Structure pair	Sequence alignment score	Number of aligned residues	rmsd of pruned atom pairs (Å)
SprB/Fjoh_1123	238.8	77	0.624
SprB/Fjoh_3952	131.4	67	0.976
SprB/Fjoh_4750	161.7	72	0.665

Table S3. Sequence alignment scores, number of aligned residues and rmsd of predicted structure of SprB CTD aligned to predicted structures of the CTDs of Fjoh_1123, Fjoh_3952 and Fjoh_4750.