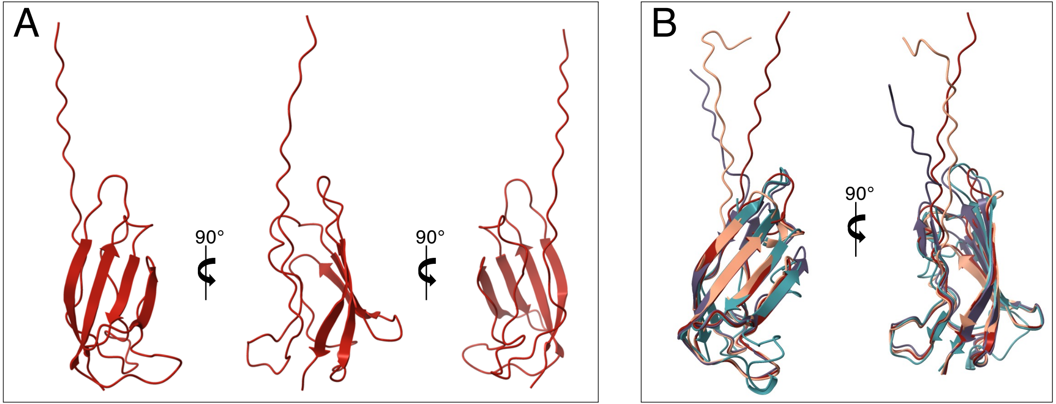

Figure S1. Predicted structure of the CTD of SprB, and its alignment to CTDs of Fjoh_1123 (orange), Fjoh_3952 (blue) and Fjoh_4750 (violet). (A) The structure of the last 100 amino acids of SprB **(A)**, Fjoh_1123, Fjoh_3952 and Fjoh_4750 have been predicted using Alphafold3 (Abramson et al., 2024), with respective pTM scores of 0.82, 0.83, 0.85 and 0.86. Predicted structures of Fjoh_1123, Fjoh_3952 and Fjoh_4750 were aligned to the predicted structure of the CTD of SprB using ChimeraX-1.9 **(B)** For each pair of structures, sequence alignment scores, number of aligned residues and rmsd of these aligned residues are listed in **Table S3**.