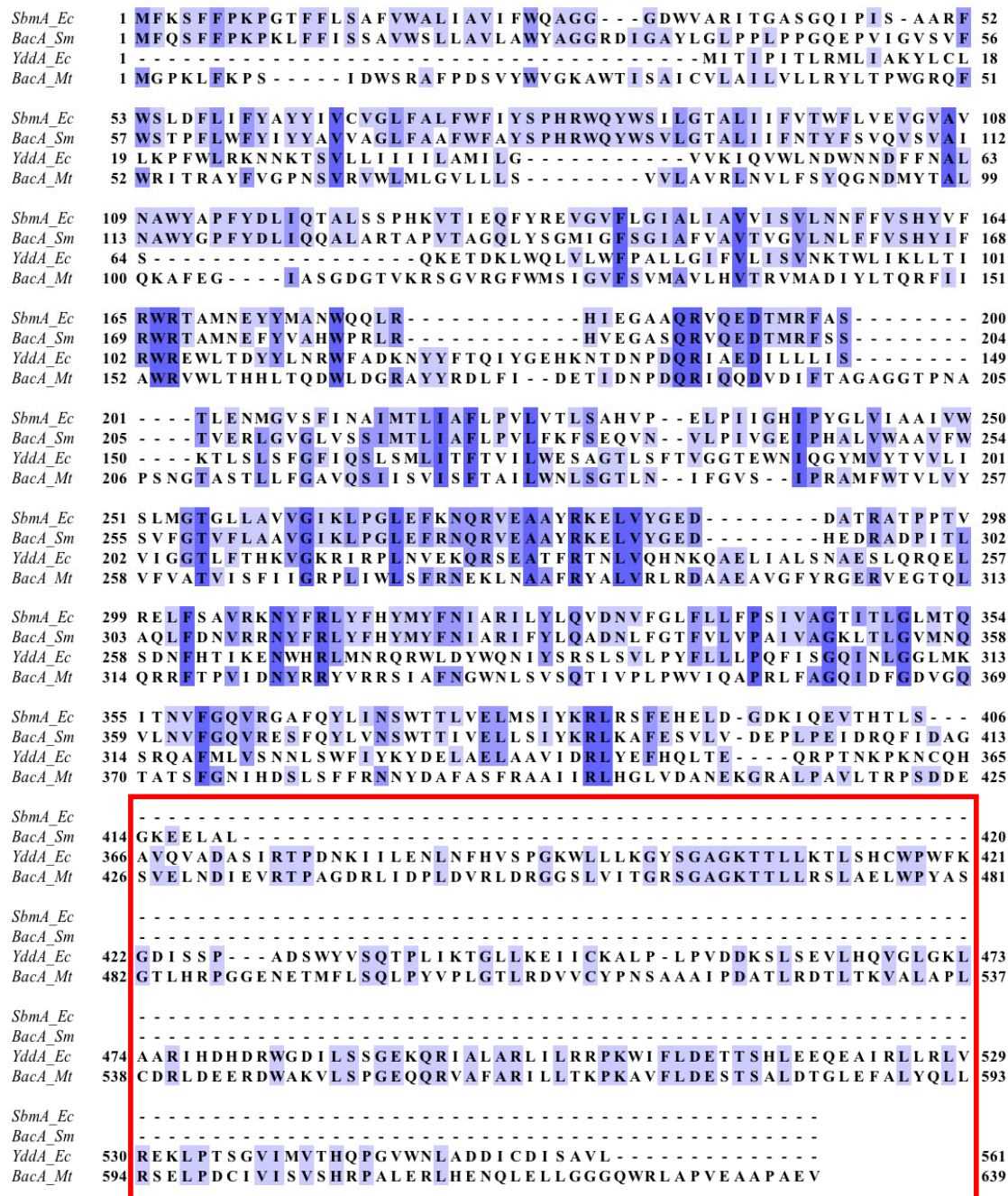


SUPPLEMENTARY FIGURES

SUPPLEMENTAL FIGURE S1

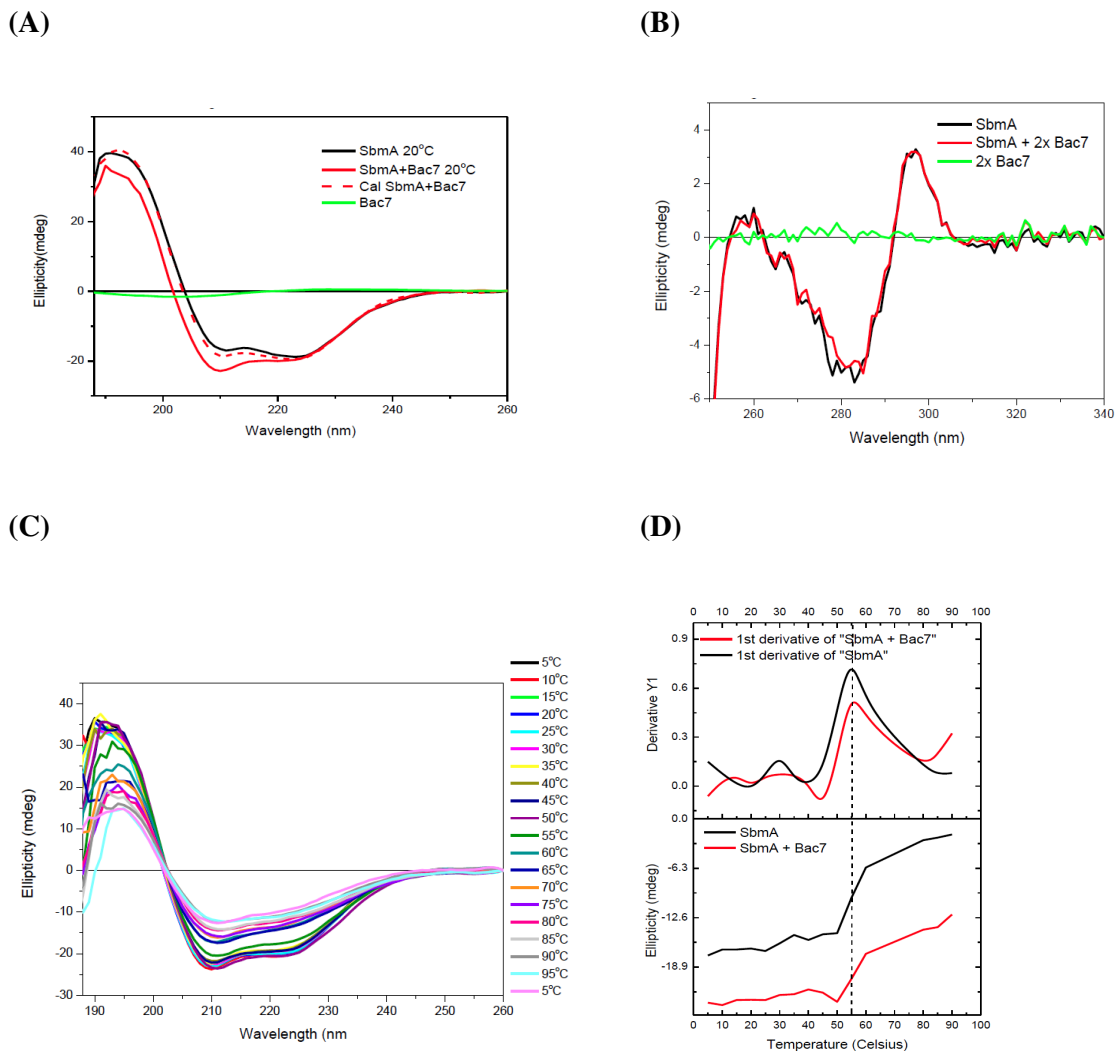


**FIGURE S1. SbmA/BacA sequence alignment.** Alignment of amino acid sequences of SbmA proteins from *E. coli* (Ec) (UNIPROT: P0AFY6), BacA from *S. meliloti* (Sm) (UNIPROT: Q08120), YddA from *E. coli* (UNIPROT: P31826) and BacA from *M. tuberculosis* (Mt) (UNIPROT: Q50614) using the CLUSTALW program in Jalview. The Ec

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SbmA shares 63.4 % identity with the Sm BacA, 23.3 % with Ec YddA and 19 % with Mt BacA. The percent identity was calculated using pairwise alignment in JalView. Residues that are >90% identical are shown in dark blue, residues that are 50% identical are blue and those that are less than 25% in light blue. The Ec SbmA and Sm BacA proteins lack an NBD coding region; the NBD of Ec YddA and Mt BacA is highlighted within a red box.

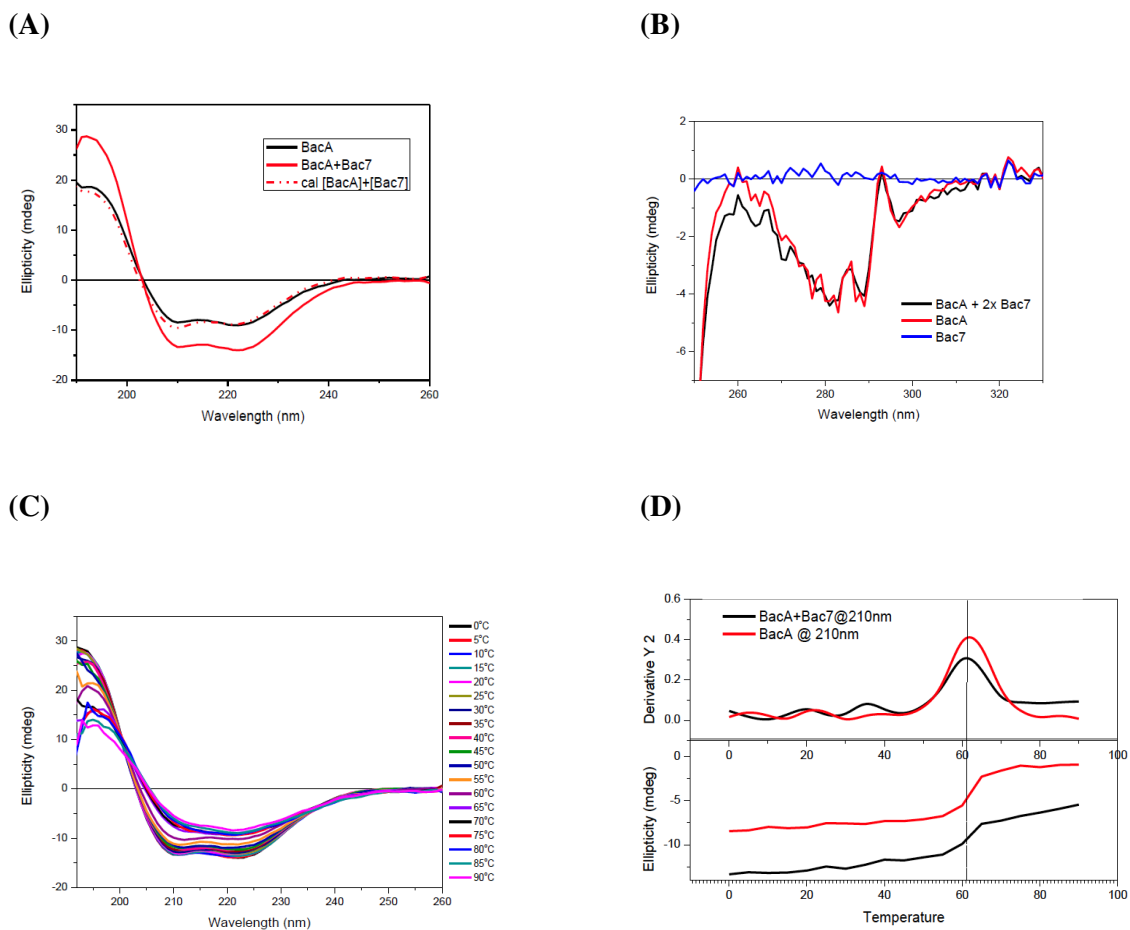
SUPPLEMENTAL FIGURE S2



**FIGURE S2. Binding studies of SbmA and Bac7 by CD spectroscopy.**

(A) Far UV measurements of SbmA (black line), SbmA-Bac7 mixture (red line) and Bac7 (green line). The theoretical secondary structure of the complex (red dotted line) is different from the measured data. (B) Near UV measurements did not show any significant changes to the aromatic environment. (C) Thermal denaturation studies on the SbmA-Bac7 complex at different temperatures. (D) Binding of Bac7 to SbmA does not stabilize the protein.

SUPPLEMENTAL FIGURE S3



**FIGURE S3. Binding studies of BacA and Bac7 by CD spectroscopy.**

(A) Far UV measurements of BacA (black line) and BacA-Bac7 mixture (red line). The theoretical secondary structure of the complex (red dotted line) is different from the measured data. (B) Near UV measurements did not show any significant changes to the aromatic environment. (C) Thermal denaturation studies on the BacA-Bac7 complex at different temperatures. (D) Binding of Bac7 to BacA does not appear to provide thermal stabilization.