

Fig. S3. Analytical ultracentrifugation of *CIRV* p19. (A) Equilibrium run at 18000 rpm, 20°C, (B) sedimentation velocity at 40000 rpm, 20°C, (C) Calculation of the sedimentation coefficient. Analysis of data was performed as described in the Materials and Methods

section. The calculated sedimentation coefficient was s(app) = 2.74 S. From the equilibrium, the corresponding molecular mass was determined to be 46 +/- 4 kDa independently of protein concentration (theoretical mass of *CIRV* p19 monomer 19.479 kDa). These data confirmed the purified p19 to form a protein dimer (22, 23).