

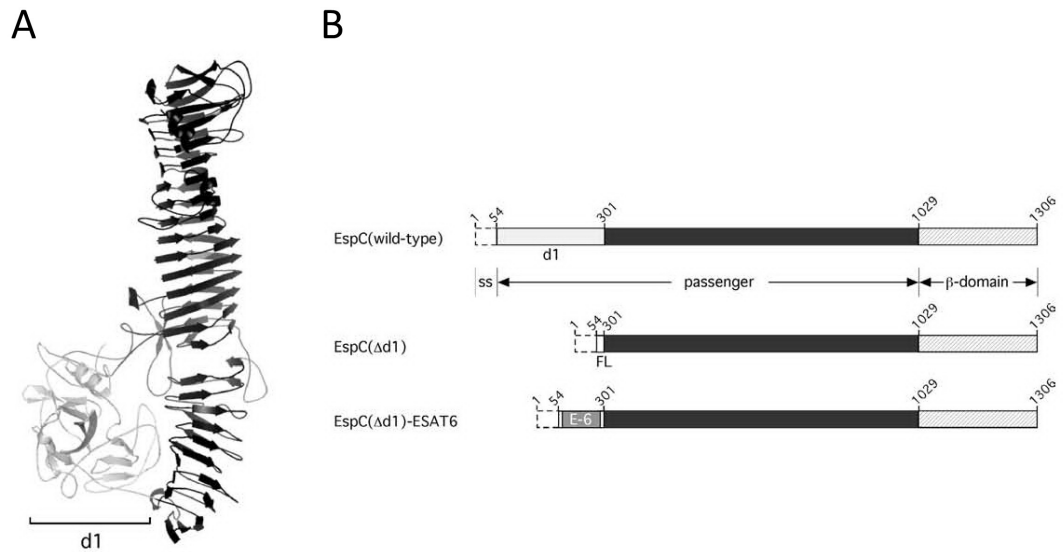


**Fig. S7. Cartoons EspC-ESAT6 fusion.** (A) Cartoon of a structural model of the passenger domain of EspC [Swiss-Prot: Q9EZE7] generated using M4T homology modeling [1]. Side domain 1 (*d1*) is in light grey. The remainder of the passenger domain, including the  $\beta$ -stem domain, is in black. (B) Schematic representation of EspC derivatives used. Wild-type EspC is synthesized as a 1306 amino acid (aa) precursor that is organized in three domains: (i) an N-terminal cleavable signal sequence (*ss*) (aa 1-53), (ii) a passenger domain (aa 54-1028) and (iii) an OM integrated  $\beta$ -domain (aa 1029-1306). After passage of the OM, the passenger is cleaved from the  $\beta$ -domain via an autocatalytic mechanism that involves hydrolysis of the peptide bond between two asparagines at position 1028 and 1029 of the EspC precursor [2]. The predicted domain *d1* is indicated. The remainder of the passenger domain, including the  $\beta$ -stem domain, is in black. “FL” denotes flexible linker. “E-6” indicates ESAT6.

## References

1. Rykunov D, Steinberger E, Madrid-Aliste CJ, Fiser A: Improved scoring function for comparative modeling using the M4T method. *J Struct Funct Genomics* 2009, 10(1):95-99.
2. Dautin N, Barnard TJ, Anderson DE, Bernstein HD: Cleavage of a bacterial autotransporter by an evolutionarily convergent autocatalytic mechanism. *EMBO J* 2007, 26(7):1942-1952.