Fig. S2. Schematic representation of Hbp derivatives used in the study. Hbp is synthesized as a 1377 amino acid (aa) precursor that is organized in three domains: (i) an N-terminal cleavable signal sequence (ss; aa 1-52), (ii) a secreted passenger domain (aa 53-1100) and (iii) an OM integrated C-terminal β-domain (aa 1101-1377). Side domains d1-d5 and the autochaperone domain (ac) of the passenger domain are indicated. The remainder of the passenger domain, including the β-stem is in black. After passage of the OM, the passenger is cleaved from the β-domain via an autocatalytic mechanism that involves hydrolysis of the peptide bond between two asparagines at position 1100 and 1101 of the Hbp precursor [1, 2]. Substitution of these asparagines by a glycine and serine, respectively, prevents cleavage [3], denoted X. Numbers displayed above the diagrams correspond to the amino acid positions of the wild-type Hbp precursor, calculated from the N-terminus. Insertion of a 9-11 amino acid long flexible linker (FL) comprising glycine and serine residues, as well as insertion of the mycobacterial antigen ESAT6 (E-6), is indicated.

References