

a)

b)

**Figure 5S. Pdbsum plots.** a) Ramachandran plot of the CagY assembled multimer of 14 chains showed 95% residues in most favored regions, 3.6% in additional allowed regions, and 0.6% in generously allowed regions. The secondary structure of chain A of the CagY assembled multimer, showing the 28 disulfide bonds predicted and present only in the MRR