SUPPLEMENTARY FIGURES

SUPPLEMENTAL FIGURE S1

SbmA_Ec BacA_Sm	1 MFK S F F P K P G T F F L S A F VWAL I A V I F WQ A G G G DWV A R I T G A S G Q I P I S - A A 1 MF Q S F F P K P K L F F I S S A VWS L L A V L A WY A G G R D I G A Y L G L P P L P P G Q E P V I G V S 1 M T T P I T I P M T A V V I A V V A G G R D I G A Y L G L P P L P P G Q E P V I G V S	R F 52 V F 56
BacA_Mt	1 MGPKLFKPSIDWSRAFPDSVYWVGKAWTISAICVLAILVLLRYLTPWGR	Q F 51
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	53 WS L D F L I F Y A Y Y I V C V G L F A L FWF I Y S PH RWQ YWS I L G T A L I I F V T WF L V E V G V 57 WS T P F LWF Y I Y Y A V V A G L F A A FWF A Y S PH RWQ YWS V L G T A L I I F N T Y F S V Q V S V 19 LK P FWL RK N NK T S V L L I I I I L AMI L G V V K I Q V W L N D W N N D F F N 52 WR I T R A Y F V G P N S V R V WLM L G V L L S V V L A V R L N V L F S Y Q G N D M Y T	AV 108 AI 112 AL 63 AL 99
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	109 NAWYA P F Y D L I Q T A L S S P HK V T I E Q F Y RE V G V F L G I A L I A V V I S V L N N F F V S H Y 113 NAWYG P F Y D L I Q Q A L A R T A P V T A G Q L Y S G M I G F S G I A F V A V T V G V L N L F F V S H Y 64 S	VF 164 IF 168 II 101 II 151
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	165 RWR T AMNE Y YMA NWQQLR H I EGAA QR VQE D TMRF A S H I EGAA QR VQE D TMRF A S 169 RWR T AMNE F Y VAHWPRLR H VEGAS QR VQE D TMRF S S 102 RWR EWLT D Y YLNRWF ADKN Y Y FTQ I YGEHKNTDN P DQR I A E D I L L L I S 152 AWR VWLTHHLTQ DWLDGRA Y YRDLF I DET I DN P DQR I QQD V D I F TAGAGGT P	200 204 149 NA 205
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	201 TLENMGVSFINAIMTLIAFLPVLVTLSAHVP ELPIIGHIPYGLVIAAI 205 TVERLGVGLVSSIMTLIAFLPVLFKFSEQVN VLPIVGEIPHALVWAAV 150 KTLSLSFGFIQSLSMLITFTVILWESAGTLSFTVGGTEWNIQGYMVYTVV 206 PSNGTASTLLFGAVQSIISVISFTAILWNLSGTLN IFGVS IPRAMFWTVL	VW 250 FW 254 LI 201 VY 257
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	251 SLMGTGLLAVVGIKL PGLEFKNQRVEAAYRKELVYGED DATRATPP 255 SVFGTVFLAAVGIKL PGLEFRNQRVEAAYRKELVYGED HEDRADPI 202 VIGGTLFTHKVGKRIRPLNVEKQRSEATFRTNLVQHNKQAELIALSNAESLQRQ 258 VFVATVISFIIGRPLIWLSFRNEKLNAAFRYALVRLRDAAEAVGFYRGERVEGT	ΓV 298 ΓL 302 ΕL 257 QL 313
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	299 RELFSAVRKNYFRLYFHYMYFNIARILYLQVDNYFGLFLLFPSIVAGTITLGLM 303 AQLFDNVRRNYFRLYFHYMYFNIARIFYLQADNLFGTFVLVPAIVAGKLTLGVM 258 SDNFHTIKENWHRLMNRQRWLDYWQNIYSRSLSVLPYFLLLPQFISGQINLGGL 314 QRRFTPVIDNYRRYVRRSIAFNGWNLSVSQTIVPLPWVIQAPRLFAGQIDFGDV	Г <mark>Q</mark> 354 NQ 358 ИК 313 GQ 369
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	355 ITNVFGQVRGAFQYLINSWTTLVELMSIYKRLRSFEHELD - GDKIQEVTHTLS - 359 VLNVFGQVRESFQYLVNSWTTIVELLSIYKRLKAFESVLV - DEPLPEIDRQFID 314 SRQAFMLVSNNLSWFIYKYDELAELAAVIDRLYEFHQLTE QRPTNKPKNC 370 TATSFGNIHDSLSFFRNNYDAFASFRAAIIRLHGLVDANEKGRALPAVLTRPSD	406 AG 413 QH 365 DE 425
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	414 GKEELAL 366 AVQVADASIRTPDNKIILENLNFHVSPGKWLLLKGYSGAGKTTLLKTLSHCWPW 426 SVELNDIEVRTPAGDRLIDPLDVRLDRGGSLVITGRSGAGKTTLLRSLAELWPY	 420 FK 421 AS 481
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	422 GDISSPADSWYVSQTPLIKTGLLKEIICKALP-LPVDDKSLSEVLHQVGLG 482 GTLHRPGGENETMFLSQLPYVPLGTLRDVVCYPNSAAAIPDATLRDTLTKVALA	 KL 473 PL 537
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	474 AARIHDHDRWGDILSSGEKQRIALARLILRRPKWIFLDETTSHLEEQEAIRLLR 538 CDRLDEERDWAKVLSPGEQQRVAFARILLTKPKAVFLDESTSALDTGLEFALYQ	 L V 529 L L 593
SbmA_Ec BacA_Sm YddA_Ec BacA_Mt	530 REKLPTSGVIMVTHQPGVWNLADDICDISAVL 594 RSELPDCIVISVSHRPALERLHENQLELLGGGQWRLAPVEAAPAEV	561 639

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

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.