SUPPLEMENTARY TABLES

Supplementary Table-1: List of bacterial species and strains used in this work and there related infections

Supplementary Table-2: Seventy five common conserved proteins of four *C. pseudotuberculosis* strains, *Y. pestis, C. diphtheriae, C. ulcerans, and multiple strains of M. tuberculosis*, *C. glutamicum*, and *E. coli*. Analysis of their pathogenic island association, COG, and pathway involvements are presented.

Supplementary Table-3: The common conserved inter-species bacterial PPI was made using conserved common 75 *E. coli* proteins and using VisANT tool.

> **3a):** These 75 proteins interact with other proteins and form a PPI network having 1674 interactions involving 666 interacting nodes (proteins). Total 27 pathways that include both bacterial essential survival and virulence can be mapped. Methods that are behind this PPI are also listed.
>
> **3b):** Internal interactions of these 75 proteins form a PPI network having 142 interactions. Total 23 pathways that include both bacterial essential survival and virulence can be mapped. Methods that are behind this PPI are also listed.

Supplementary Table-4: Fourteen common conserved proteins of four *C. pseudotuberculosis* strains, *Y. pestis, M. tuberculosis, C. glutamicum, C. diphtheriae, C. ulcerans*, and *E. coli*, that interact with 122 host proteins. The complete functional annotations of all 14 proteins, their virulence, the analysis of essentiality and host homology, and the interactions with host proteins are listed.

Supplementary Table-5: Pathway analysis of 122 interacting host proteins using DAVID and the ToppGene Suite. Most of the proteins are found in well-known bacterial infection-related pathways including integrin-mediated signaling, endocytosis, TLR signaling, immunity, apoptosis, and inflammation. The host proteins and corresponding pathogen proteins are also represented.

Supplementary Table-6: ToppGene Suite-based Gene Set Enrichment Analysis results for host proteins that interact with the 14 pathogen proteins.

Supplementary Table-7: Active residues of four cavities in the Ack protein.

Supplementary Table-8: GOLD fitness scores for the top 5 compounds for each cavity of the Ack protein.