



Supplementary figure 4

The complete region between the final helix of CA and the first Zn finger of NC modelled as an alpha helix using Chimera compared to the solved structure of the cucumber mosaic virus coat protein helix for illustrative purposes (colouring as in Figure 3D). The left hand panel shows the most likely hydrophobic face the right hand panel shows the left hand panel rotated 180°. The 18-residue region considered in the helical wheel corresponds to a 24 Å alpha-helix (Figure 3C).