

**P023** Structural studies of protein–RNA interactions in Viral Capsids  
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The interaction between the bacteriophage MS2 capsid and a 19 nt stem-loop operator within the viral genome has long been regarded as the paradigm for the study of sequence specific protein–RNA interactions. Thus far, the structures of over 20 complexes between coat protein and RNA stem-loops with base substitutions and chemical modifications have been determined by X-ray crystallography. Recently the structure of a complex between coat protein and a modified stem-loop with the highest binding affinity yet determined has been elucidated. The structure allows an explanation of the high affinity to be proposed, and also confirms the important role of the torsional flexibility of the sugar-phosphate backbone for complex formation. It is hoped that the success of the MS2 project can be emulated using the recombinant  $T=1$  icosahedral capsid of Satellite Tobacco Necrosis Virus (STNV), the structure of which has been resolved to 1.45Å. The size of STNV and the fact that the entire capsid accommodates the asymmetric site within the crystal makes the capsid ideal for use as a scaffold for the structural determination of short RNA sequences.