

# Structural biology of viruses

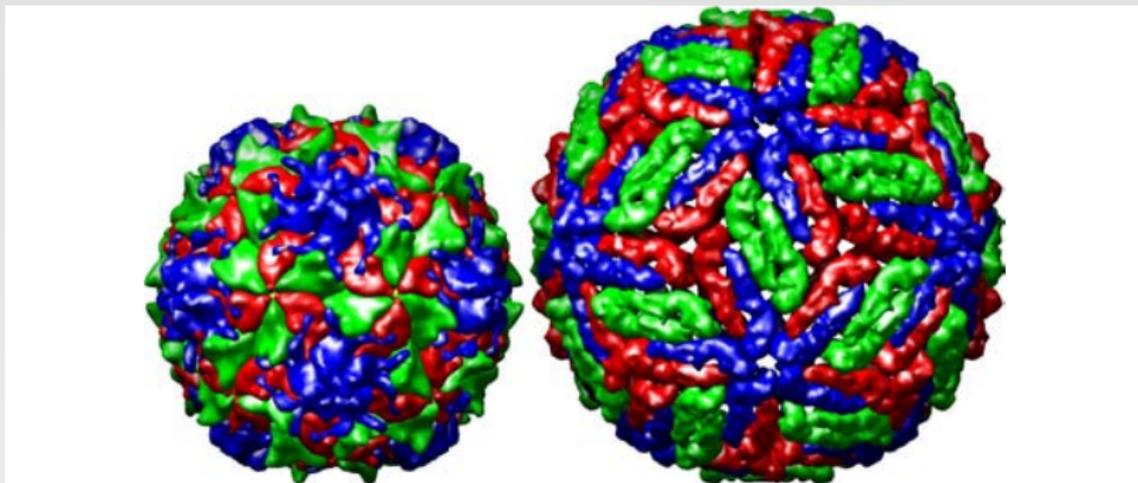
Biophysical Chemistry 1, Fall 2010

Coat proteins

DNA/RNA packaging

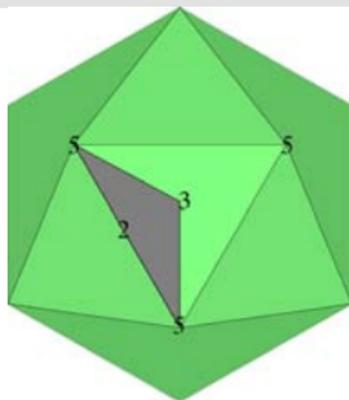
Reading assignment: Chap. 15

# Virus particles self-assemble from coat monomers



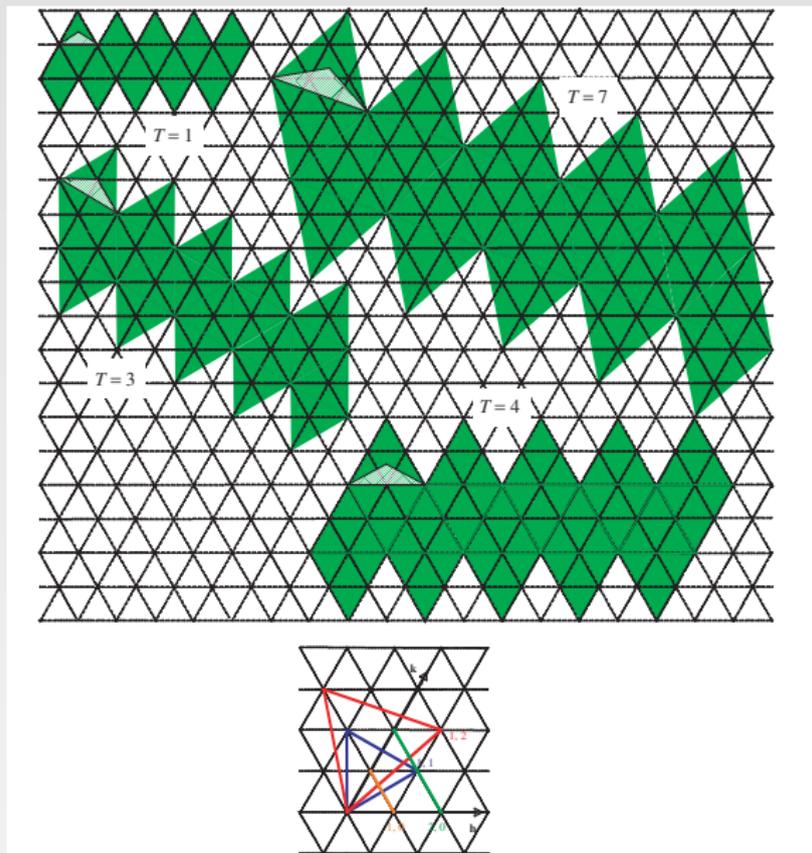
**FIGURE 15.1** ■ Schematic drawings of virus particles. *Left:* Poliovirus, a simple icosahedral virus with a diameter of about 300 Å (based on a crystal structure). *Right:* Flavivirus, an enveloped virus with a crystal diameter of about 470 Å (based on a cryo-EM model with models of coat protein molecules from a crystal structure fitted into the cryo-EM density). The colors denote subunits in different environments as discussed below. From VIPER (<http://viperd.b.scripps.edu/>).

# Icosahedral coats are the most common ones

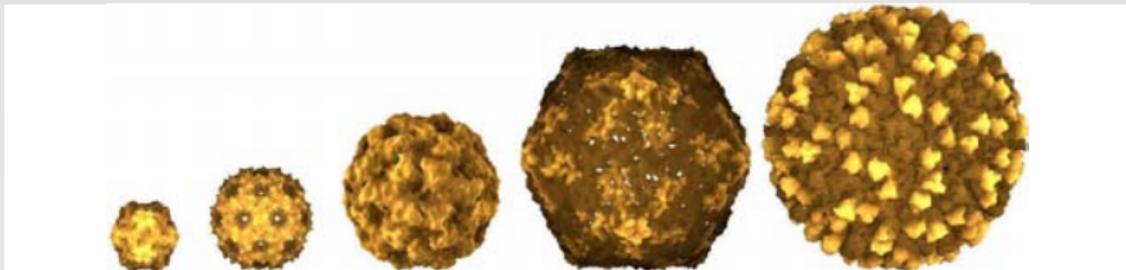


**FIGURE 15.2** ■ An icosahedron showing the positions of the five-, three- and two-fold symmetry axes. The repeated unit is marked in gray. This is only one of many possible choices of the repeated unit.

# Interactions can be viewed in two dimensions



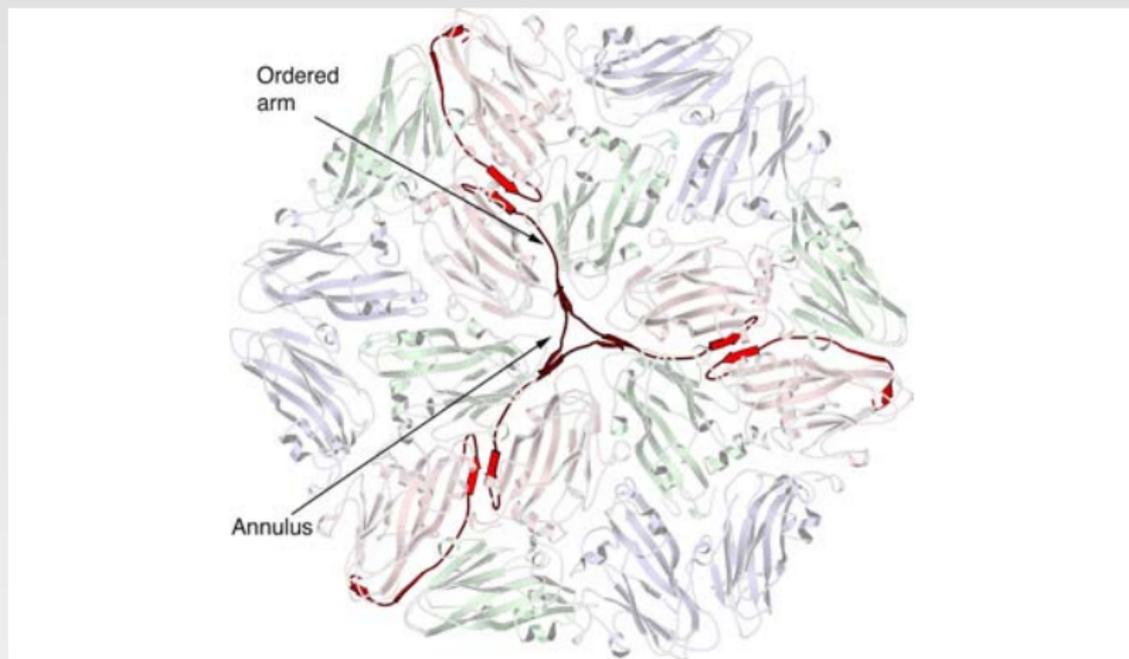
# Various triangulation numbers



**FIGURE 15.4** ■ Viruses with triangulation numbers 1, 3, 4, 7 and 13 showing their relative sizes. The surface of the virus particles is shaded according to its distance from the center, darker being closer. Some particles have an icosahedral shape, but the particles all have icosahedral symmetry. The drawings are based on the crystal structures (from left to right) of satellite tobacco necrosis virus, phage MS2, *Nudaurelia capensis*  $\omega$  virus, phage HK97 and the bluetongue virus. From VIPER (<http://viperd.b.scripps.edu/>).

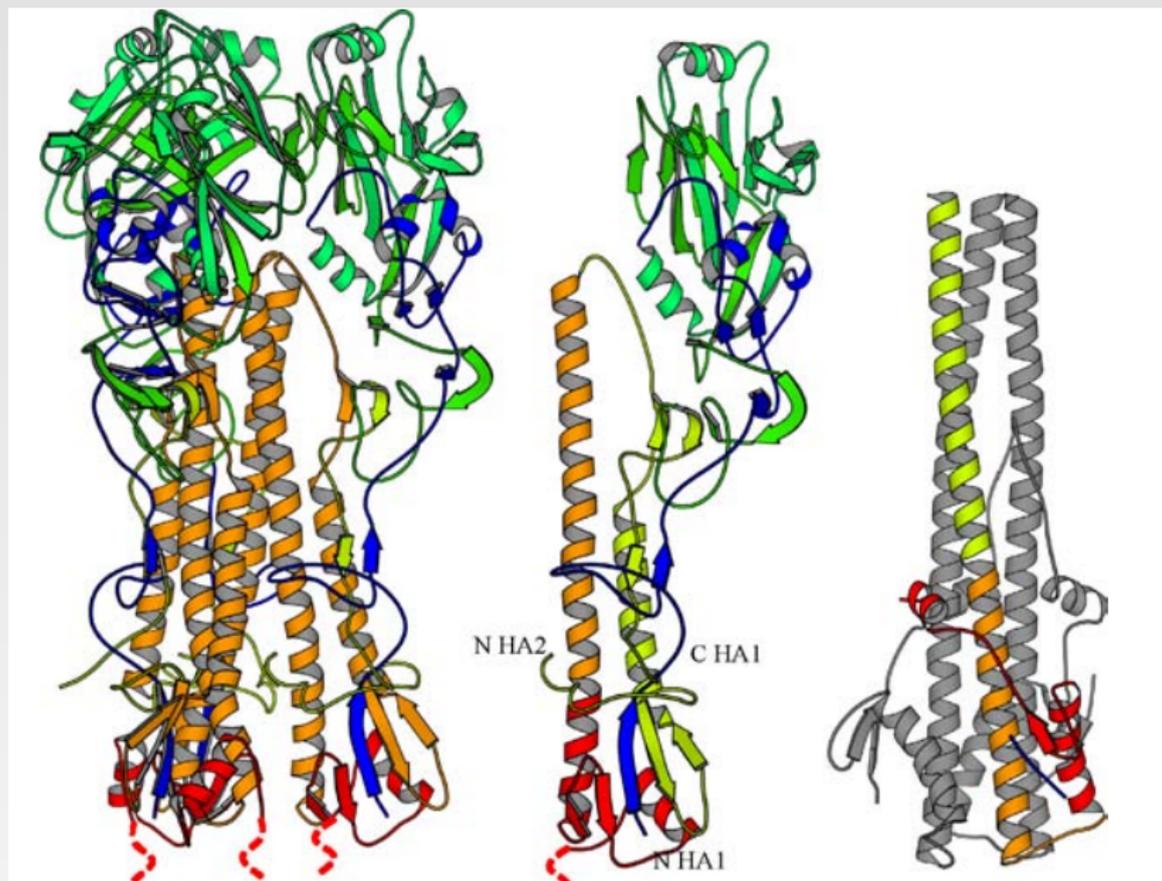


# Interdigitation often stabilizes coats

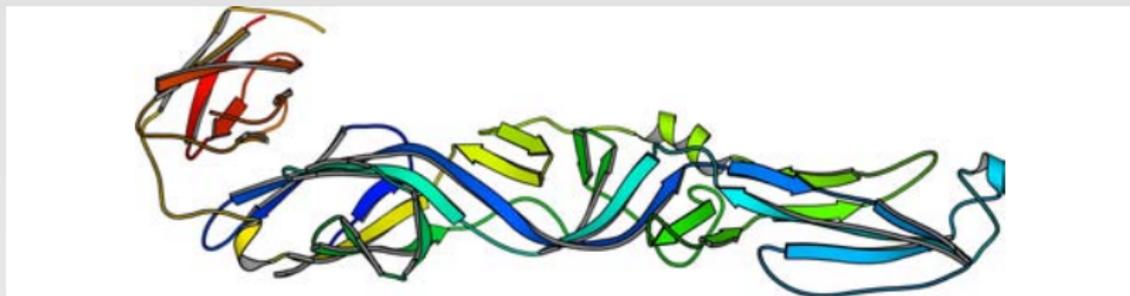


**FIGURE 15.7** ■ The arrangement of 18 subunits around the three-fold (quasi-six-fold) axis in the southern cowpea mosaic virus. The partially ordered arm in one of the subunits (marked in red) interacts with arms from symmetry-related subunits at the three-fold axis (beta annulus, indicated with an arrow). In this virus, the N-terminal 23 amino acids are disordered in all subunits. This region contains several positively charged residues and probably interacts with the viral RNA, which is asymmetric.

# Cell entry: hemagglutinins

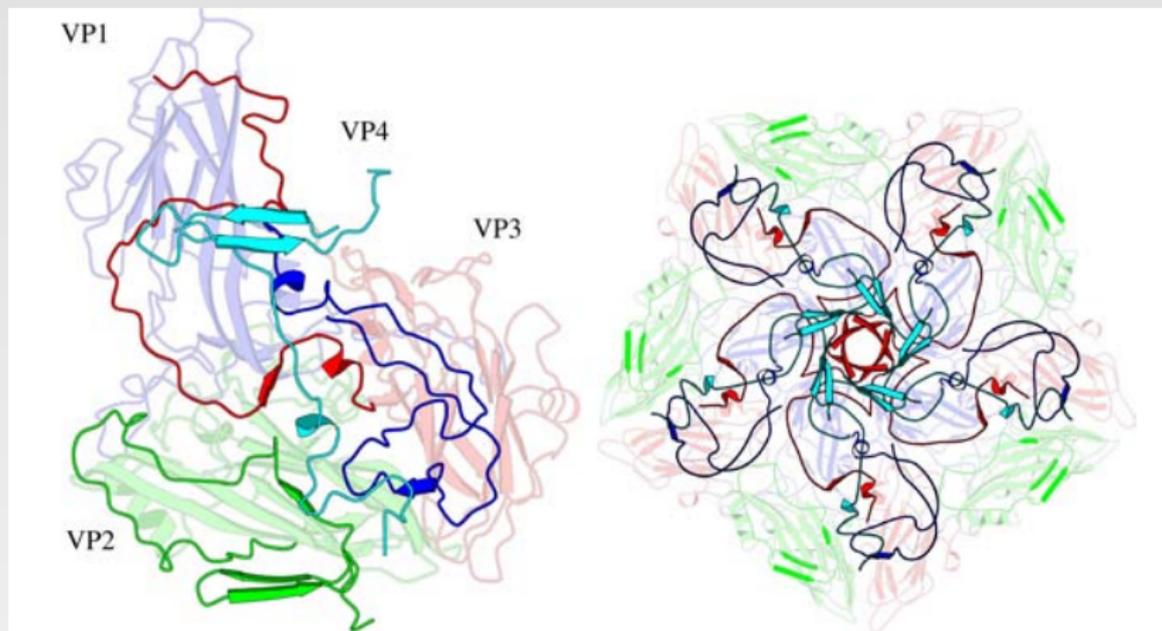


# Cell entry: simple viruses

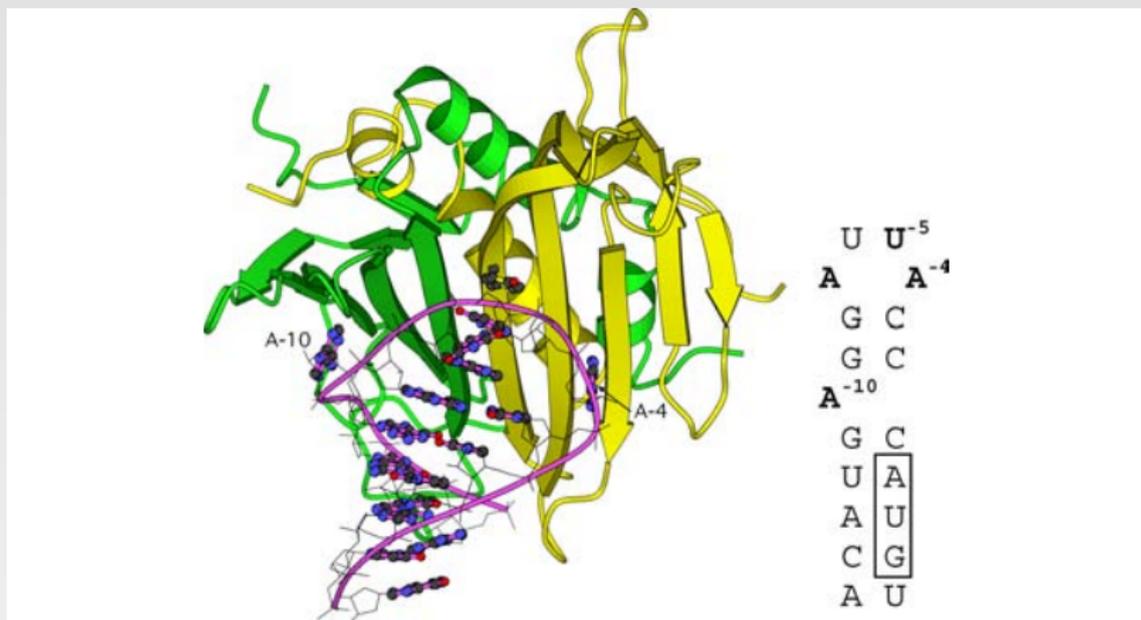


**FIGURE 15.9** ■ The E1 protein from the Semliki Forest virus, an alphavirus (PDB: 119W). The coloring is from N-terminal (blue) to C-terminal (red). The fusion peptide is the loop at the extreme right of the molecule and is hidden through contacts to another protein in a homodimer. The anchor to the viral membrane is at the C-terminus of the protein, but this part of the protein was removed before crystallization and is therefore not seen here.

# Cell entry: poliovirus architecture



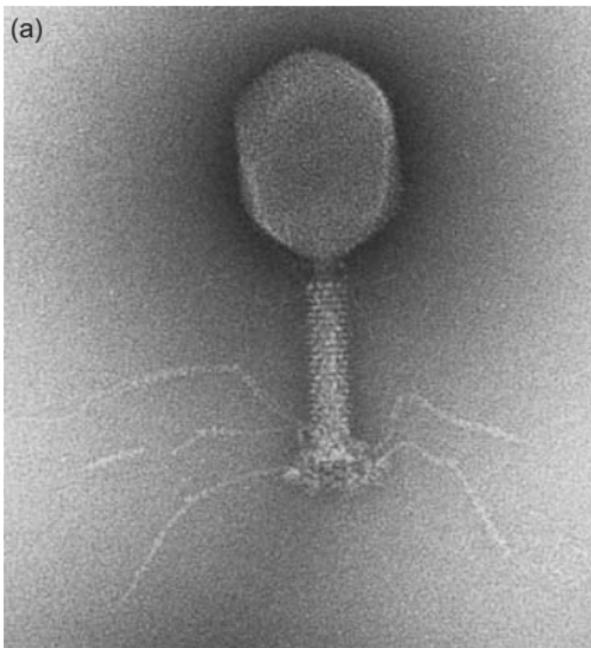
# Getting the right RNA back into the virus



**FIGURE 15.12** ■ The binding of the RNA hairpin by the MS2 dimer (PDB: 1ZDI). Adenine bases  $-10$  and  $-4$  are bound in corresponding pockets in the two monomers of the dimer, and uracil base  $-5$  is stacked to a tyrosine sidechain in one of the subunits. To the *right*, the secondary structure of the hairpin is shown. The initiation codon of the replicase subunit is boxed.

# Genome packaging in bacteriophage

(a)



(b)

