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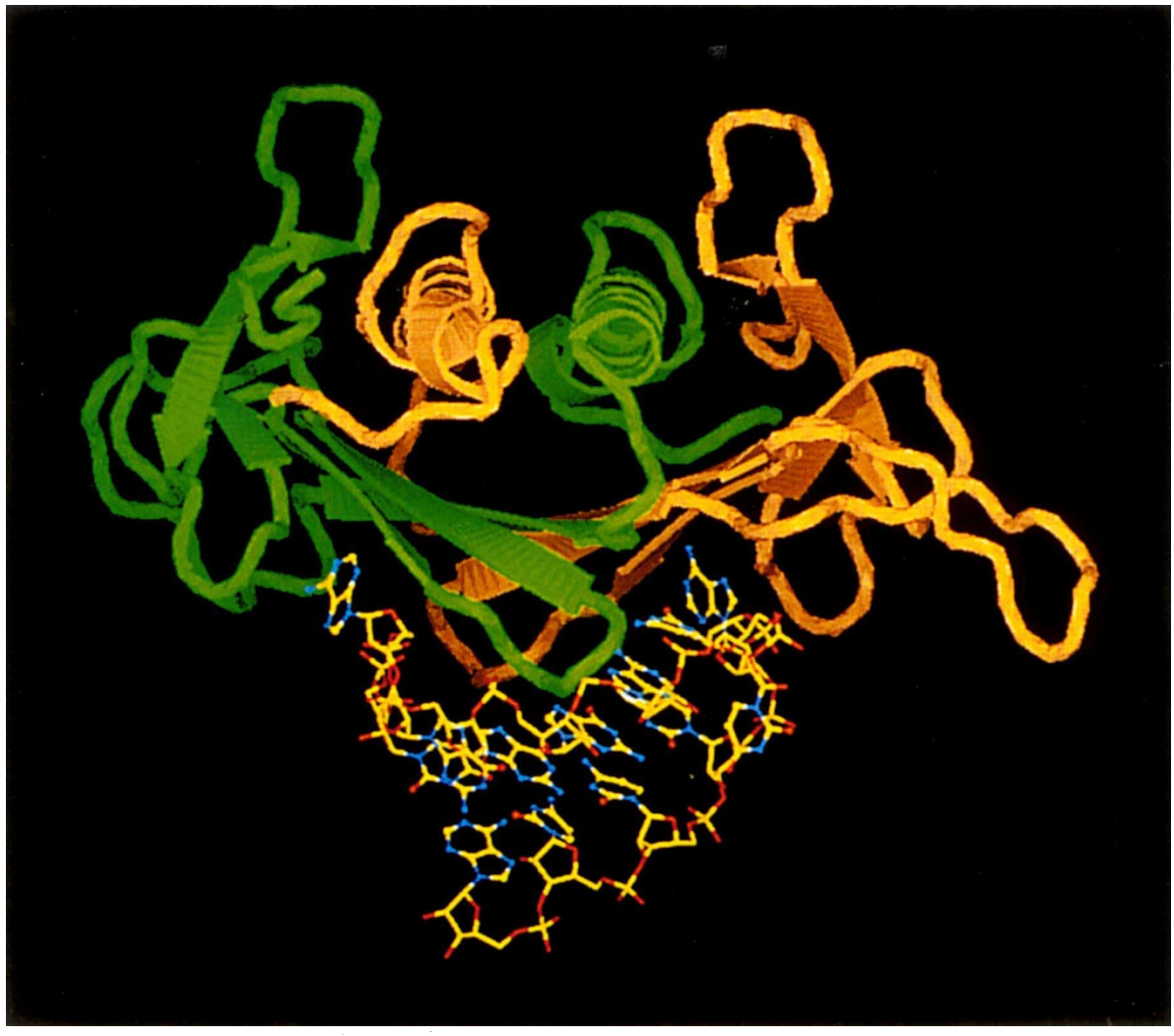
If the coat fits...



Unlike the DNA-binding proteins, a large number of whose structures have been determined, little is known about the detail of sequence-specific interactions between proteins and RNA. To date the only high resolution structures of sequence-specific protein/RNA complexes have been those of tRNA synthetases. The structure of the protein coat from bacteriophage MS2 in complex with a 19 base oligonucleotide (Valegård K., Murray J.B., Stockley P.G., Stonehouse N.J. & Liljas L. *Nature* **371**, 623–626) goes some way to addressing this imbalance.

Bacteriophage MS2 is an icosahedral virus whose coat is comprised of 180 identical proteins. Due to the constraints of icosahedral symmetry the protein occupies three different environments and takes up subtlety different conformations dependent on the position being occupied. Viral coat proteins are involved in organising the viral genome (in this case RNA) however this interaction is difficult to resolve in native virus structures. The viral nucleic acid is isolated from the crystal environment by the capsid and so does not conform to the symmetry essential for the resolution of its structure. Here this difficulty was surpassed by growing crystals of empty capsids and soaking them with a 19 base oligonucleotide. This ligand is small enough to bind identically at all the potential sites within the capsid.

The oligonucleotide used contained the initiation codon for the viral replicase gene. *In vivo* this sequence is specifically bound by the coat protein, achieving the dual effects of ordering the RNA within the virus and instigating virion assembly by shutting off replicase synthesis. The structure shows the oligonucleotide forming a hairpin structure maintained by Watson-Crick base pairing and bound to a dimer of coat proteins (either a symmetric dimer lying on a 2-fold symmetry axis or, as shown here, a dimer formed by non-symmetry related proteins; note the different conformations adopted by the two proteins). Detailed analysis of this interaction, as well as the determination of complexes with RNA and protein mutants, will help bring our understanding of RNA recognition up to, if not beyond, that for DNA.

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