Figure S2.

A)
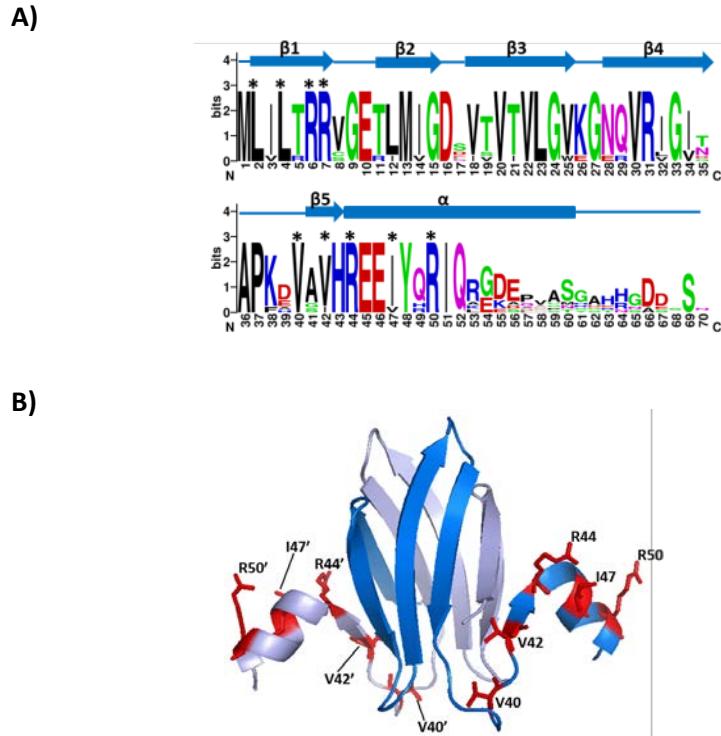

B)

Figure S2. Graphical representation of the multiple sequence alignment and structural model of RsmA of *Xanthomonas citri* subsp. citri. A) Sequences of RsmA homologous proteins were used to generate this representation using the WebLogo server (http://weblogo.berkeley.edu/) [110], in which the height of the residue symbol indicates the degree of conservation and the numbers refer to residue positions in RsmA. RsmA secondary structure was predicted by Phyre (http://www.sbg.bio.ic.ac.uk/~phyre/) [49]. In the predicted XCC RsmA secondary structure, boxes indicate alpha-helices and arrows indicate β-strand motifs. **B)** The RsmA structure model was obtained using the Swiss-Model Repository program with the *E. coli* CsrA structure as a model [PDB: 1Y00, [47]]. The structure was generated using PyMOL [111]. The critical residues involved in RNA binding are highlighted in A) with stars and in B) with sticks in the RsmA three-dimensional structure model [32,33].