Supporting Information

Krieg *et al.* 10.1073/pnas.0809406106

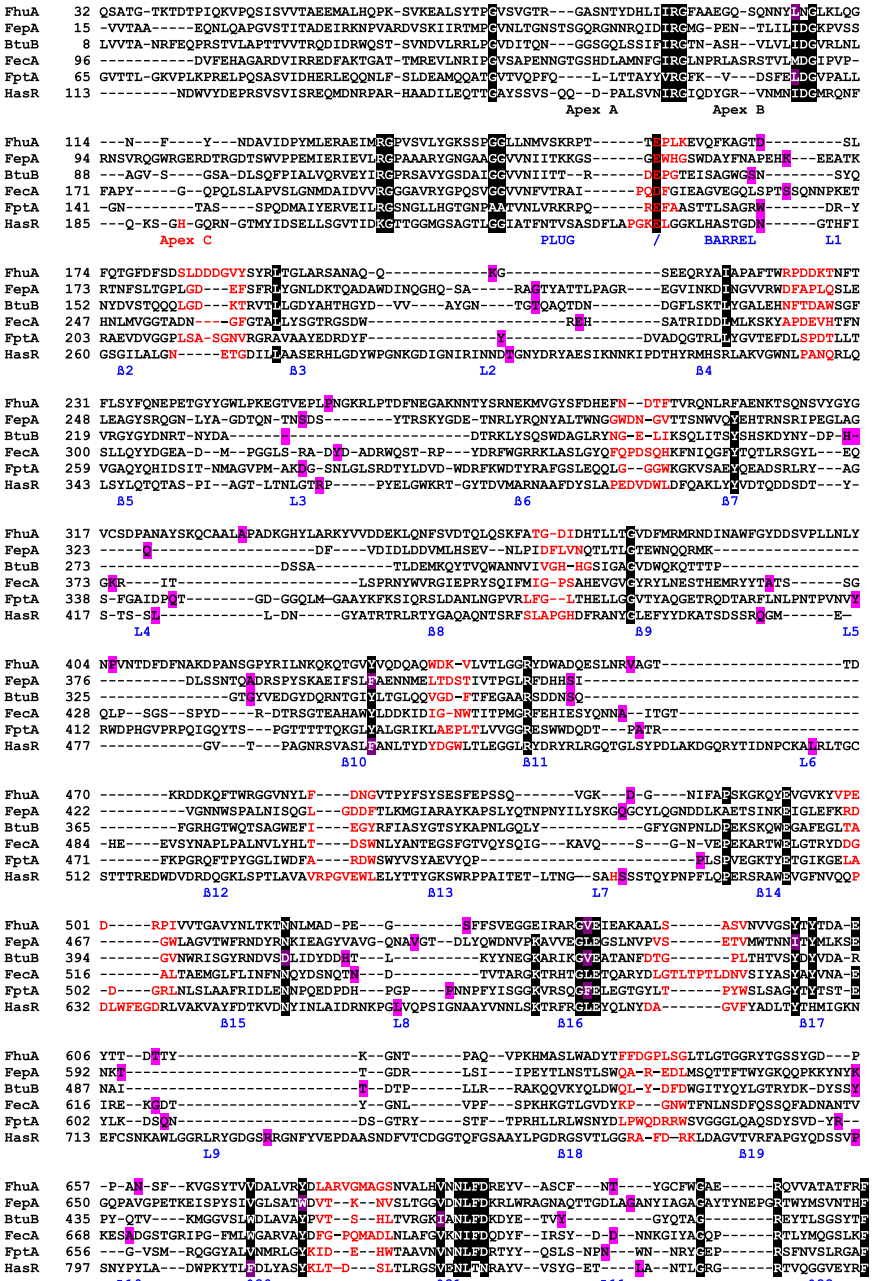

Fig. S1. Structural alignment of TonB/HasB-dependent receptors. The superposition was made with the program MUSTANG (1) and adjusted manually. Conserved residues are highlighted, the apex of each extracellular loop is boxed in violet, the periplasmic turns are shown in red, the 2 conserved histidines involved in heme iron ligation are shown in bold red. Residue numbers follow the PDB ID codes of superimposed structures, i.e., FhuA (1QFF), FepA (1FEP), BtuB (1NQG), FecA (1KMP), FptA (1XKW), HasR (3CSL), except that in FhuA 11 residues of an artificial internal affinity tag inserted in L5 have been deleted. The bottom line indicates the position of the cork apices, the cork/barrel border, the β-strands, and extracellular loops of the barrel.

1. Konagurthu AS, *et al.* (2006) MUSTANG: A multiple structural alignment algorithm. *Proteins* 64:559–574.