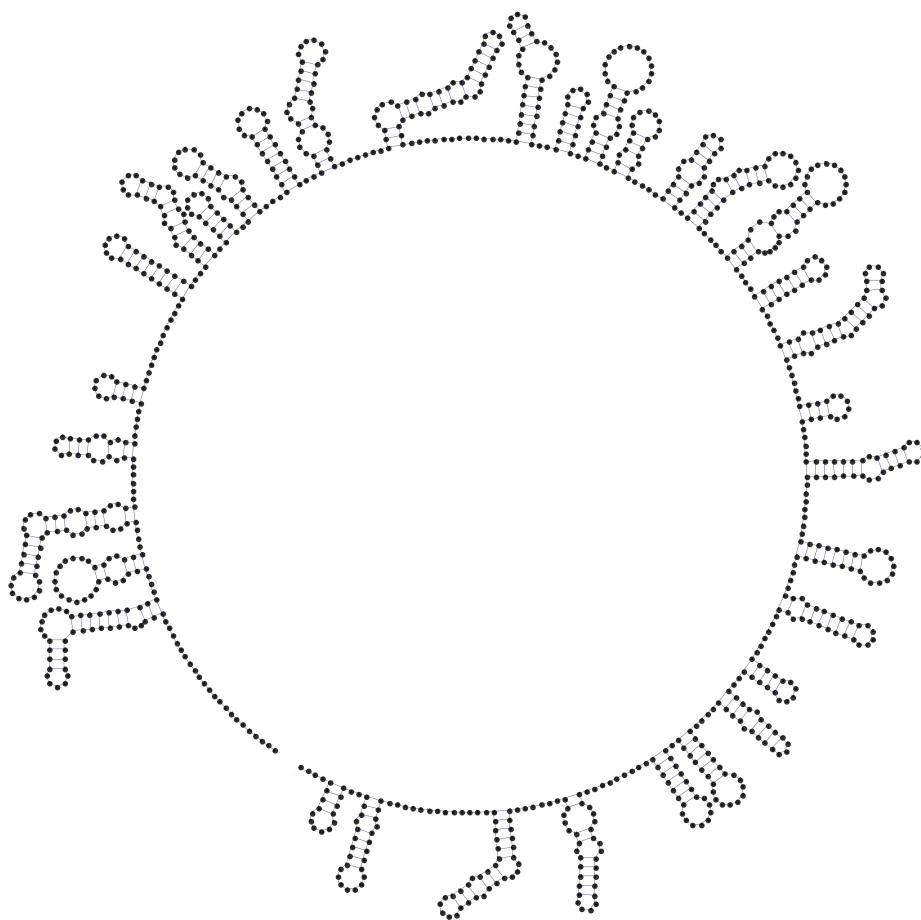


Figure S2. A low-energy secondary structure model for STMV based on thermodynamic predictions with restraints on the maximum base-pairing distance. The restraints generate a structure with 33 local stem-loop structures, similar to the structure of Schroeder *et al.* (1). This structure is lower in energy (-302 kcal/mol) than the Schroeder structure (-160 kcal/mol), but the double-helical stems contain numerous asymmetric bulges. As a consequence, the stems are bent, and a three-dimensional model based on this structure gives much worse agreement with the crystallographic data (correlation coefficient = 0.12) than does a model based on the Schroeder secondary structure (correlation coefficient = 0.56).



REFERENCE:

1. Schroeder SJ, Stone JW, Bleckley S, Gibbons T, & Mathews DM (2011) Ensemble of secondary structures for encapsidated satellite tobacco mosaic virus RNA consistent with chemical probing and crystallography constraints. *Biophysical journal* 101(1):167-175.