



Additional File 5. Figure S5 :

Sequence analysis for HrpO-like proteins. The analysis of PSPPH_2532 (Hrp_{II}O) indicates that this hypothetical protein belongs to the HrpO/YscO/FliJ family of T3SS proteins [5, 32]. The same is evident for the sequence annotated as RhcZ in the T3SS-2 of *Rhizobium* sp. NGR342. Residues predicted in α -helical conformation are indicated in yellow and unfolded regions in red. Green areas indicate ordered regions. Residues for which a high propensity for coiled-coil formation is predicted are indicated in blue rectangular. Here α -helix prediction was performed with PsiPRED, disordered prediction with FOLDINDEX and coiled coils prediction with COILS. Accession numbers or loci numbers are: AAC25065 (HrpO), P25613 (FliJ), AAB72198 (YscO), PSPPH_2532 (Hrp_{II}O), NGR_b22960 (RhcZ), NGR234_462 (Y4yJ).