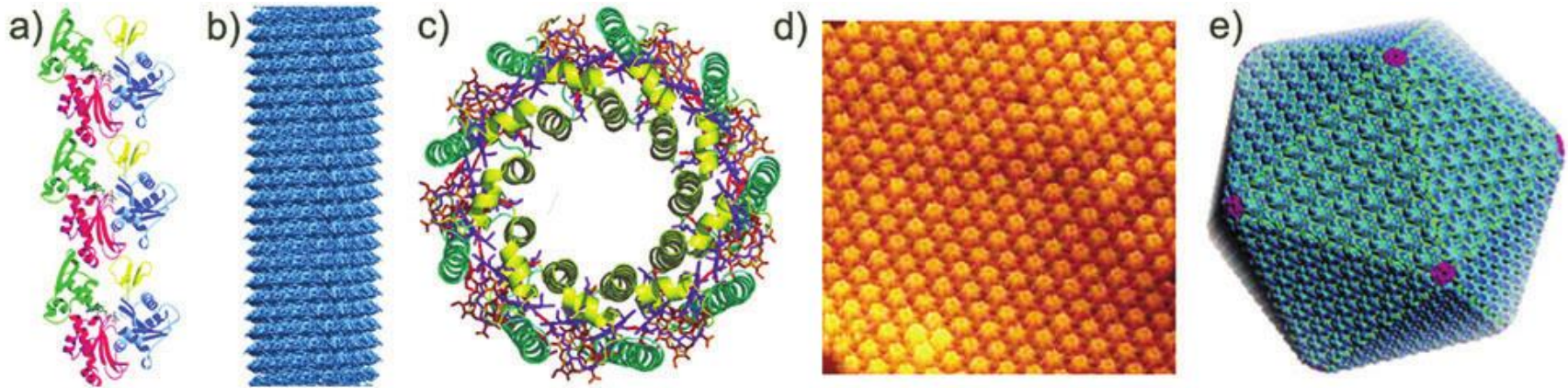


Self assembly



Shape in eukaryotic cells

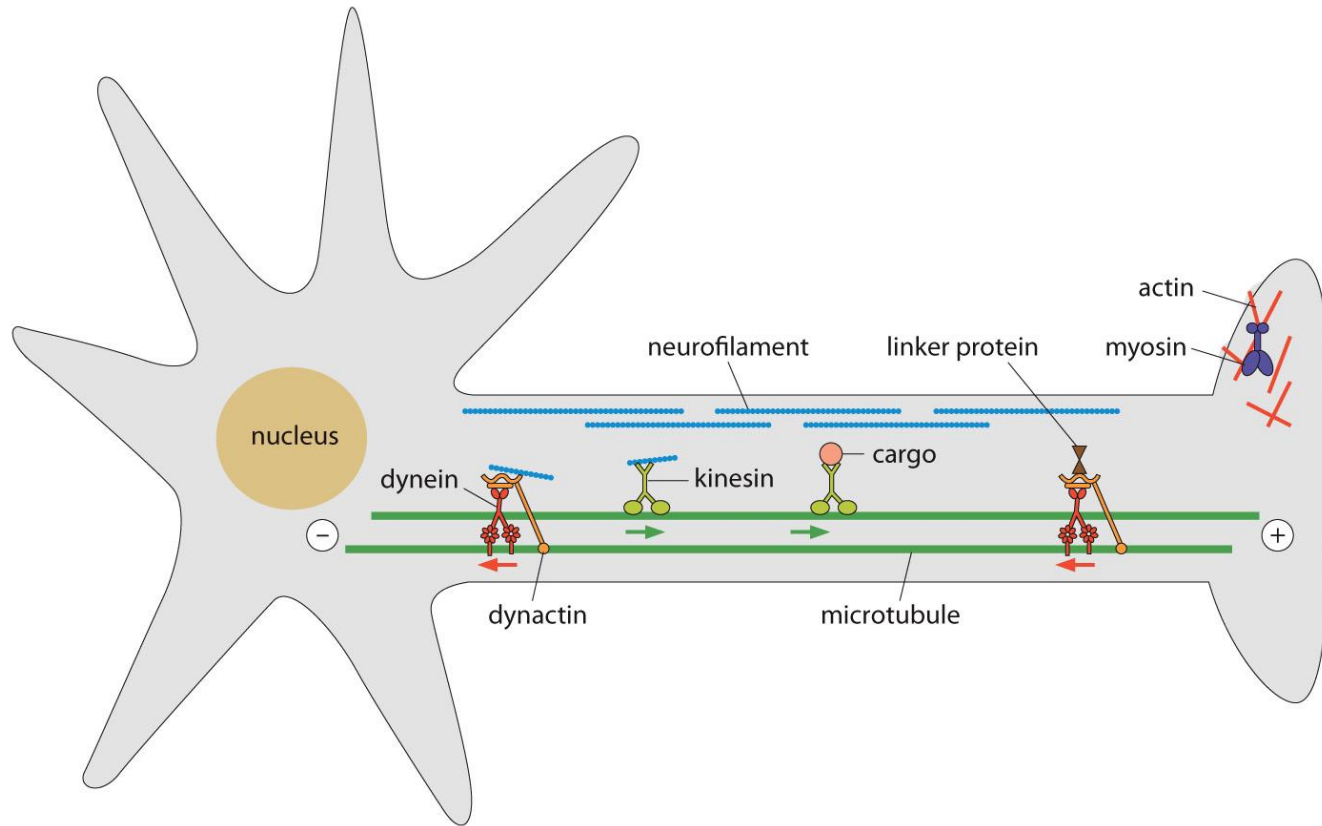


Figure 14.1 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

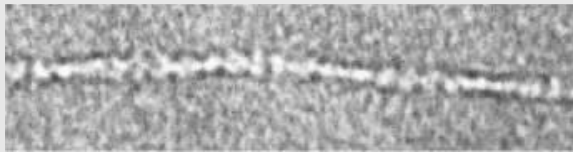
Shape in eukaryotic cells is provided by the cytoskeleton that consists of actin, tubulin, and intermediate filaments.

Bacterial cells come in a variety of different shapes, including spheres, rods, spirals, and crescents.

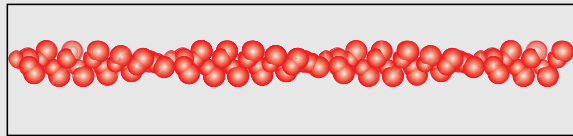
Shape is important for bacterial cells because it plays a role in cell division, helps to maximize the uptake of nutrients, and aids cell movement.

Filaments and microtubules within the cell

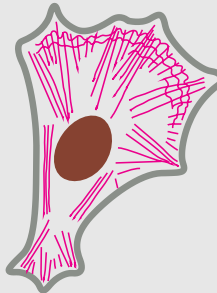
ACTIN FILAMENTS



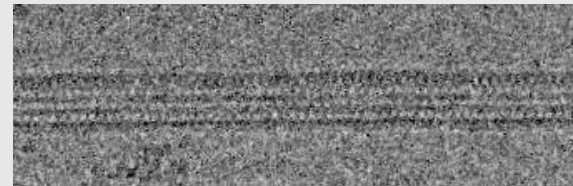
100 nm



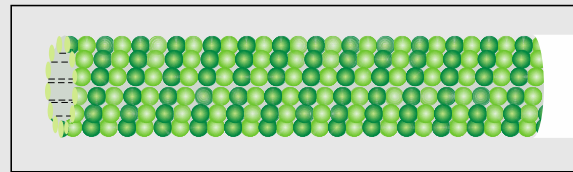
25 nm



MICROTUBULES



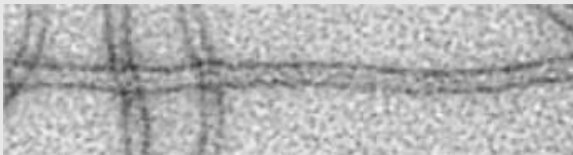
100 nm



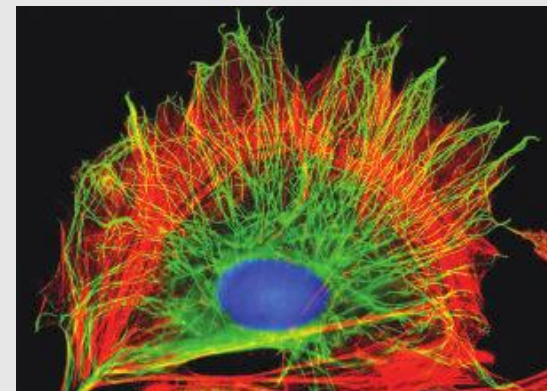
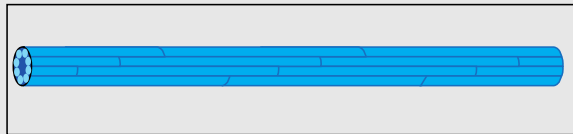
25 nm



INTERMEDIATE FILAMENTS

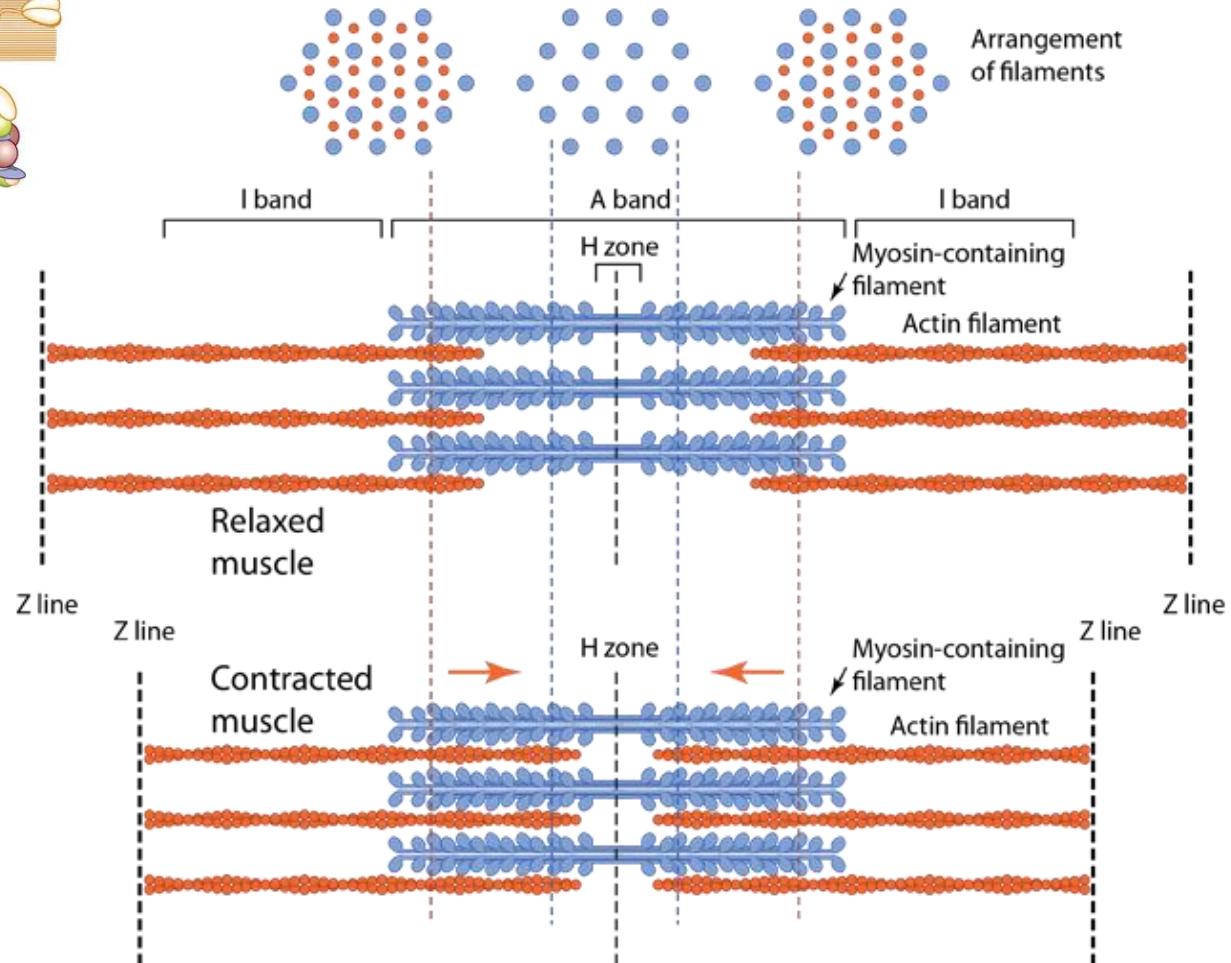
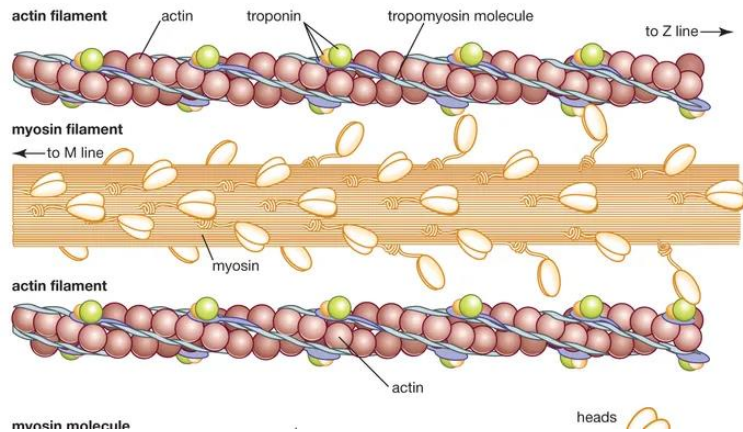


100 nm



10 μm

Actin



Actin filament

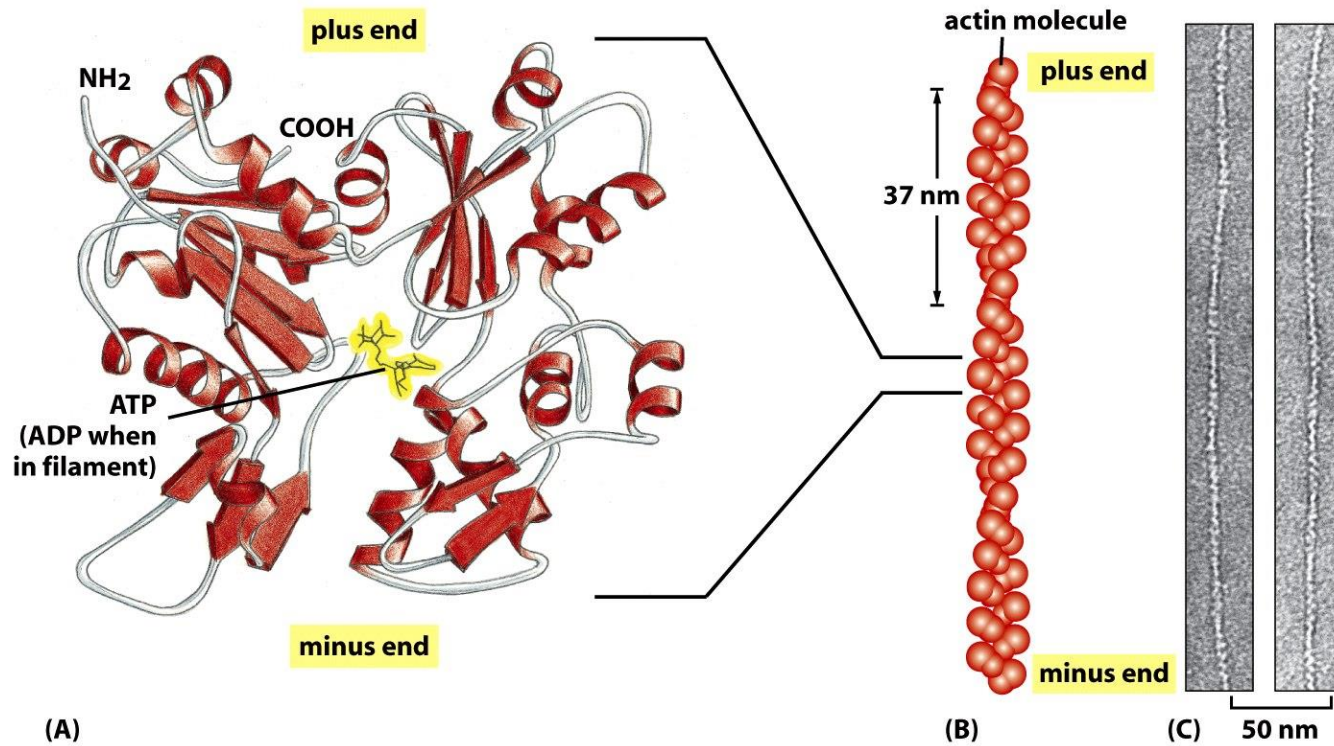
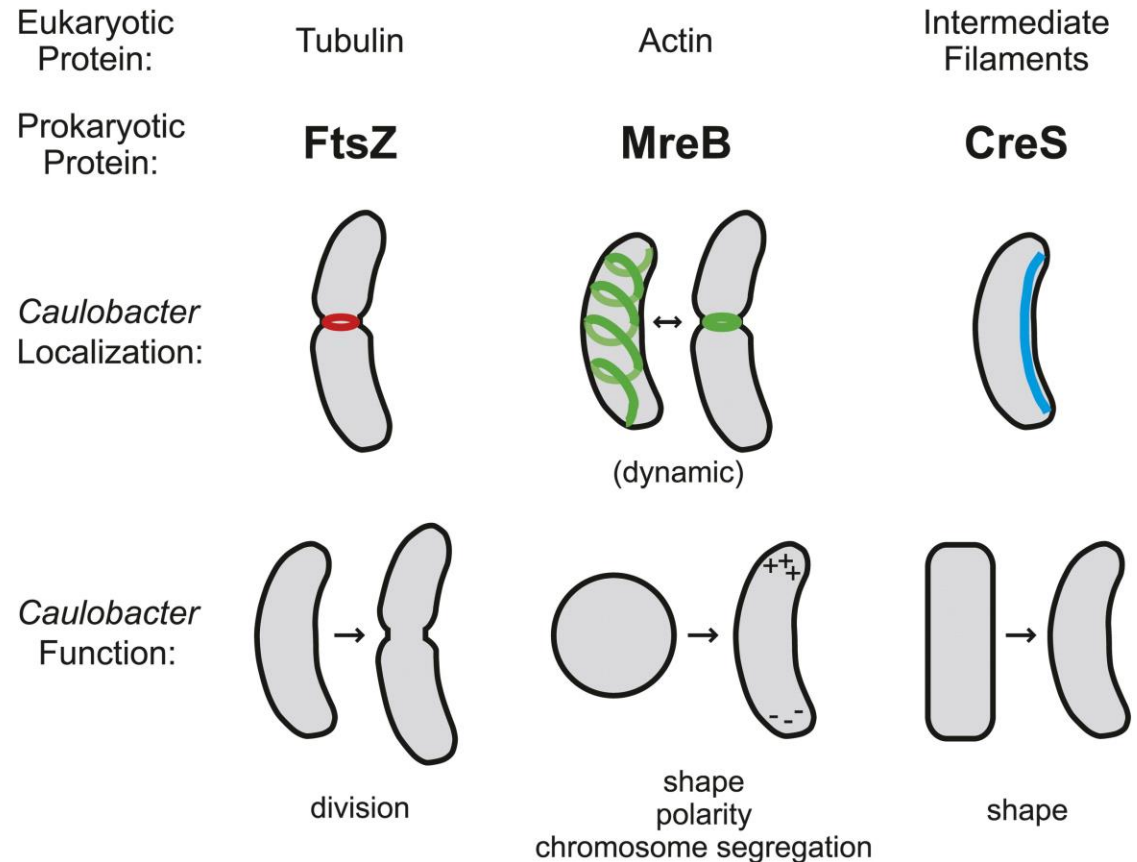


Figure 16-12 *Molecular Biology of the Cell* (© Garland Science 2008)

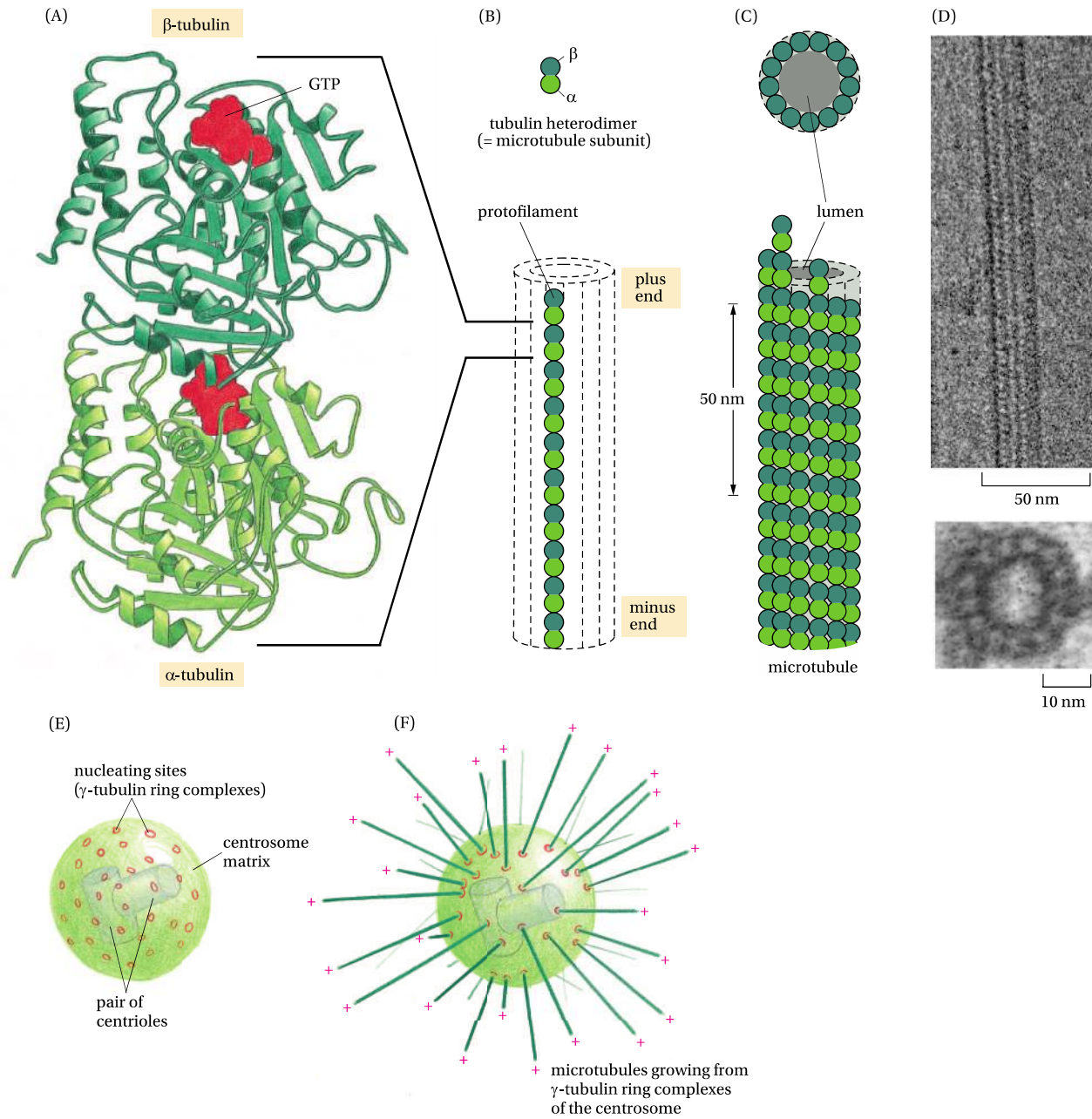
Procaryotic actin

Prokaryotes also have a dynamic, filamentous network of proteins, which are homologous to the eukaryotic cytoskeletal elements.

In non-spherical bacteria, the actin homologue MreB is essential for shape maintenance as depletion of MreB through genetic knockouts or MreB-targeted drug treatment results in misshapen cells that eventually lyse



microtubules



Dynamic instability

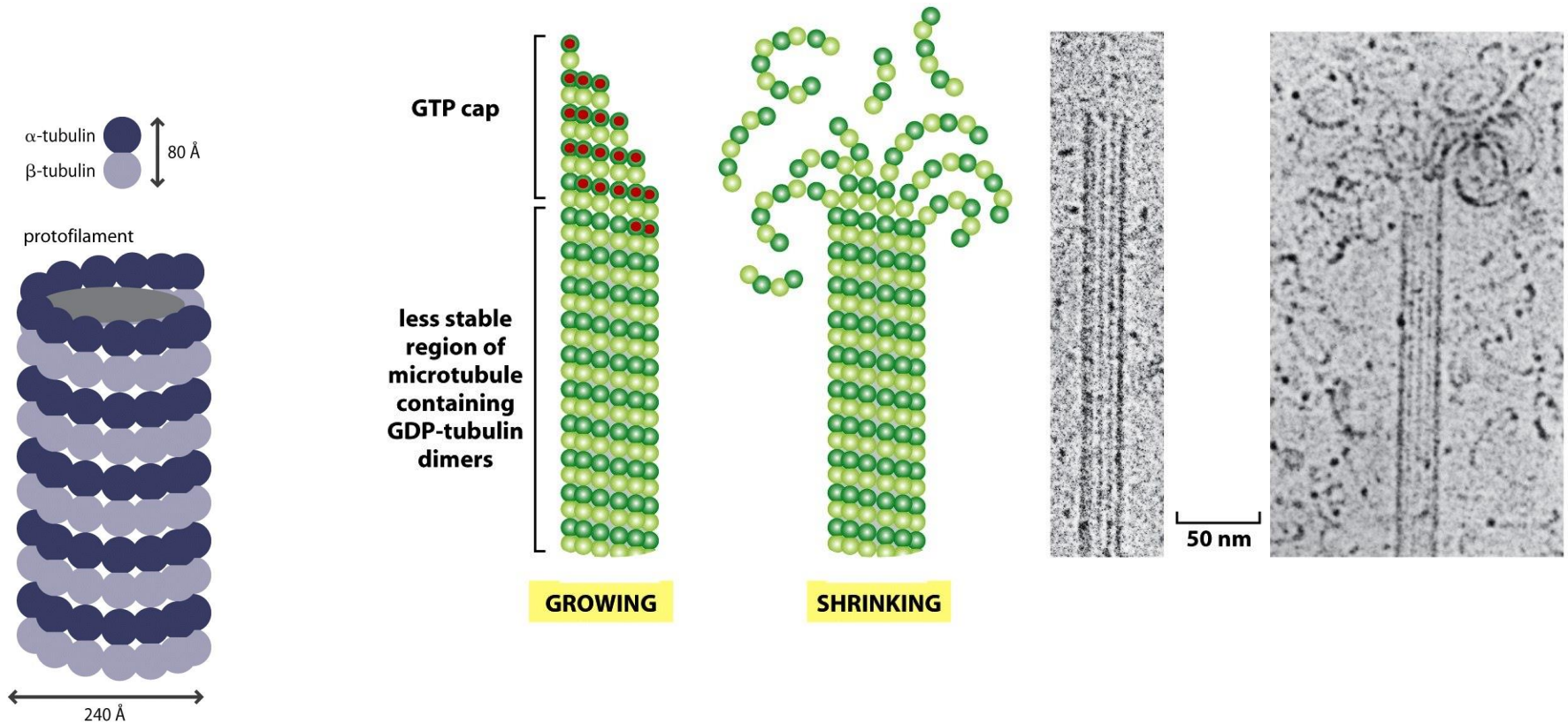


Figure 7.27 How Proteins Work (©2012 Garland Science)

Tubulin interacting proteins

TABLE 7.2 Proteins that interact with tubulin/microtubules

Protein	Function
γ -TuRC	Initiates filament formation
MAP, XMAP215	Stabilizes filaments
Tau, MAP-2	Cross-links filaments in parallel rows
Stathmin, kinesin 13, katanin	Cuts or depolymerizes filaments
+TIP, plectin	Links filament to other proteins

Fiber growth

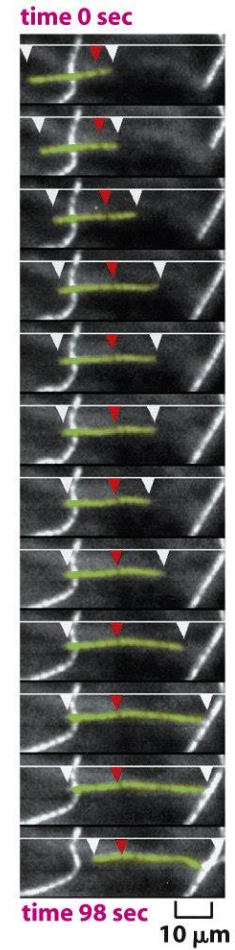
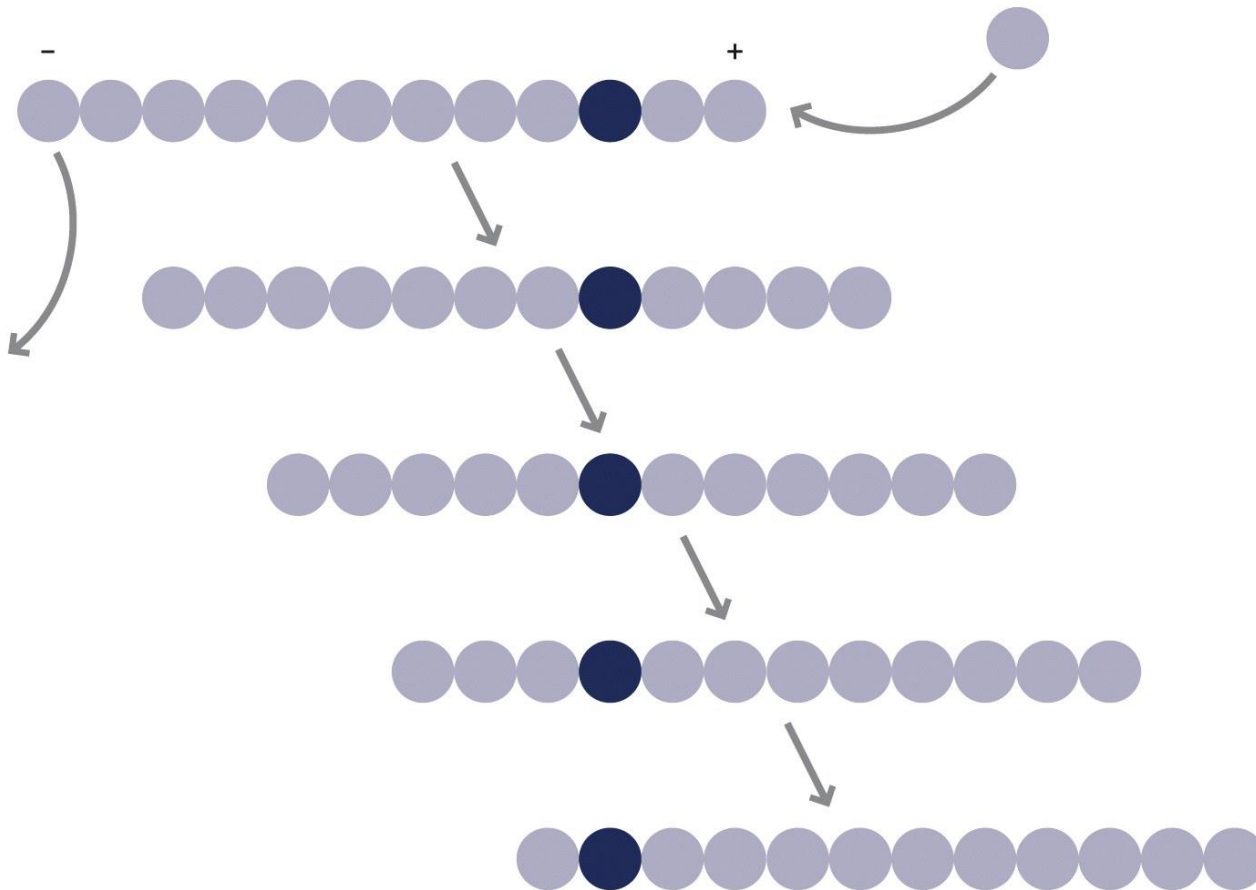
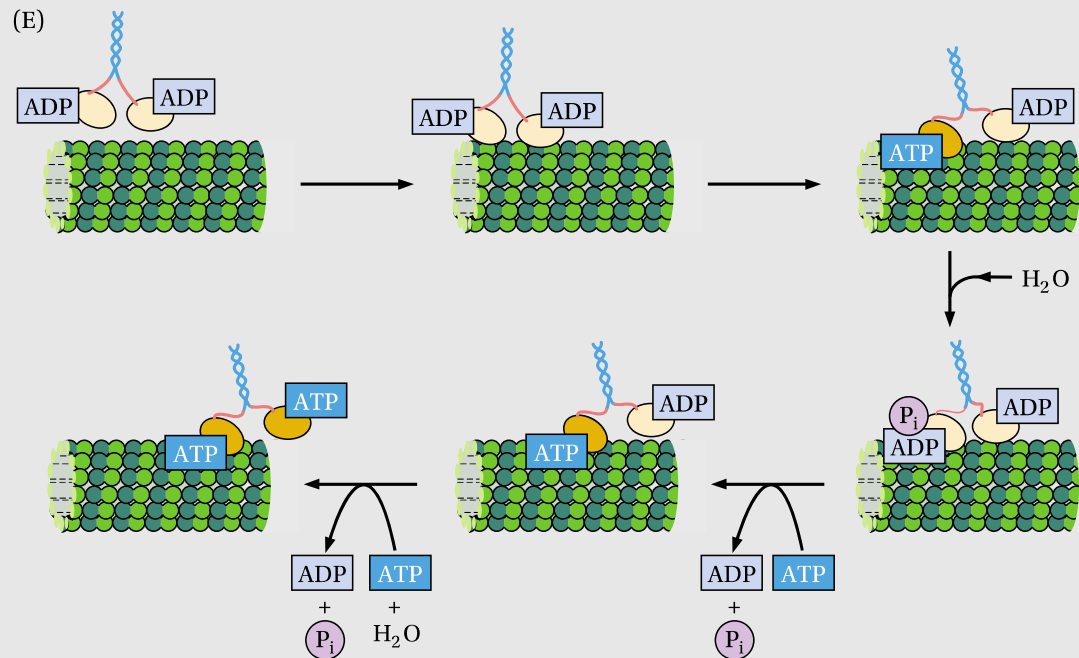
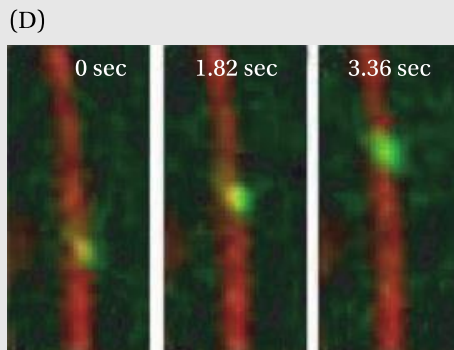
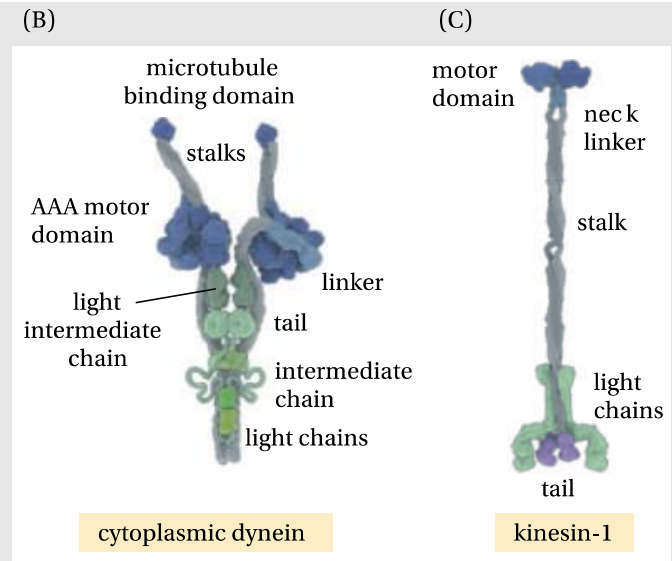
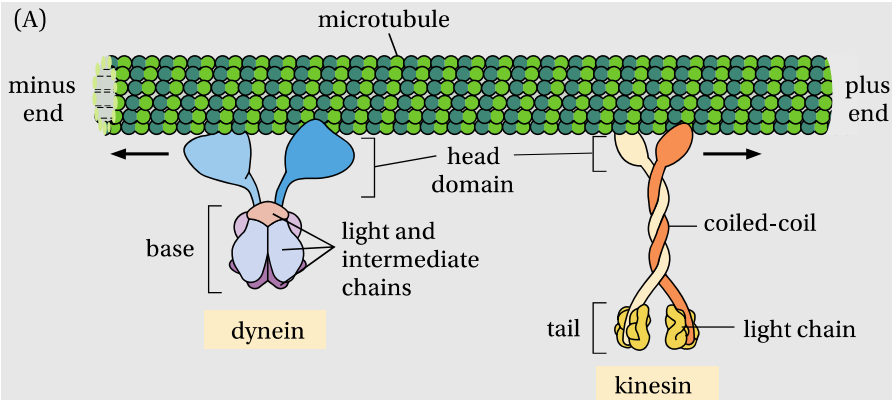


Figure 7.30 How Proteins Work (©2012 Garland Science)

kinesins and dyneins



Drugs

Table 16–2 Drugs That Affect Actin Filaments and Microtubules

ACTIN-SPECIFIC DRUGS	
Phalloidin	binds and stabilizes filaments
Cytochalasin	caps filament plus ends
Swinholide	severs filaments
Latrunculin	binds subunits and prevents their polymerization
MICROTUBULE-SPECIFIC DRUGS	
Taxol	binds and stabilizes microtubules
Colchicine, colcemid	binds subunits and prevents their polymerization
Vinblastine, vincristine	binds subunits and prevents their polymerization
Nocodazole	binds subunits and prevents their polymerization

Fluorescence microscopy

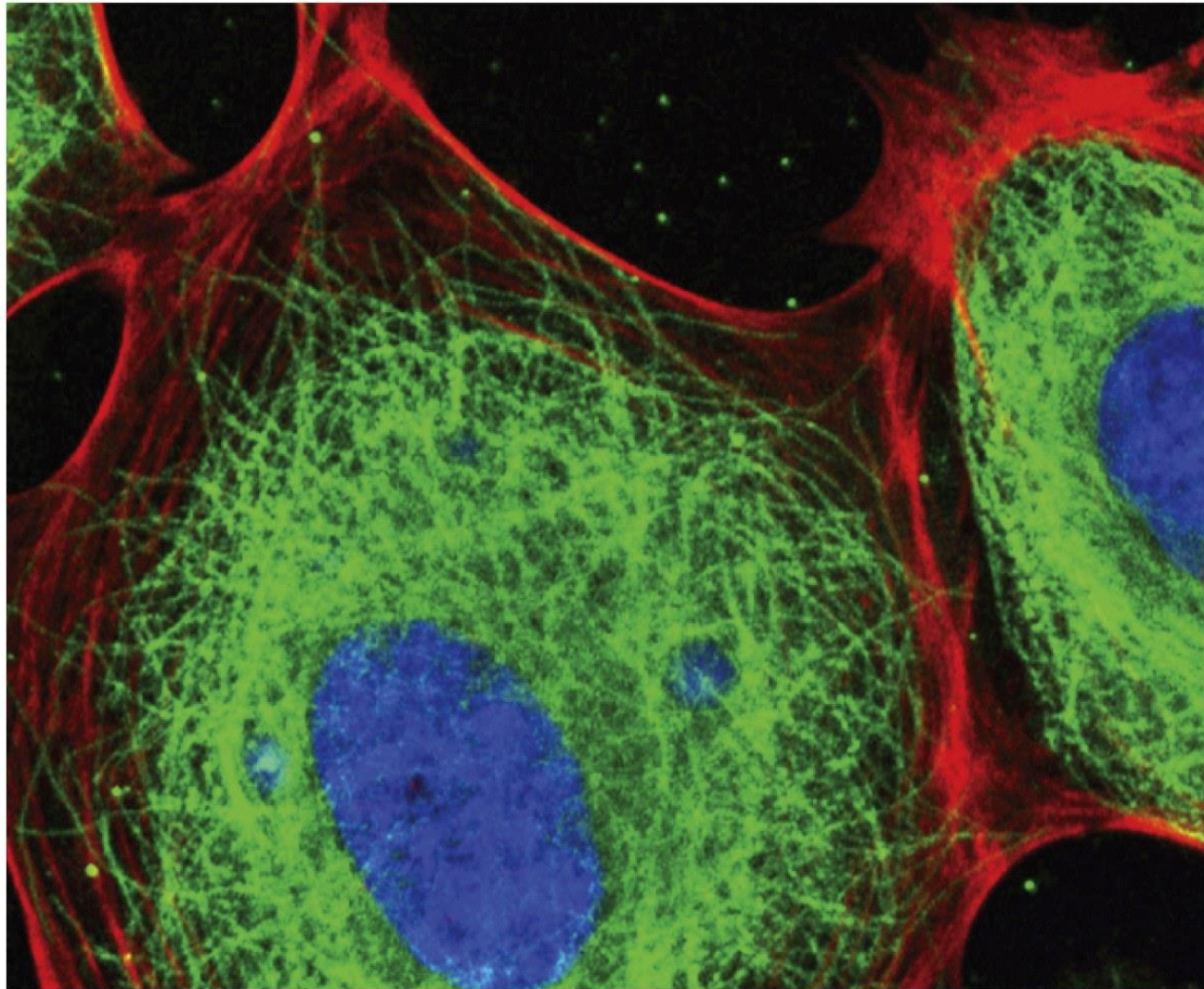
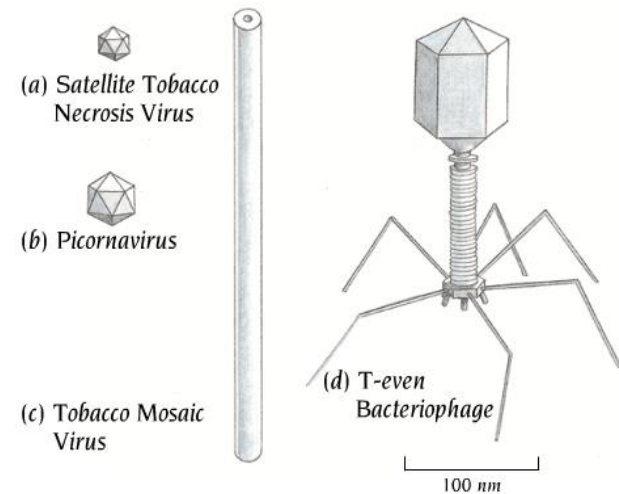
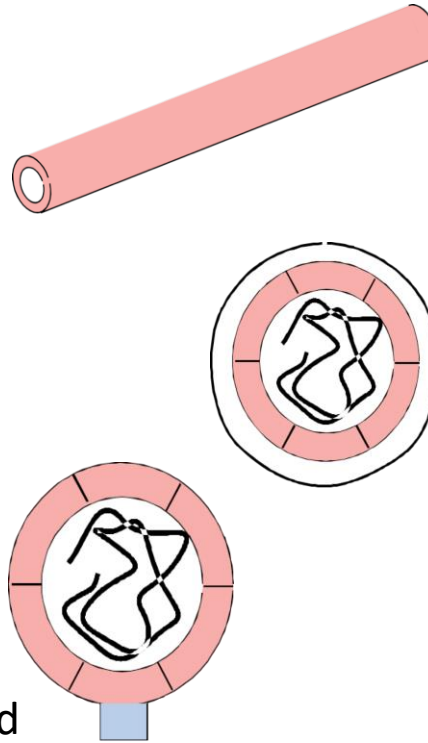


Figure 7.33 How Proteins Work (©2012 Garland Science)

Virus Structure

- Size
 - 17 nm – 3000 nm diameter
- Basic shape
 - Rod-like
 - “Spherical”
- Protective Shell - Capsid
 - Made of many identical protein subunits
 - Symmetrically organized
 - 50% of weight
 - Enveloped or non-enveloped
- Genomic material
 - DNA or RNA
 - Single- or double-stranded



Virus capsids function in

- Packaging and protecting nucleic acid
- Host cell recognition
 - Protein on coat or envelope “feels” or “recognizes” host cell receptors
- Genomic material delivery
 - Enveloped: cell fusion event
 - Non-enveloped: more complex strategies & specialized structures

Viruses

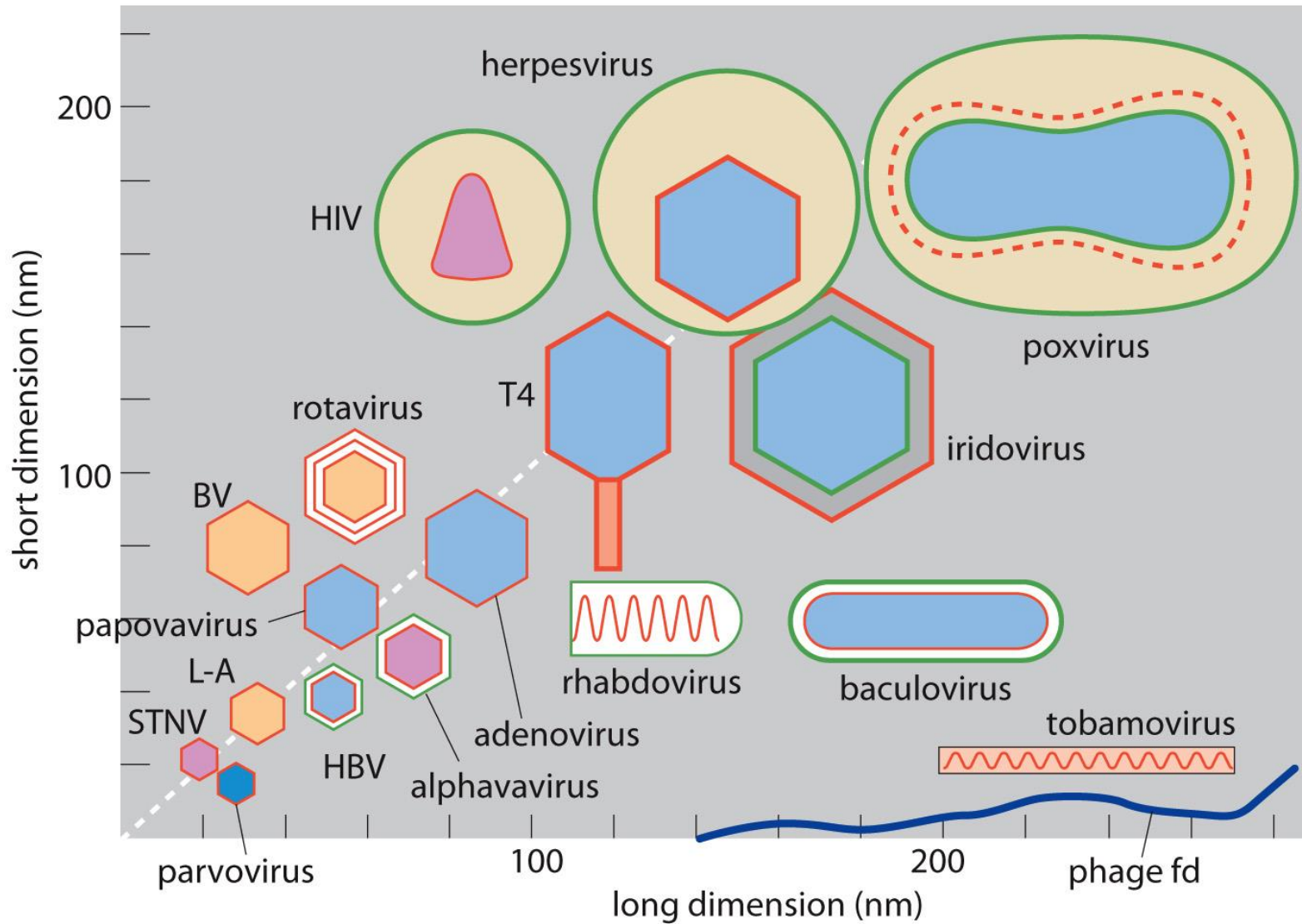
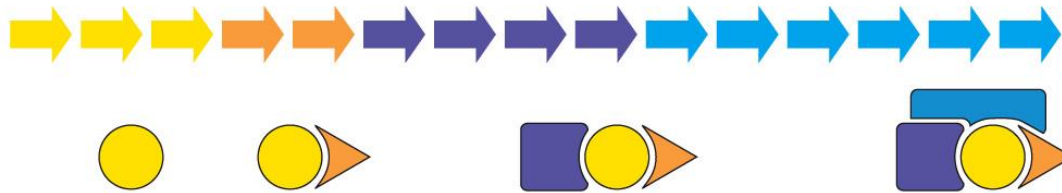


Figure 8.4 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

assembly pathways

linear assembly pathway



branched assembly pathway

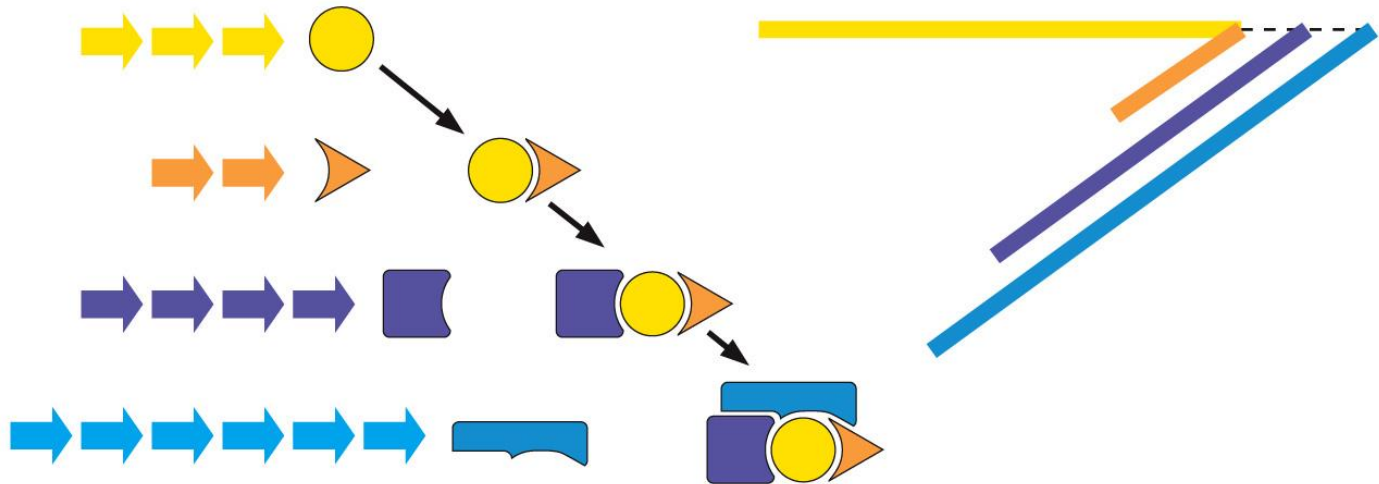


Figure 8.2a Molecular Biology of Assemblies and Machines (© Garland Science 2016)

bacteriophage T4

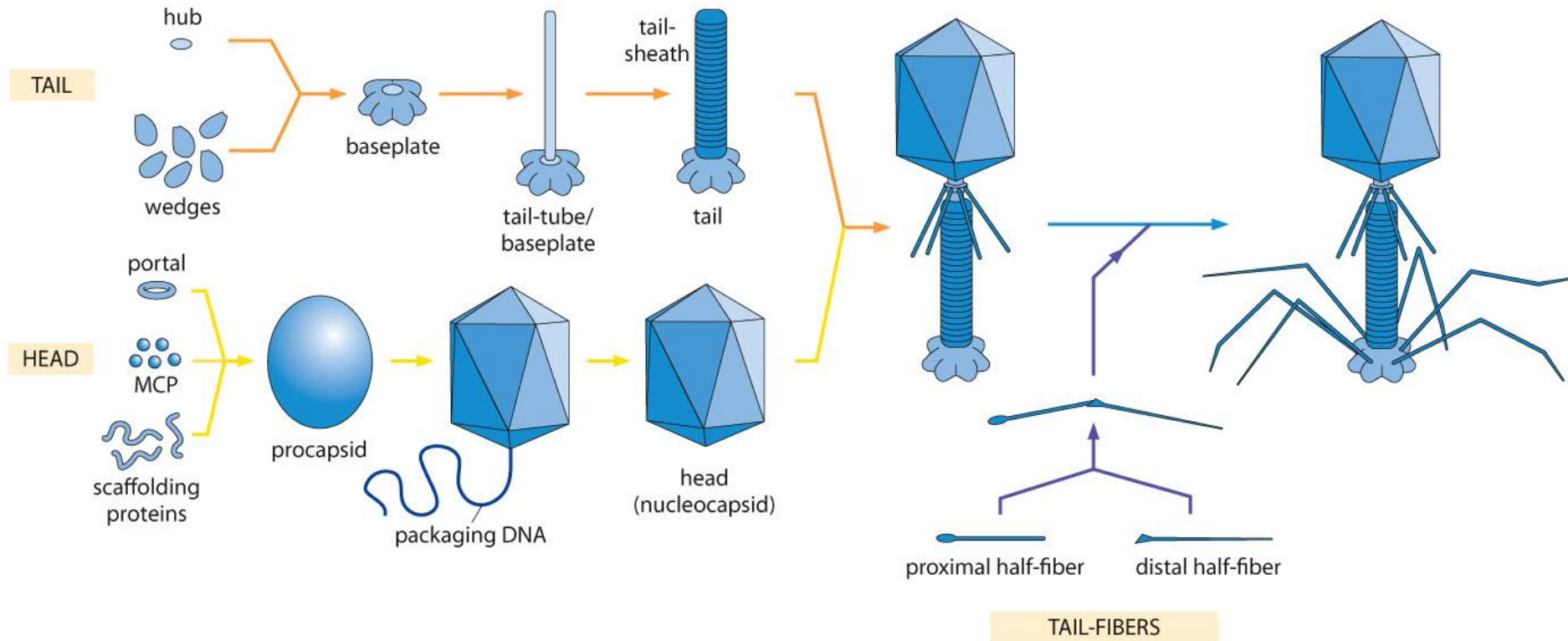


Figure 8.2b Molecular Biology of Assemblies and Machines (© Garland Science 2016)

recognition

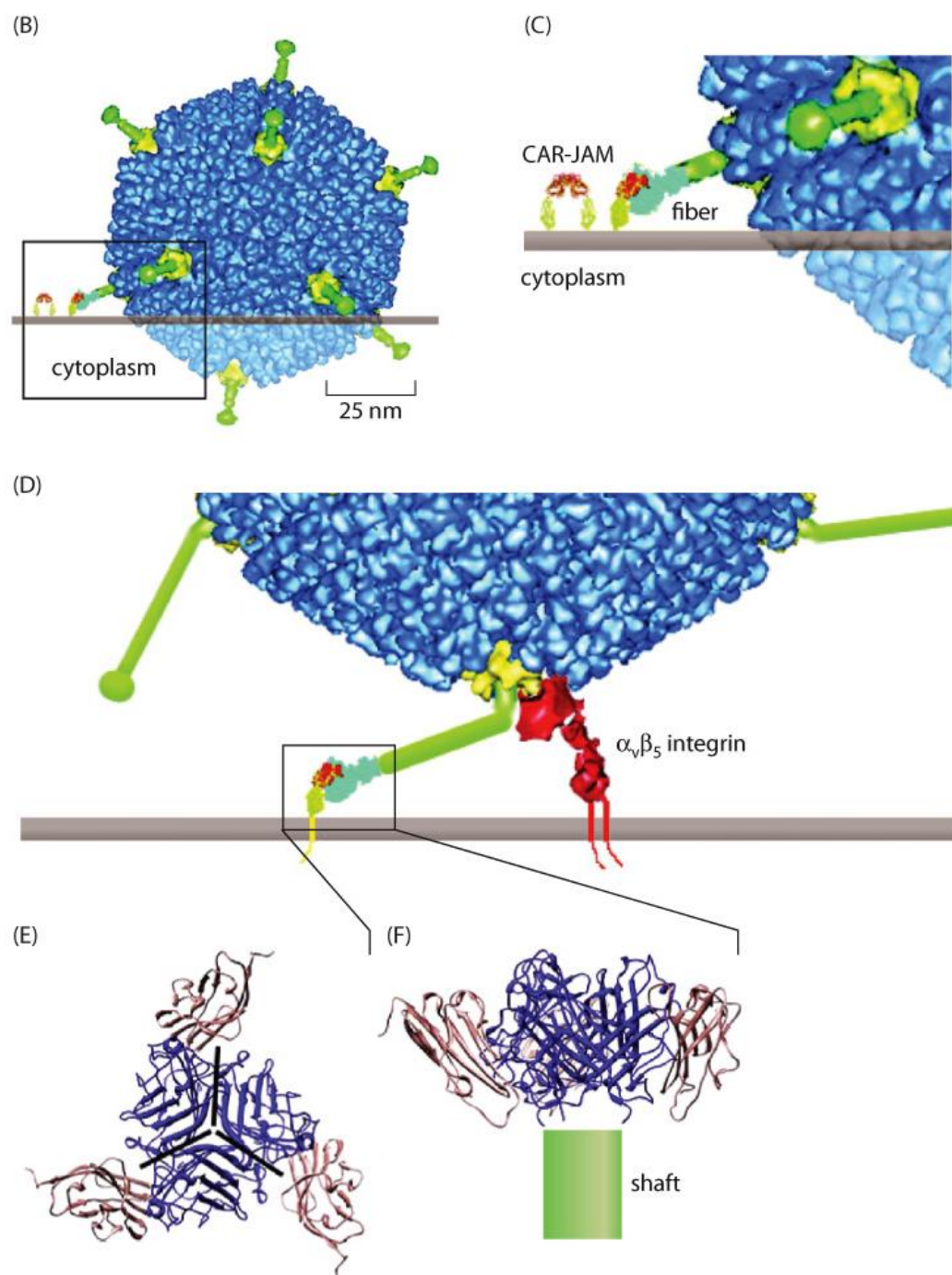
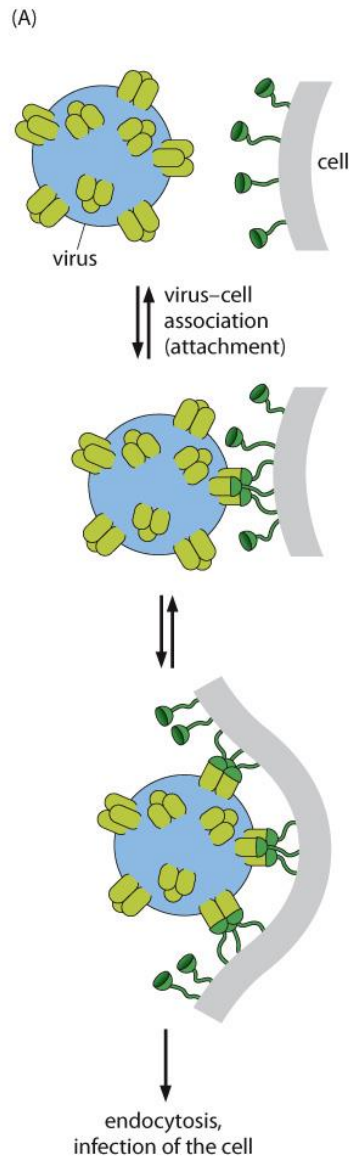
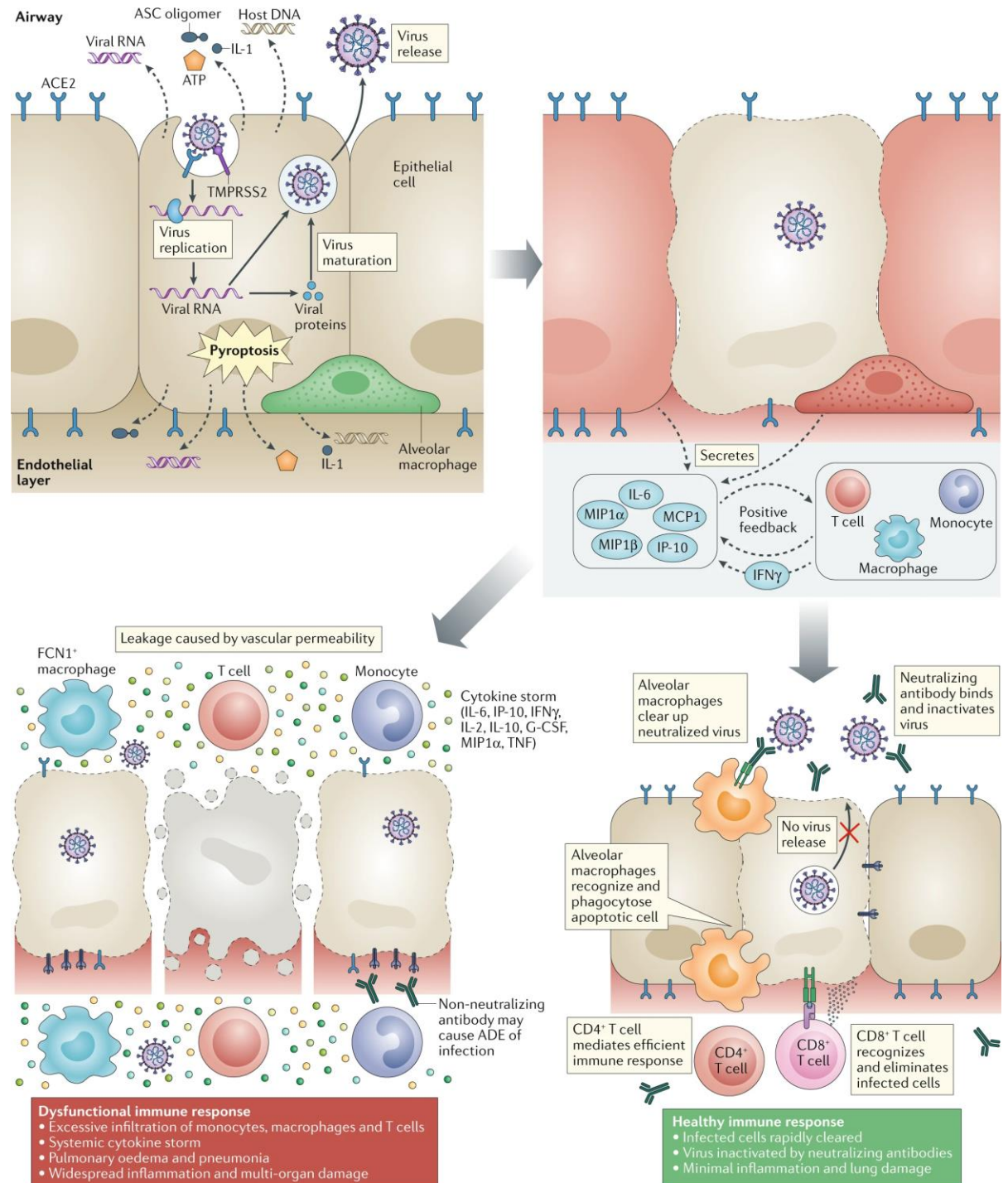


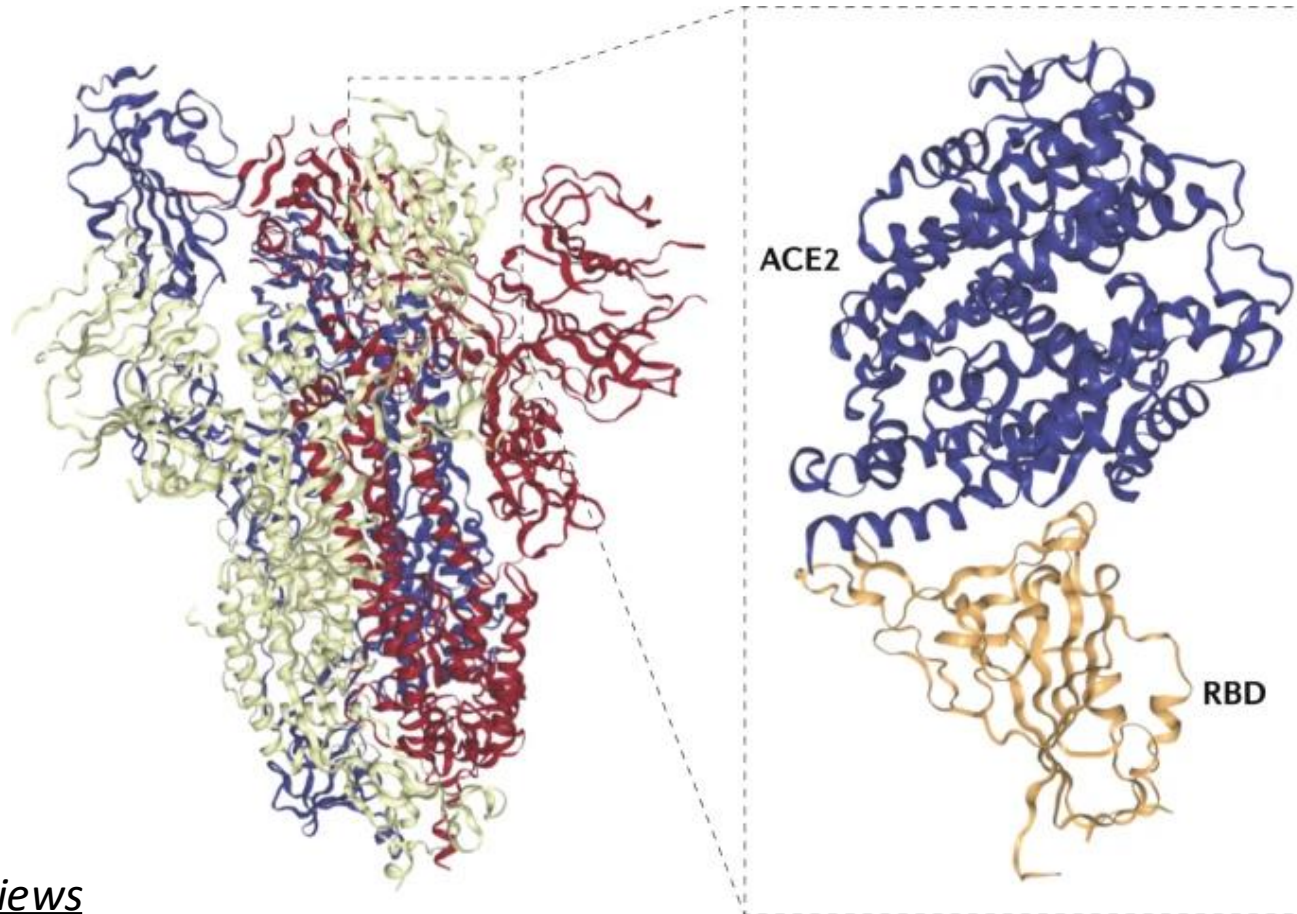
Figure 8.3 Molecular Biology of Assemblies and M.

recognition



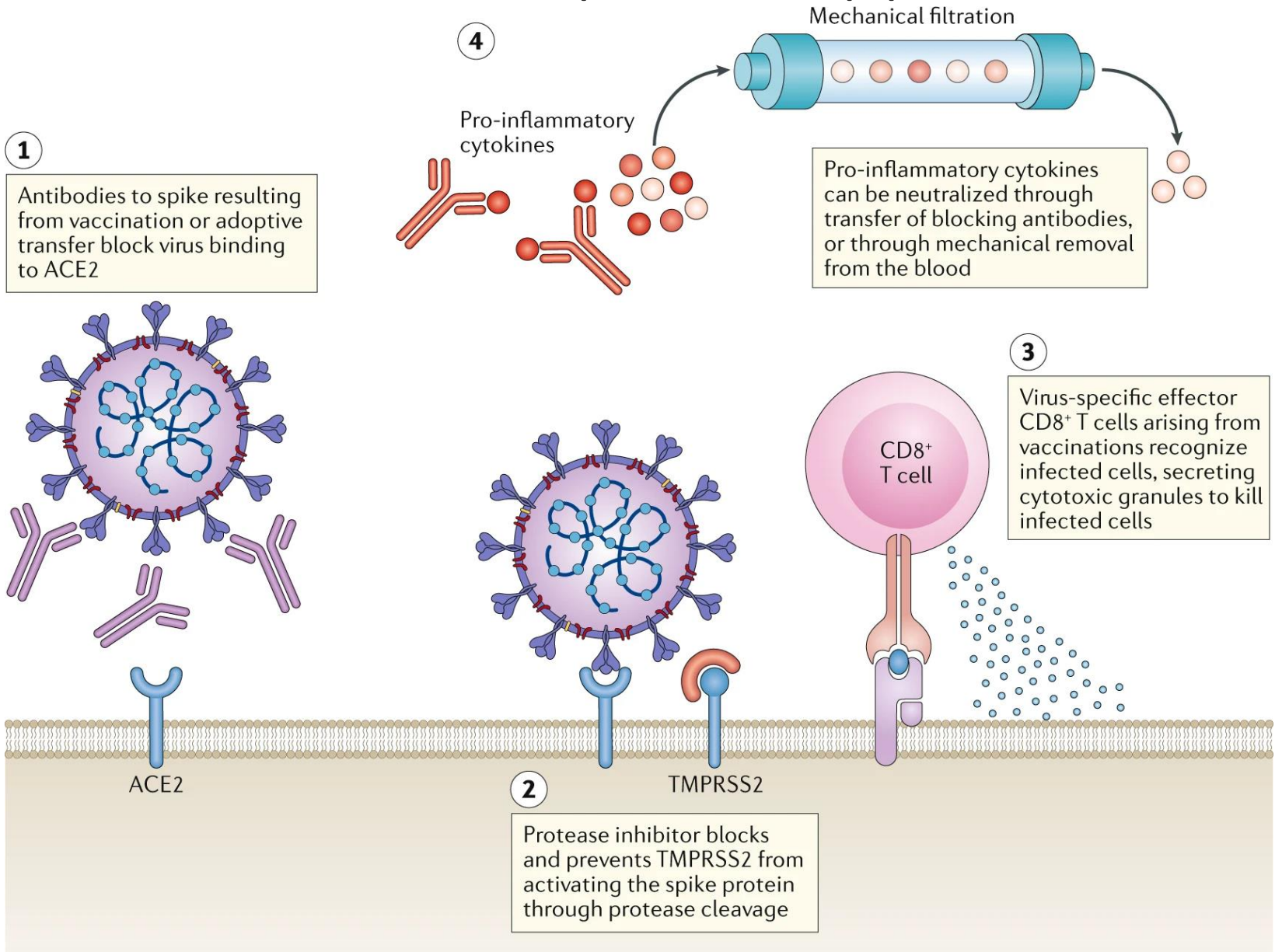
*Nature Reviews
Immunology* volume 20,
pages 363–374 (2020)

The structure of the trimeric spike protein of SARS-CoV-2.



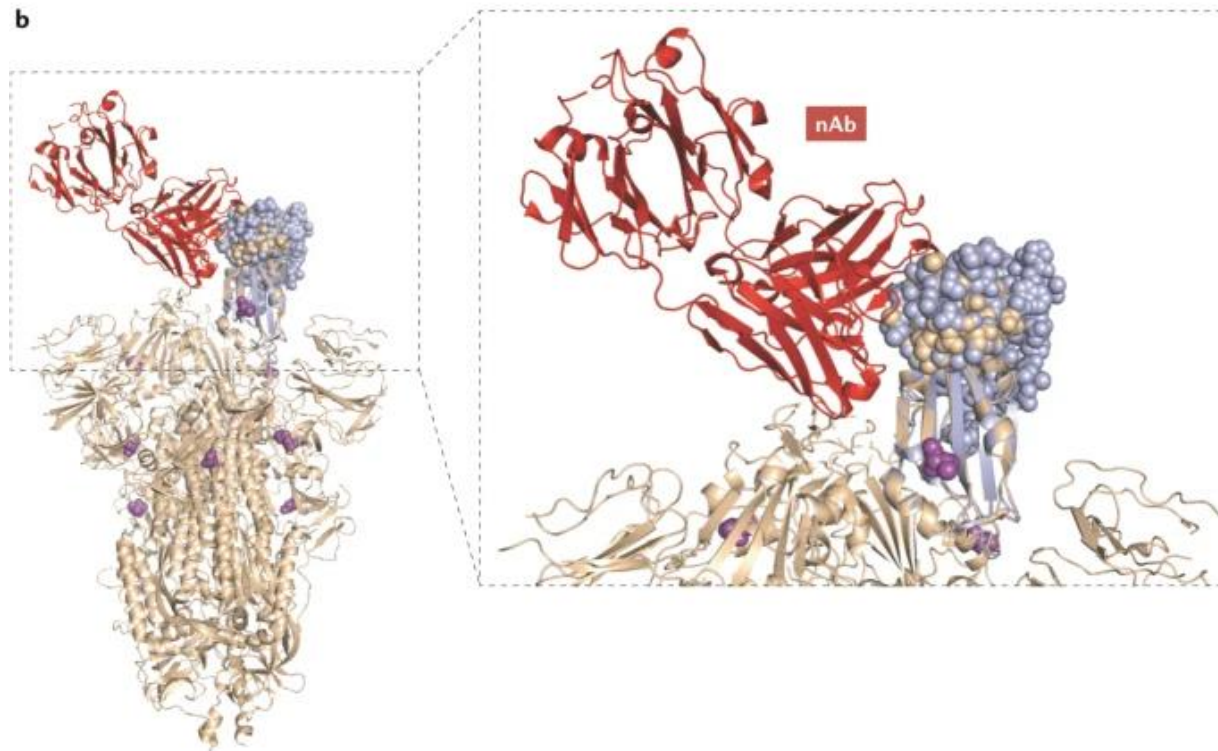
Nature Reviews
Immunology volume 20, pages 363–374
(2020)

Potential therapeutic approaches



a

SARS-CoV spike protein (316–510)	316	FPNITNLCPPFGEVFNATKFP	SVYAWERKKISNCVADYSVLYNSTFFSTFK	365
SARS-CoV-2 spike protein (338–533)	338	FPNITNLCPPFGEVFNATRFAS	SVYAWNRKRISNCVADYSVLYNSASFSTFK	387
SARS-CoV spike protein (316–510)	366	CYGVSATKLNDLCFSNVYADSFV	VKGDDVRQIAPGQTGVIADYNYKLPDD	415
SARS-CoV-2 spike protein (338–533)	388	CYGVSP	TKLNDLCFTNVYADSFVIRGDEV	RQIAPGQTGKIADYNYKLPDD 437
SARS-CoV spike protein (316–510)	416	FMGCVLAWNTRNIDATST	GNVNYKYRYLRHGKLRPFERDISNVFFSPDGK	465
SARS-CoV-2 spike protein (338–533)	438	FTGCVIAWNSNNLDSKV	GGNYYLYRLFRKSNLKPFERDISTEIQAGST	487
SARS-CoV spike protein (316–510)	466	PCT-PPALNCYWPLNDYGFYTTT	TGIGYQPYRVVVLSEFLLNAPATV	510
SARS-CoV-2 spike protein (338–533)	488	PCNGVEGFNCYFPLQSYGFQPT	NGVGYPYRVVVLSEFLLHAPATV	533

b

Icosahedral Symmetry

In 1953, Crick & Watson proposed principles of virus structure

Key insight:

Limited volume of virion capsid => nucleic acid sufficient to code for only a few sorts of proteins of limited size

Conclusion:

Identical subunits in identical environments

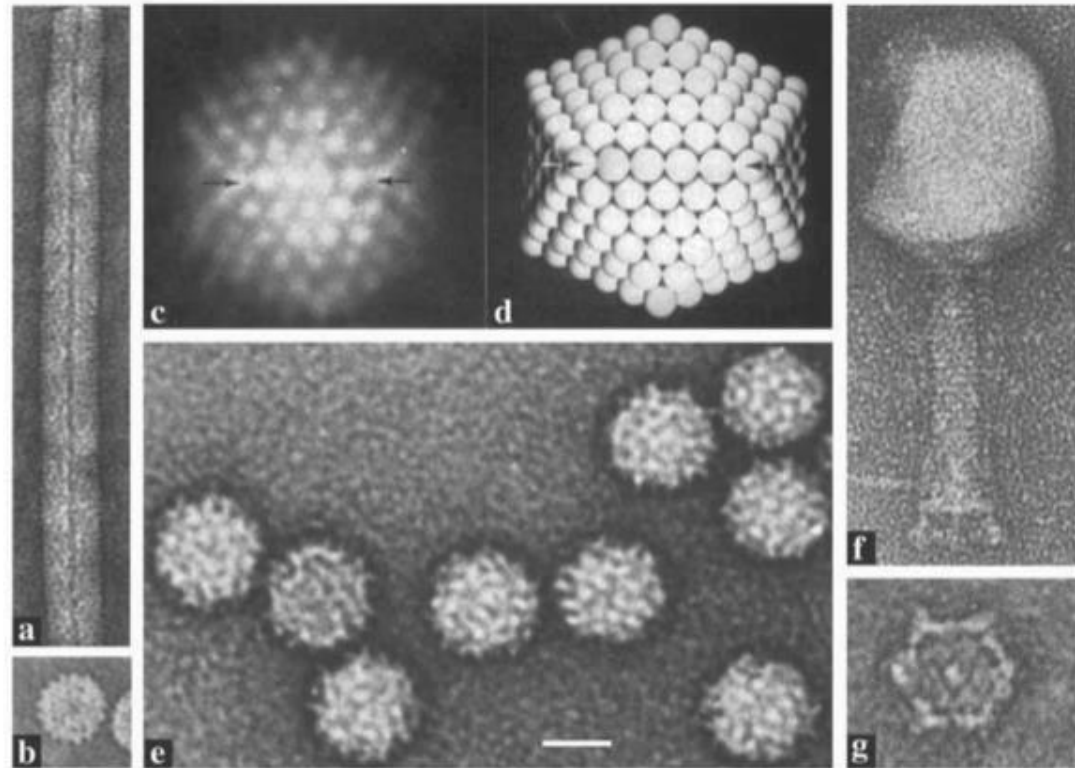
Icosahedral, dodecahedral symmetry

In 50's & 60's Klug and others confirmed that several (unrelated) "spherical" viruses had icosahedral symmetry

- (Used negative staining & electron microscopy)

• Conclusion:

- Icosahedral symmetry is preferred in virus structure



Icosahedral Symmetry



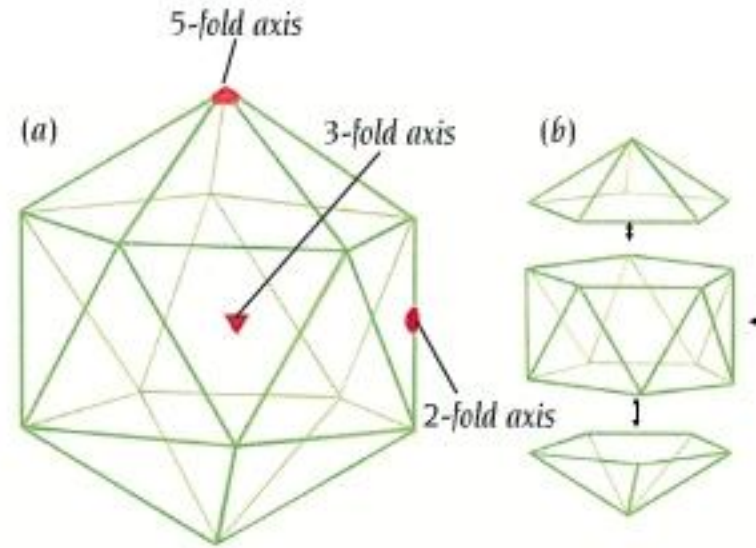
3-fold



5-fold



2-fold



12 vertices

20 faces (equilateral triangles)

5-3-2 symmetry axes

60 identical* subunits
in identical environments
can form icosahedral shell
* asymmetric

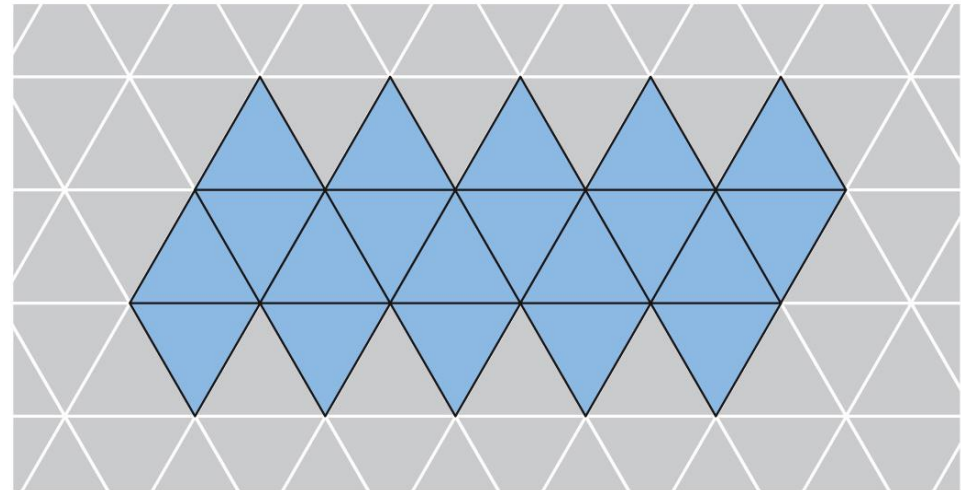


Figure 8.6 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

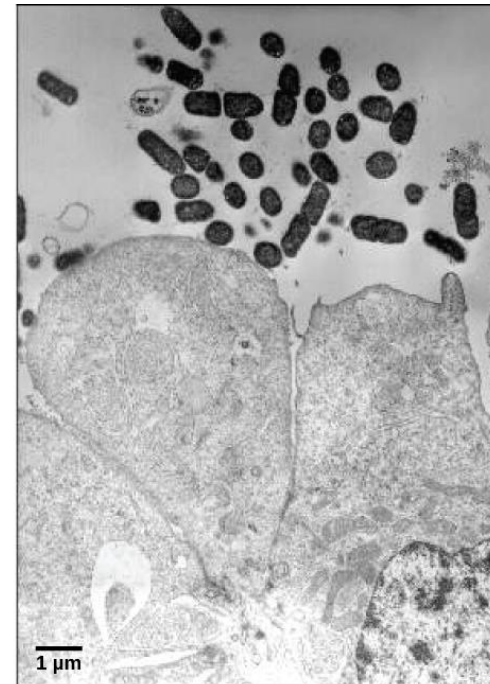
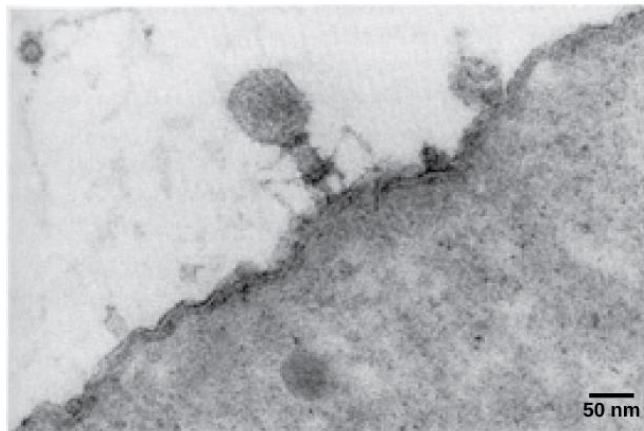
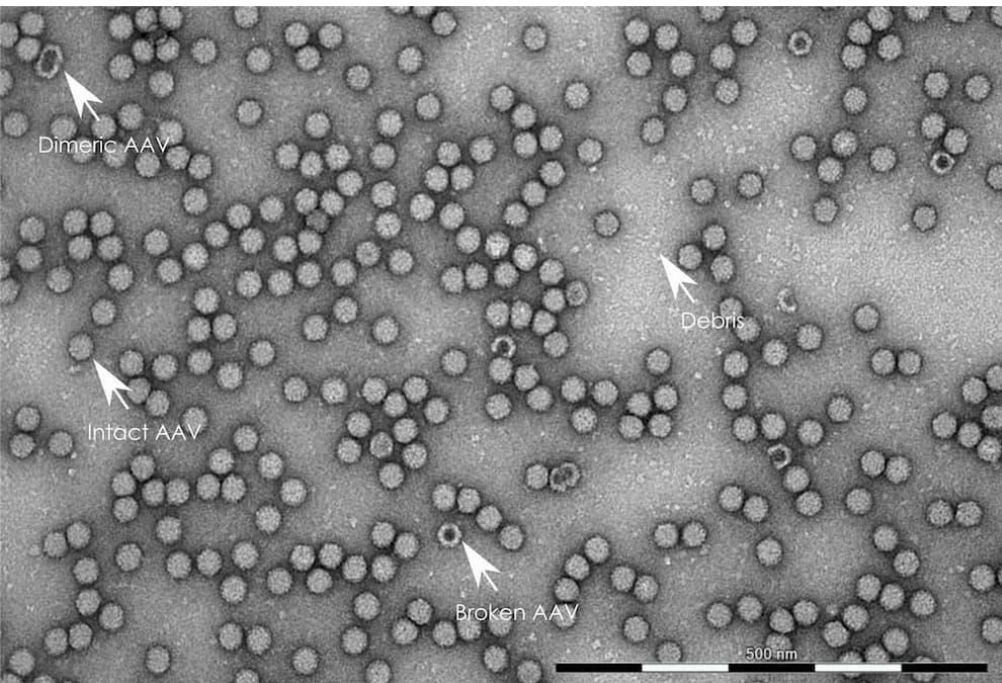
But ...

- Clear evolutionary pressure to make larger capsid
 - Using larger subunits helps very little
 - Using more subunits helps a lot
- Not possible to form icosahedral shell (of identical units in identical environments) with more than 60 subunits
- Viruses with more than 60 subunits were observed
- In 1962, Caspar & Klug proposed the theory of “quasi-equivalence”
 - Not all protein subunits are equivalent
 - “Identical” subunits in slightly different environments
 - Only certain numbers of subunits will can be packed into closed regular lattice.

X-ray Crystallography of Viruses

- Symmetry of protein shells makes them uniquely well-suited to crystallographic methods
- Viruses are the largest assemblies of biological macromolecules whose structures have been determined at high resolution

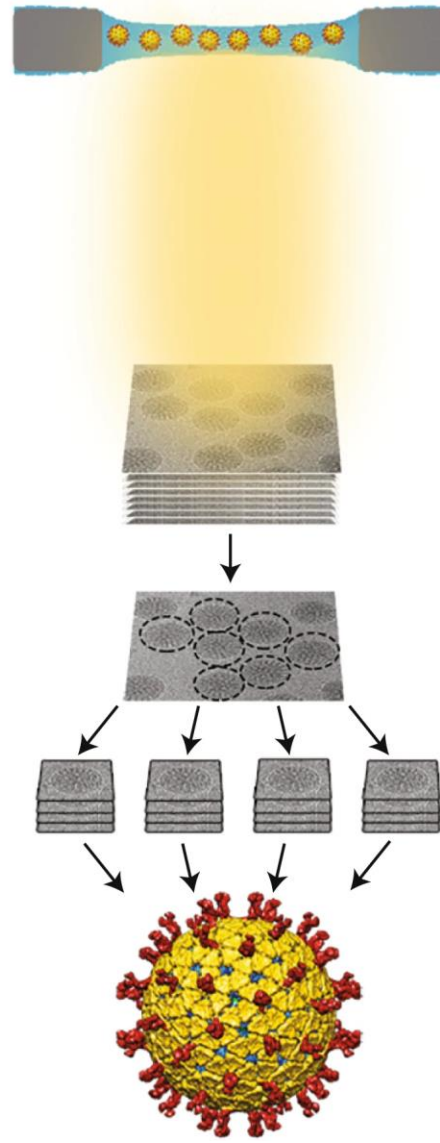
Electron Microscopy



Electron Microscopy

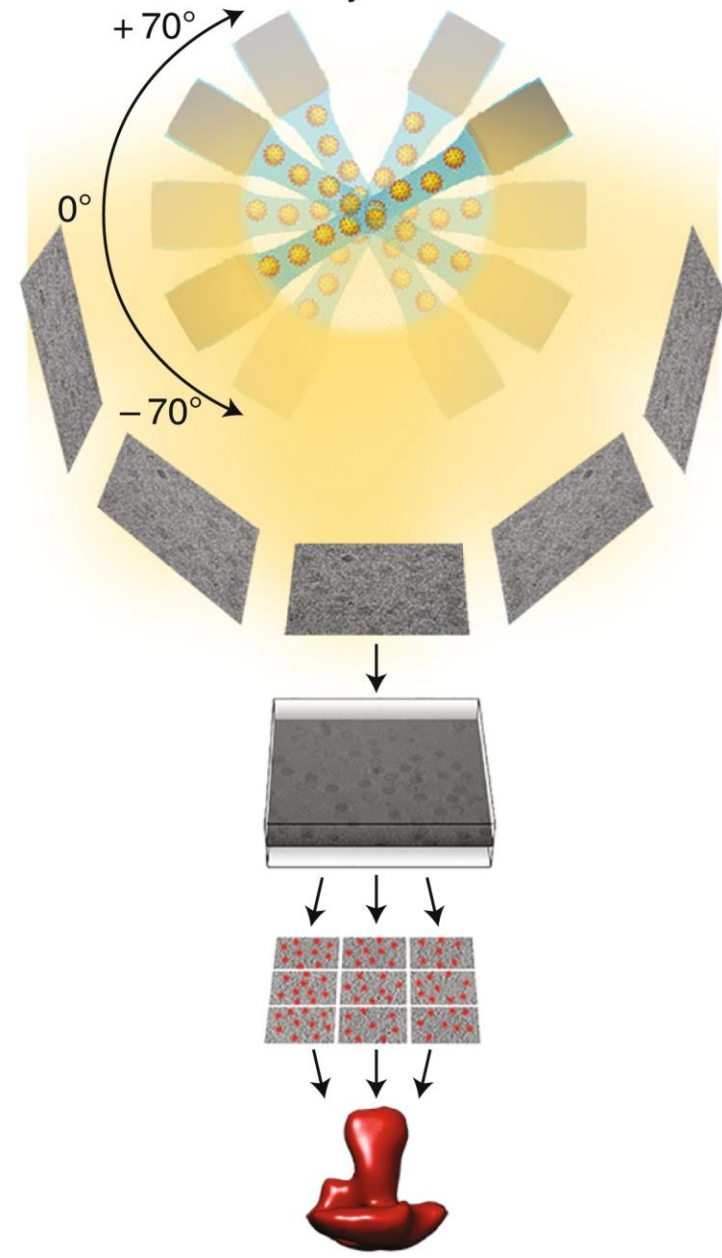
a

Cryo-EM

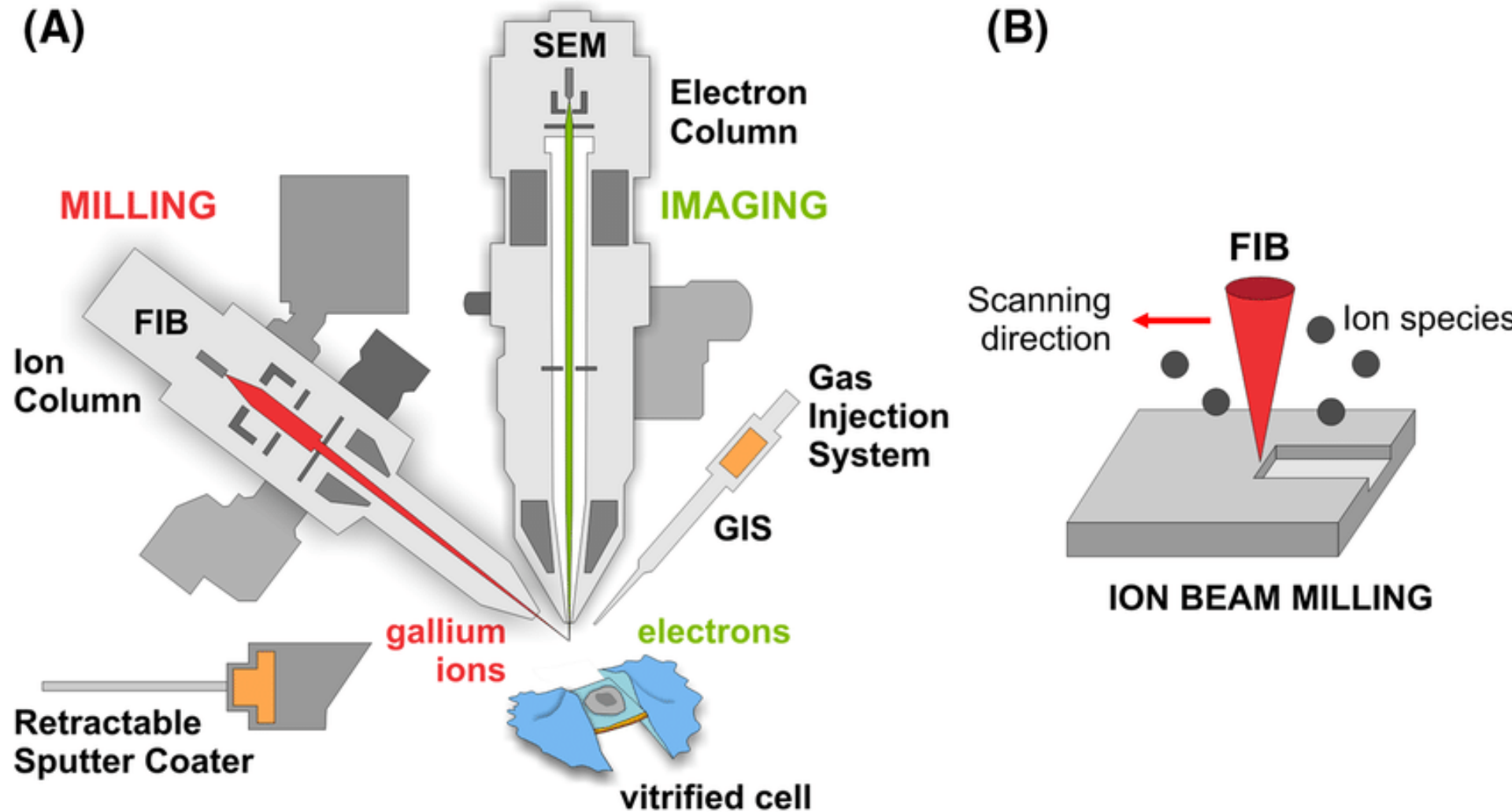


b

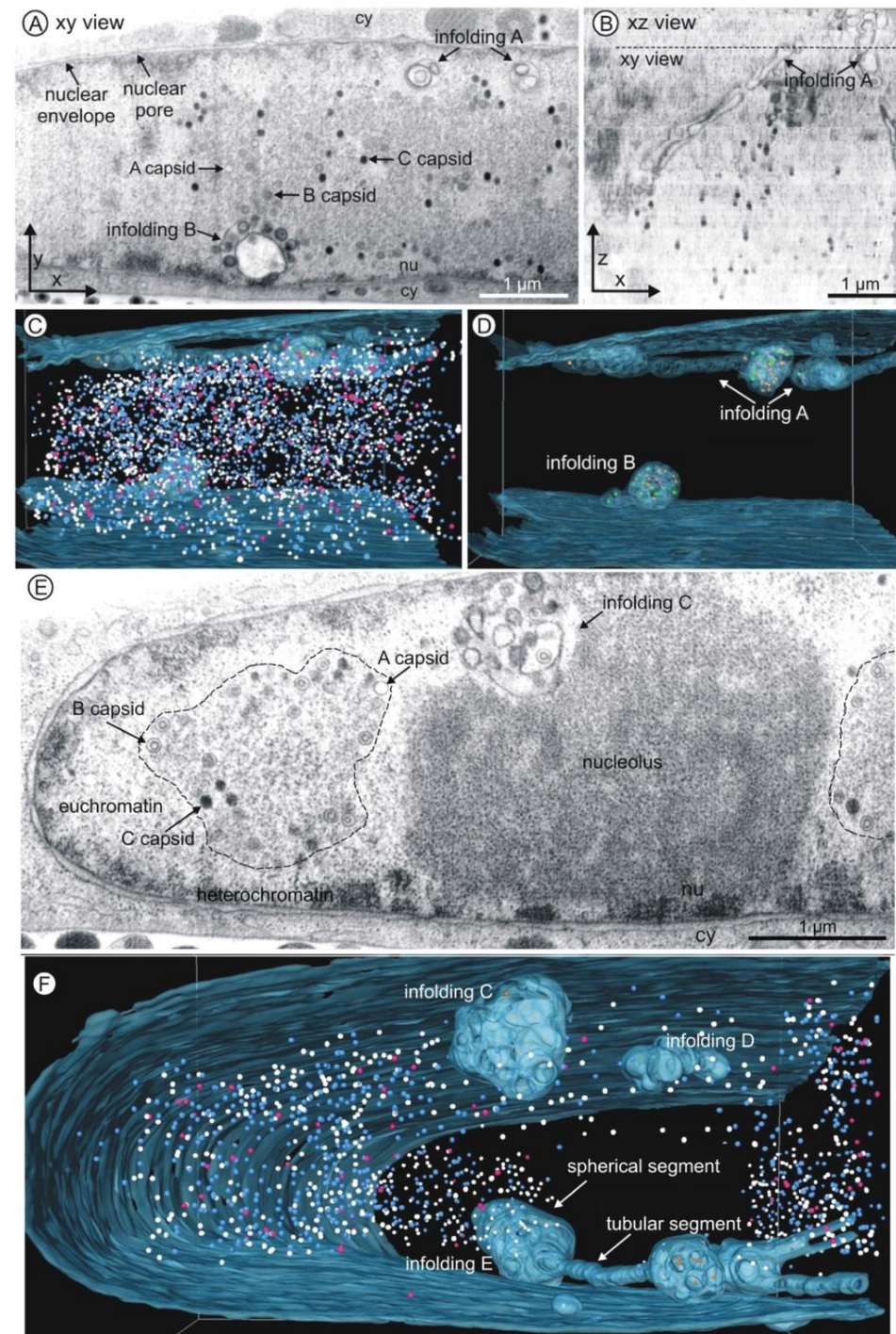
Cryo-ET



focused ion beam

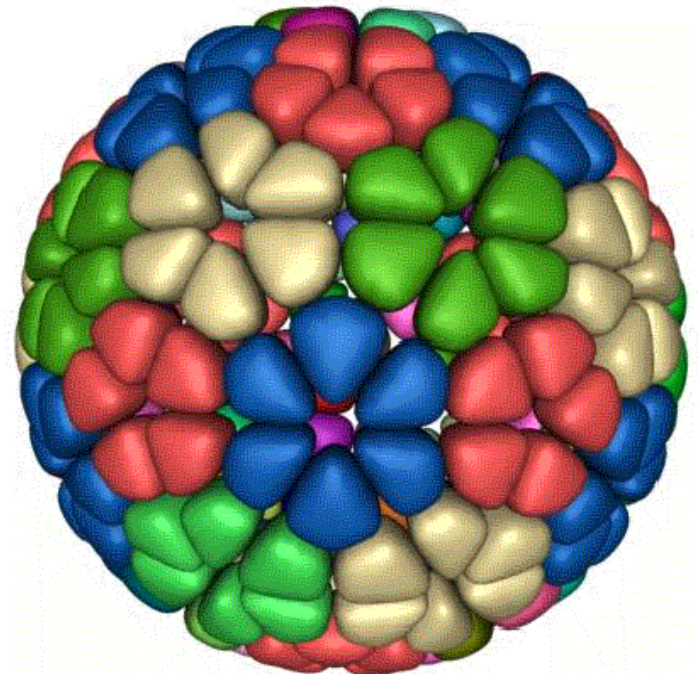
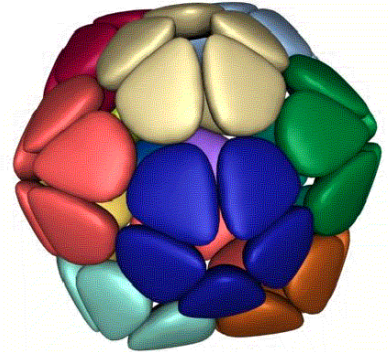


FIB/SEM tomography of an HCMV infected nucleus



Quasi-equivalence

- Subunits are in “minimally” different environments
 - Pentamers at vertices
 - Hexamers elsewhere
- Predicts packing arrangements of larger capsids
 - Shift from T1 to T4 packing
=> 8-fold increase in volume



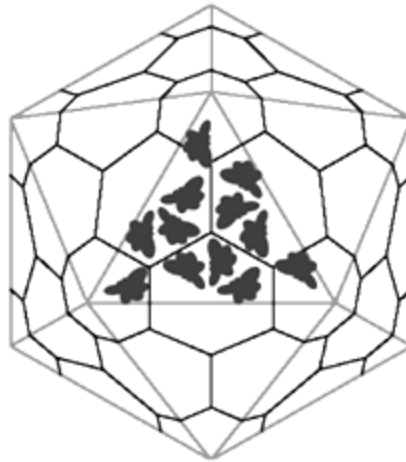
Spherical viruses have icosahedral symmetry



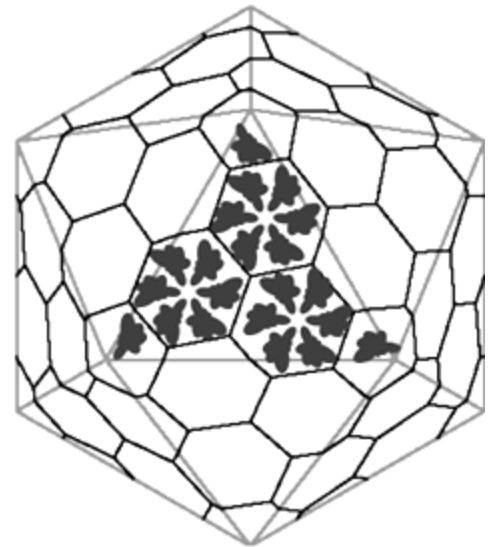
T=1



T=3



T=4

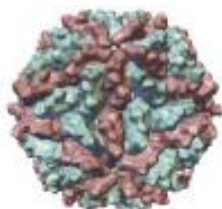


T=7

Goldberg diagram



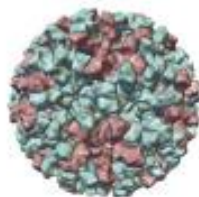
CPV T=1 286 Å
Picorna PDB 2CAS



L-A T=1 440 Å
BTV PDB 1M1C



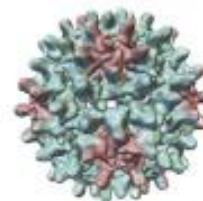
MS2 T=3 288 Å
PDB 2MS2



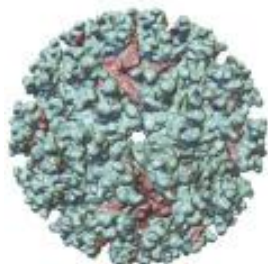
Norwalk T=3 400 Å
Picorna PDB 1IHM



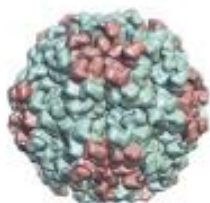
HRV14 P=3 322 Å
Picorna PDB 4RHV



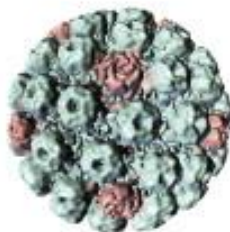
Hep-B T=4 332 Å
PDB 1QGT



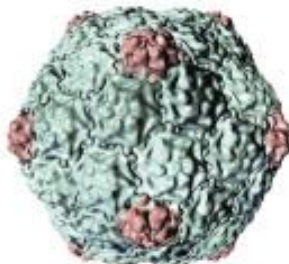
ChikV T=4 672 Å
ENV PDB 6NK5



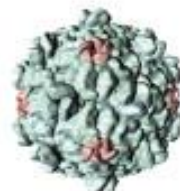
NWV T=4 432 Å
Picorna PDB 1OHF



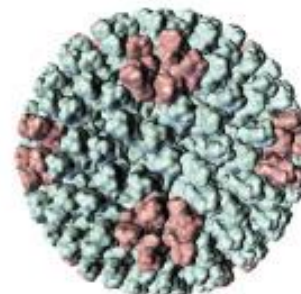
SV40 T=7d 494 Å
Picorna PDB 1SVA



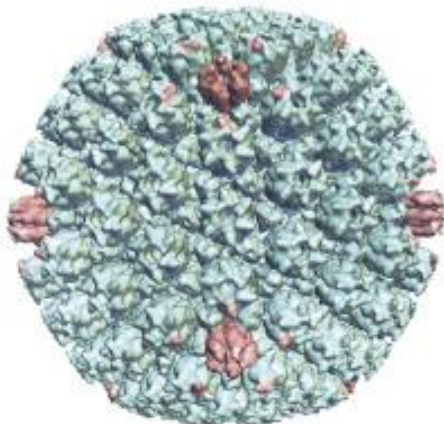
HK97 T=7l 660 Å
HK97 PDB 1OHG



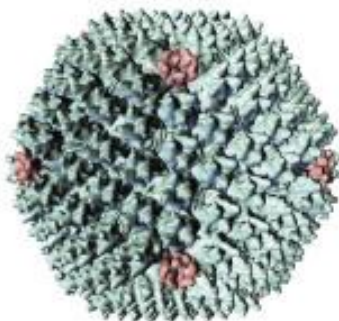
Ba Micro T=9 414 Å
PDB 6MZX



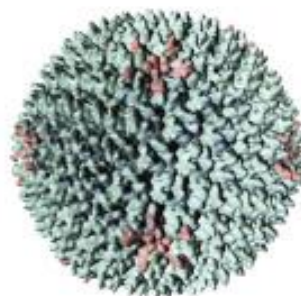
BTV T=13 705 Å
BTV PDB 2BTV



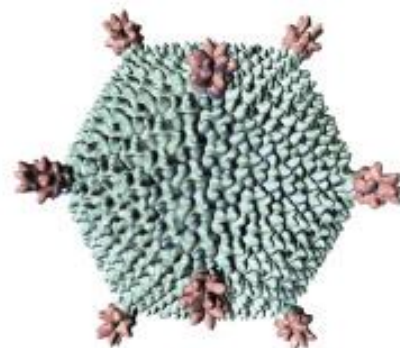
HSV T=16 1300 Å
HK97 PDB 5ZAP



Adeno P=25 940 Å
PRD1 PDB 6CVG



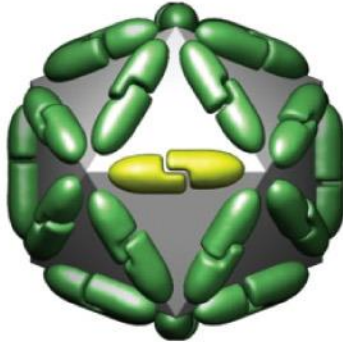
HCIV P=28d 850 Å
PRD1 PDB 6H9C



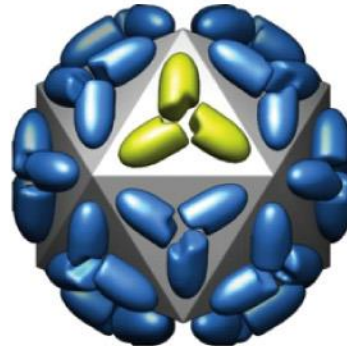
STIV P=31 970 Å
PRD1 PDB 3J31

Icosahedral capsids

(A)



(B)



(C)

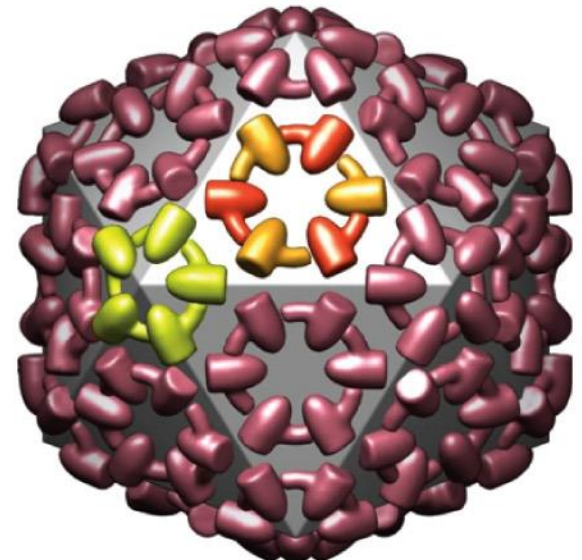
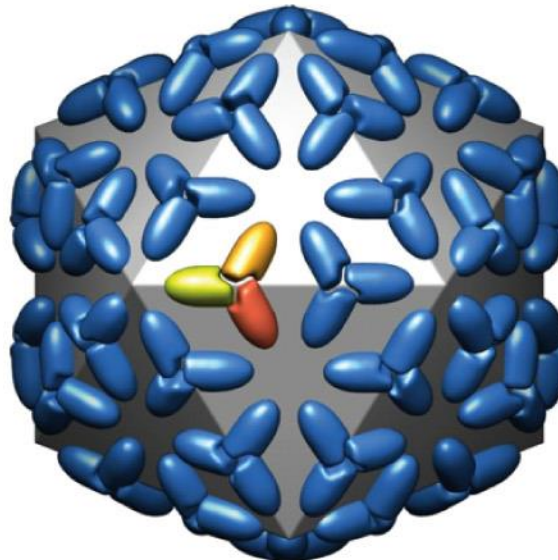
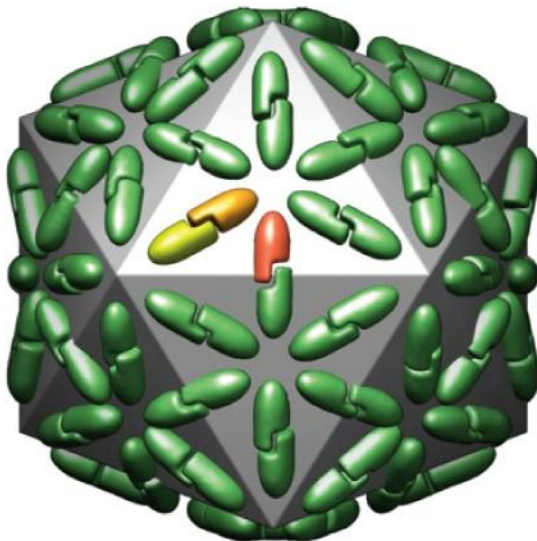
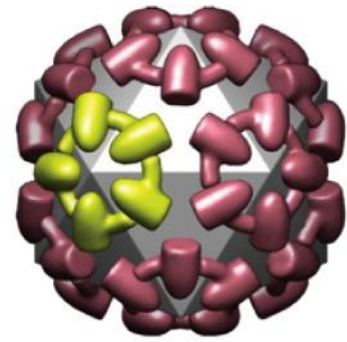


Figure 8.8 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

interactions between complementary surface patches

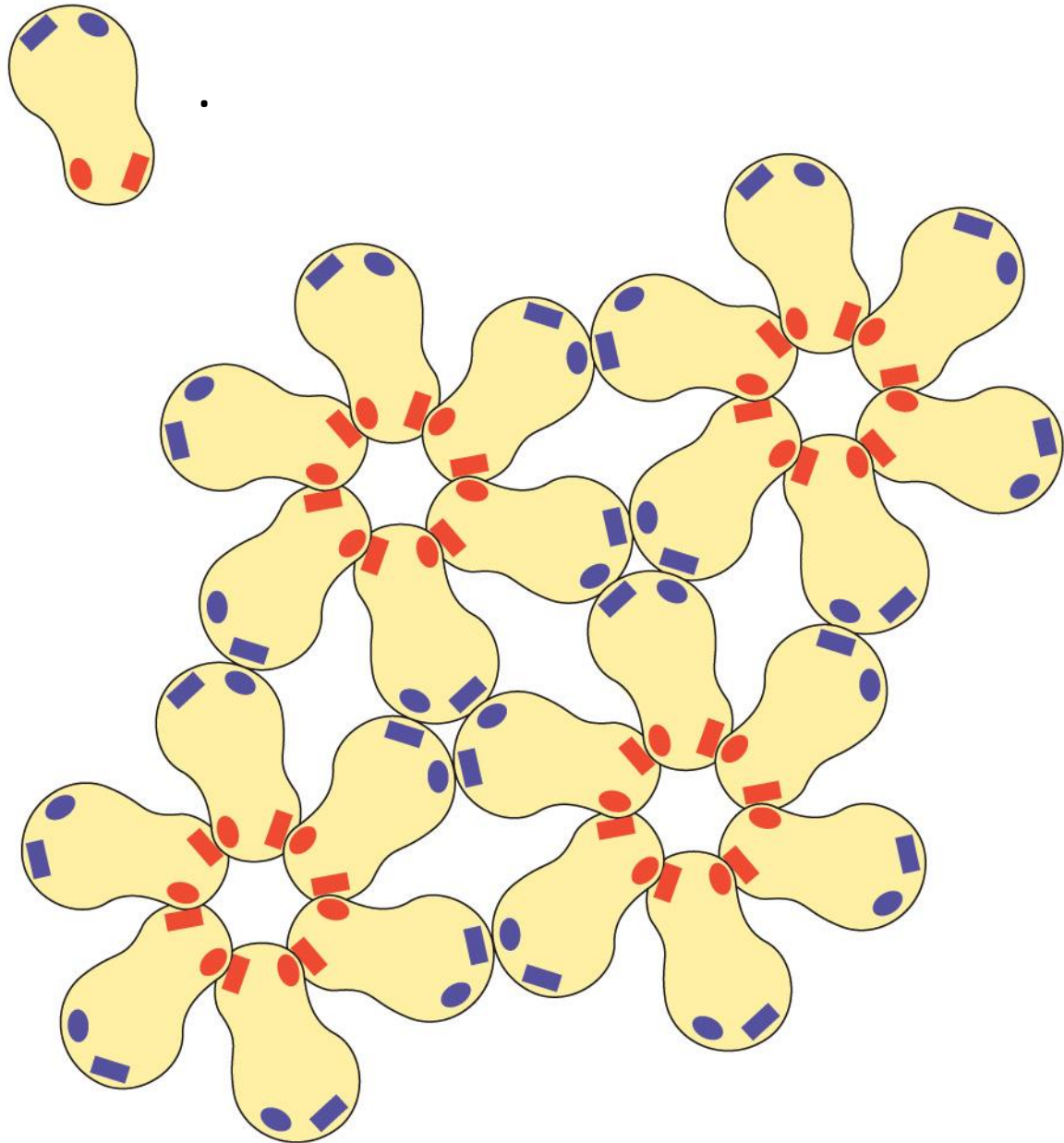


Figure 8.13 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Helical viruses

tobacco mosaic virus (TMV)

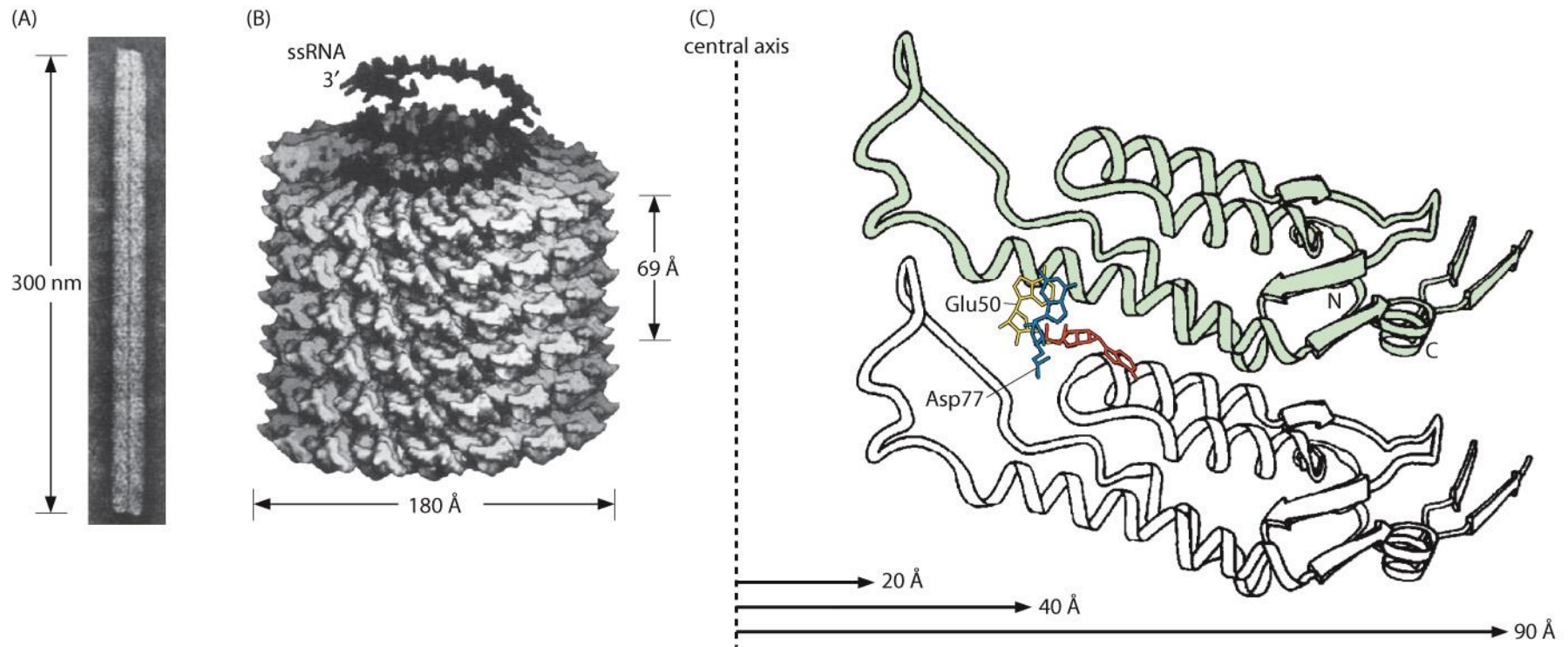
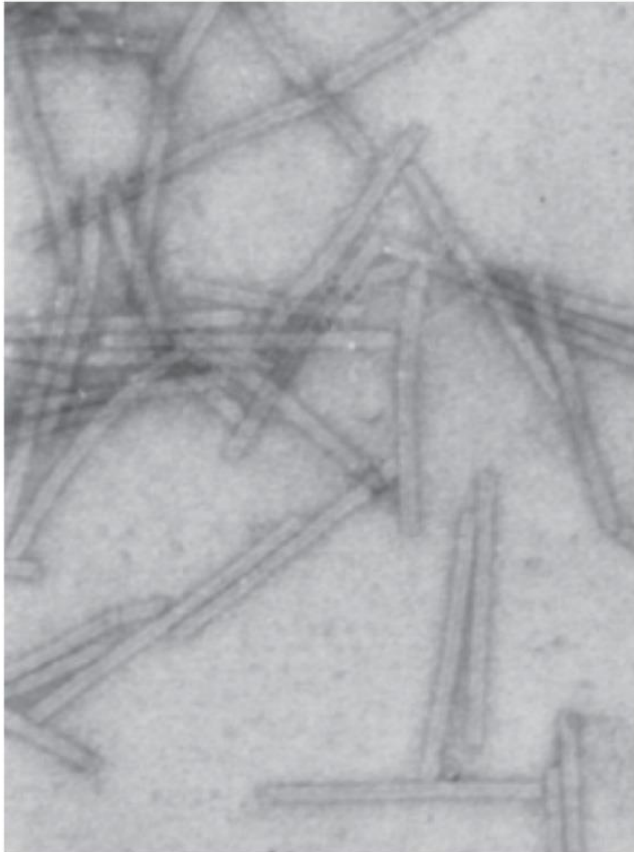


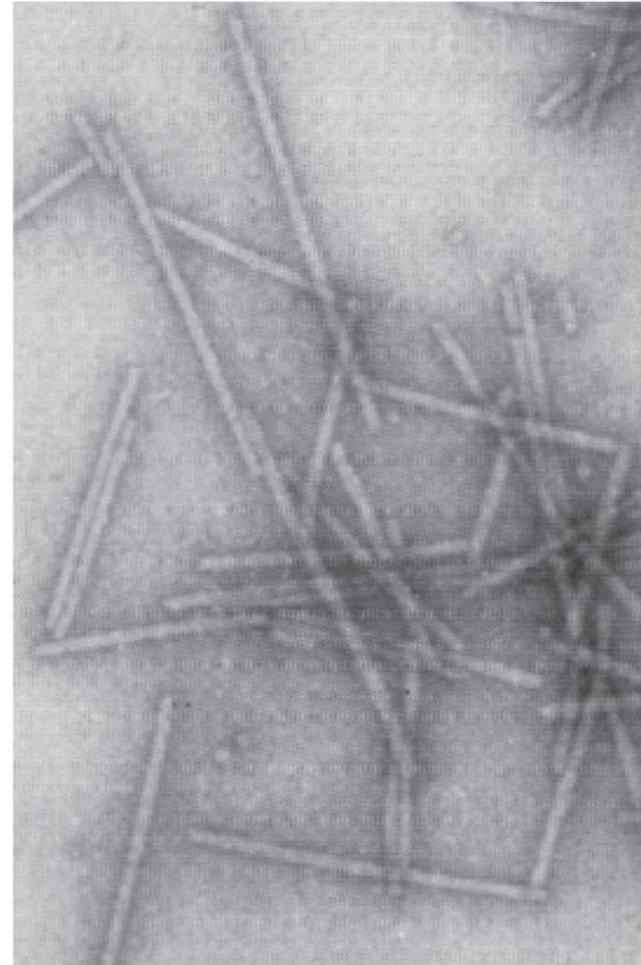
Figure 8.15 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Helical viruses

with RNA



without RNA

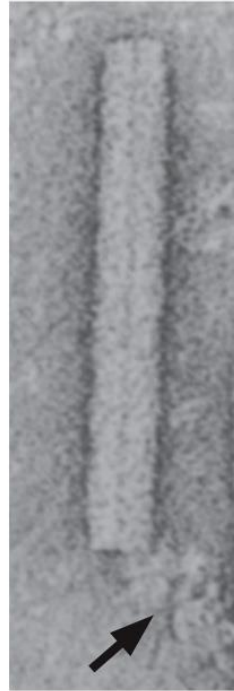


300 nm

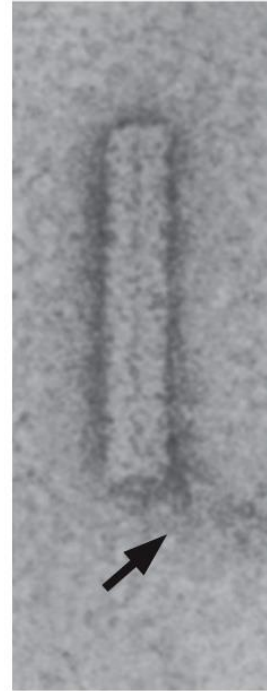
Figure 8.16 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Disassembly of TMV

(A)



high pH



detergent

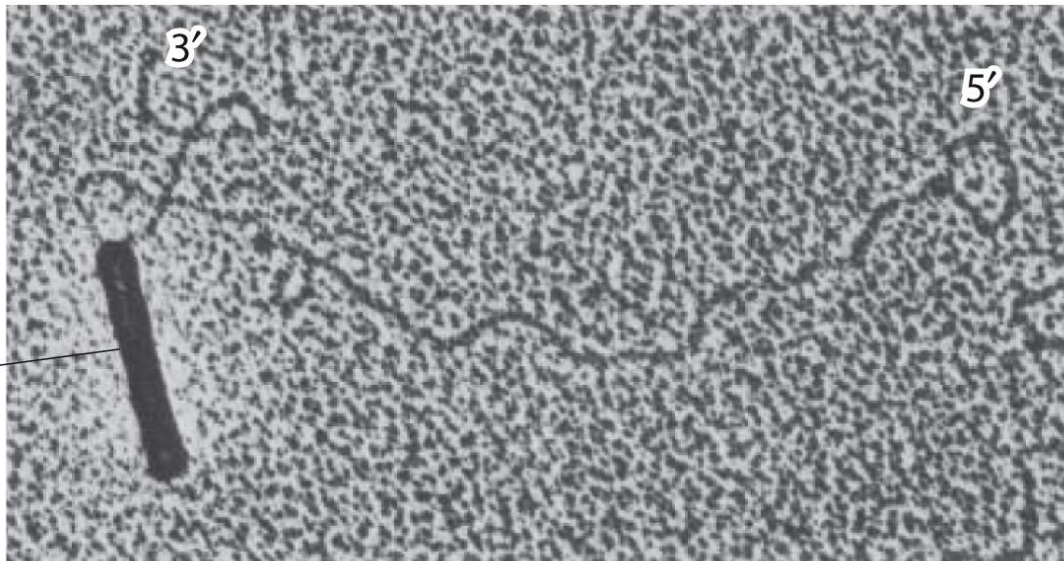
25 nm

(B)



ribosome-mediated
disassembly

Assembly of TMV



nucleoprotein
rod

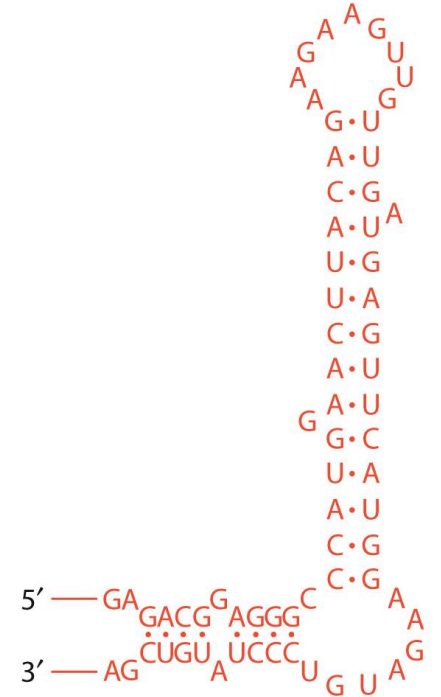
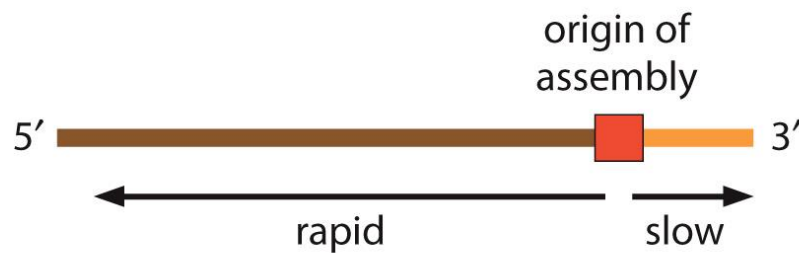


Figure 8.18a Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Assembly of TMV

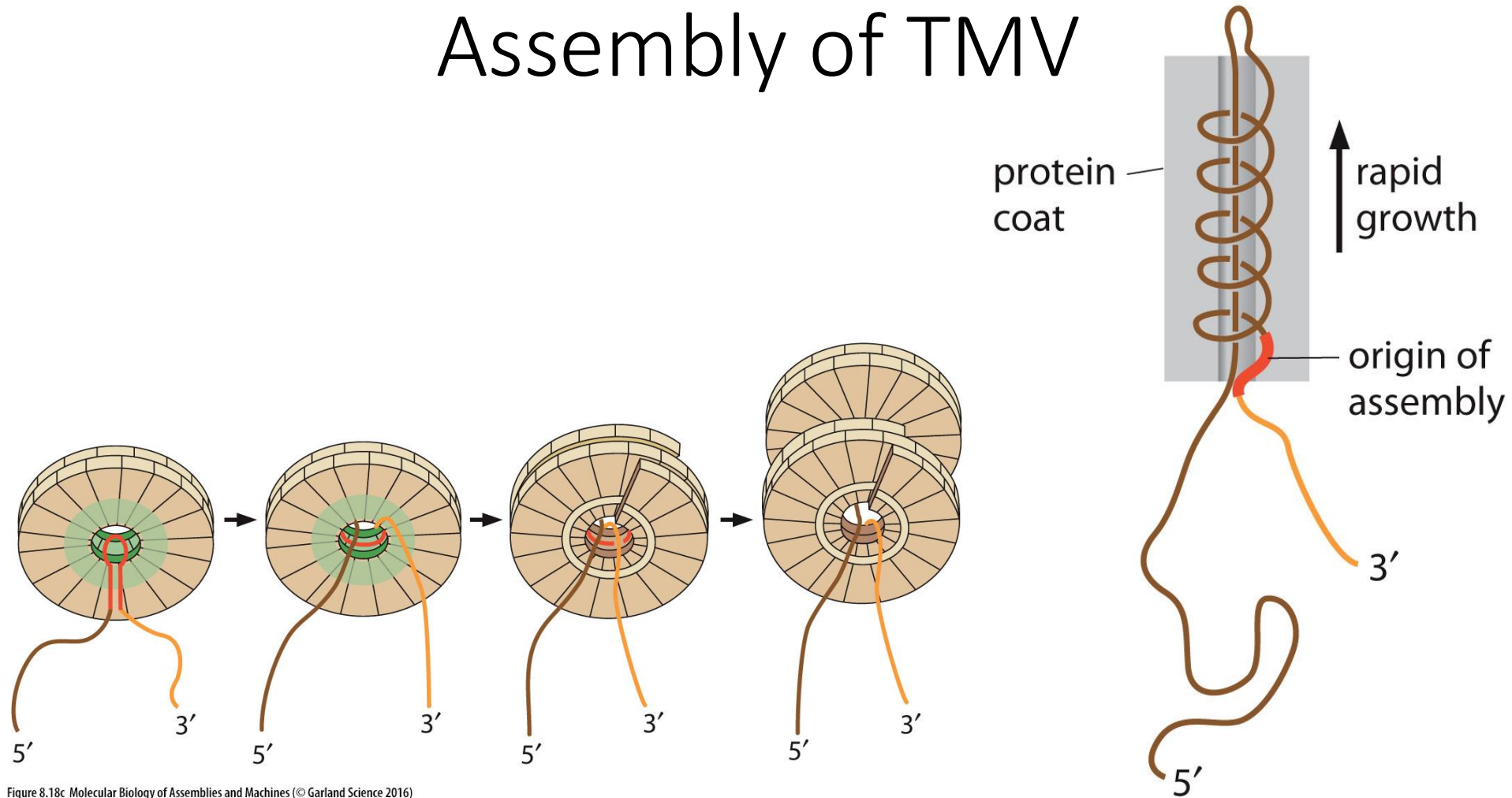
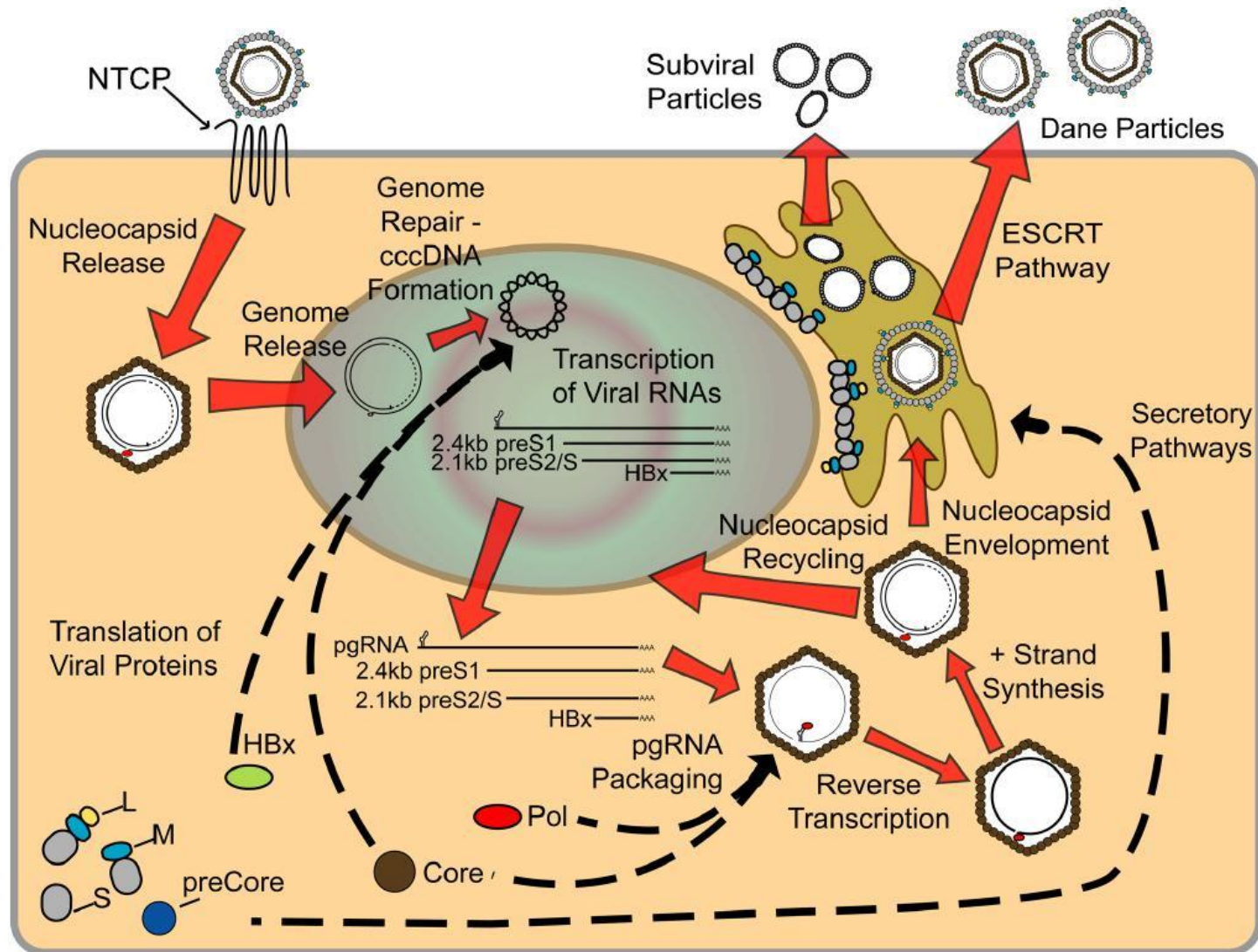


Figure 8.18c Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Figure 8.18d Molecular Biology of Assemblies and Machines (© Garland Science 2016)

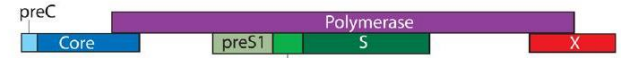
hepatitis B virus life cycle



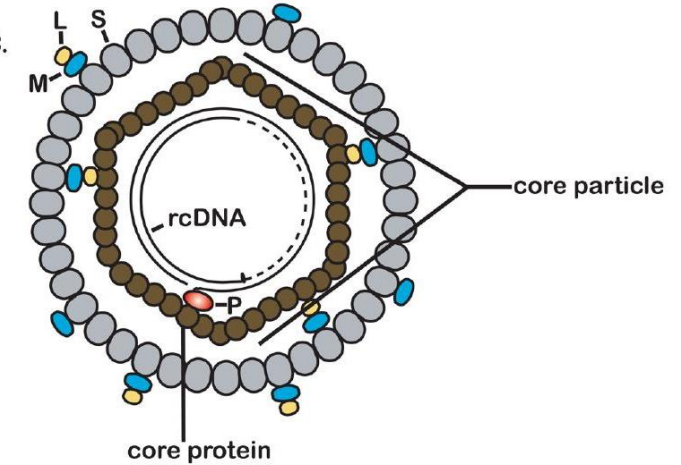
small Icosahedral viruses

hepatitis B virus

B.



C.



(B)

end of ORF C (MCP coding sequence)

Gln.Ser.Arg.Glu.Ser.Gln.Cys
 CAA.TCT.CGG.GAA.TCT.CAA.TGT.TAG.TAT.TCC.TTG.GAC.TCA.
 .AAT.CTC.GGG.AAT.CTC.AAT.GTT.AGT.ATT.CCT.TGG.ACT.CAT
 .Leu.Gly.Asn.Leu.Asn.Val.Ser.Ile.Pro.Trp.Thr.His

part of ORF P (polymerase coding sequence)

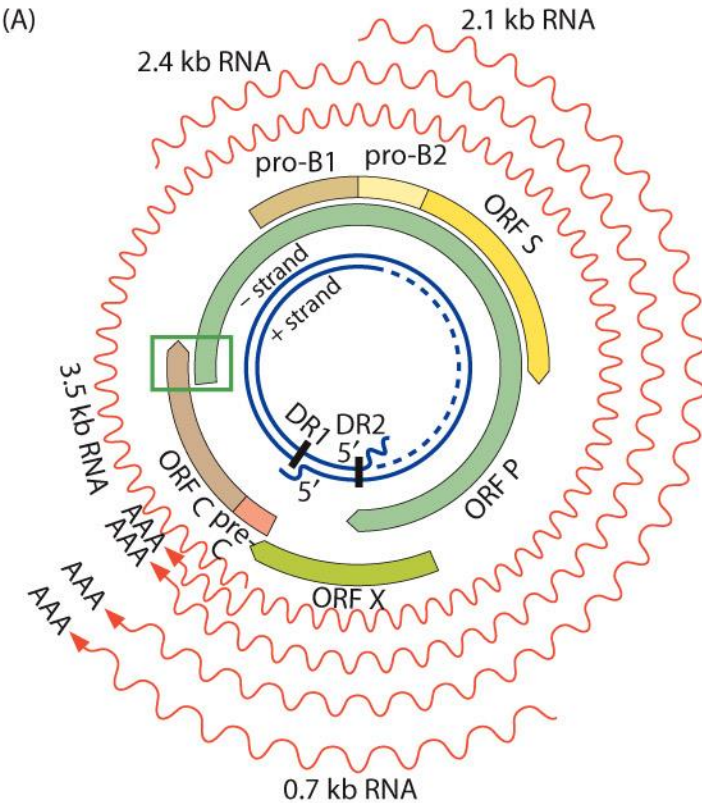
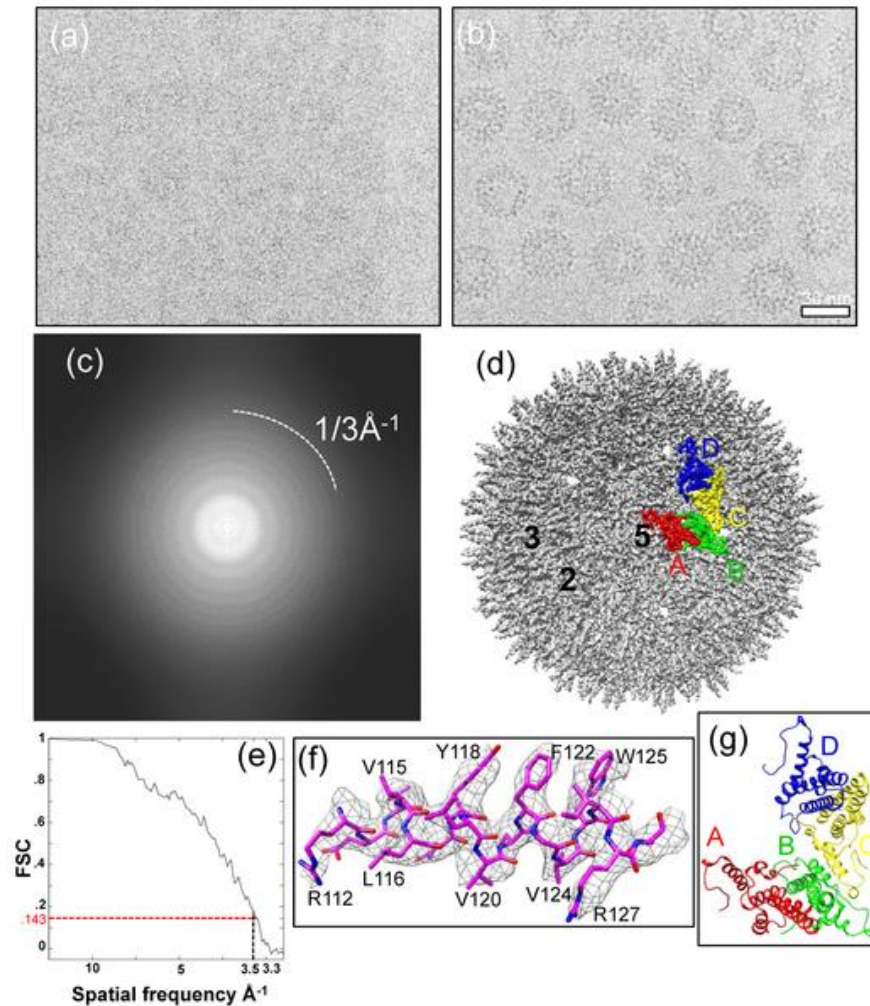
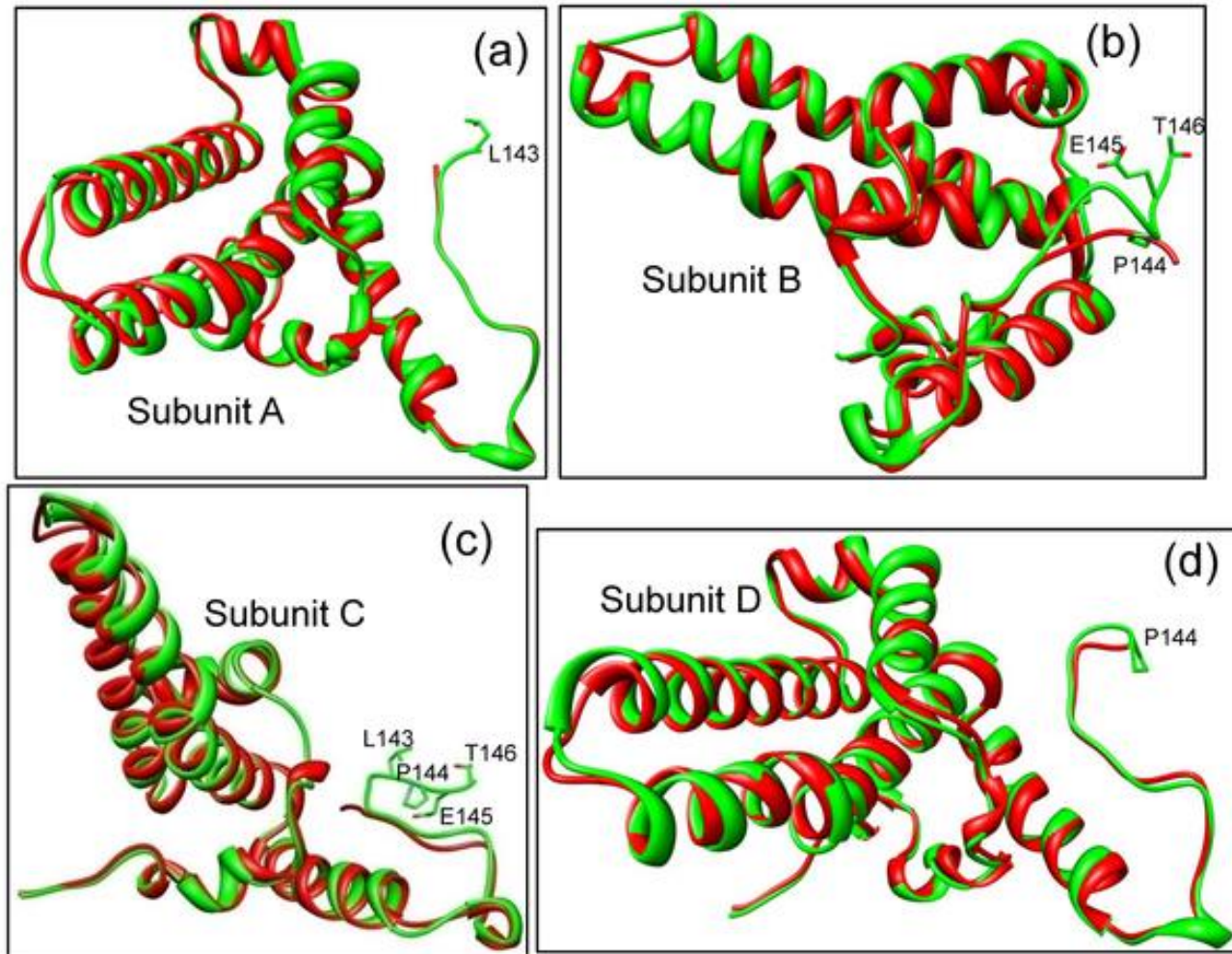


Figure 1. CryoEM and 3D reconstruction of hepatitis B virus (HBV) core assembled from full-length HBV core proteins at 3.5Å resolution.



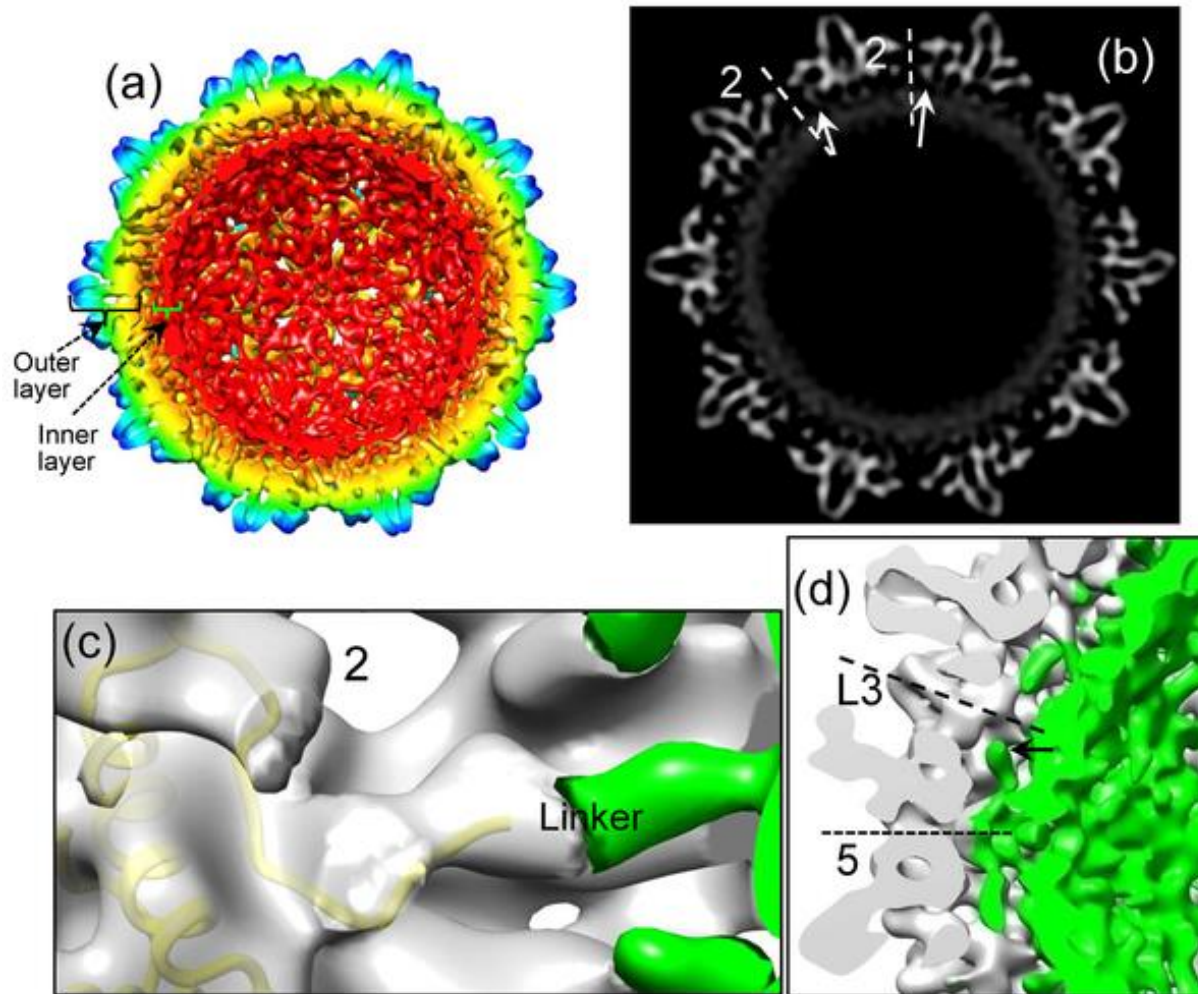
Yu X, Jin L, Jih J, Shih C, Hong Zhou Z (2013) 3.5Å cryoEM Structure of Hepatitis B Virus Core Assembled from Full-Length Core Protein. PLOS ONE 8(9): e69729. <https://doi.org/10.1371/journal.pone.0069729>
<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0069729>

Figure 2. Comparisons between corresponding cryoEM structures (green) and crystal structures (red) by superimposition.



Yu X, Jin L, Jih J, Shih C, Hong Zhou Z (2013) 3.5Å cryoEM Structure of Hepatitis B Virus Core Assembled from Full-Length Core Protein. PLOS ONE 8(9): e69729. <https://doi.org/10.1371/journal.pone.0069729>
<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0069729>

Figure 4. Maps of HBV core reconstruction filtered to 10Å resolution.



Yu X, Jin L, Jih J, Shih C, Hong Zhou Z (2013) 3.5Å cryoEM Structure of Hepatitis B Virus Core Assembled from Full-Length Core Protein. PLOS ONE 8(9): e69729. <https://doi.org/10.1371/journal.pone.0069729>
<https://journals.plos.org/plosone/article?id=10.1371/journal.pone.0069729>

neutron diffraction

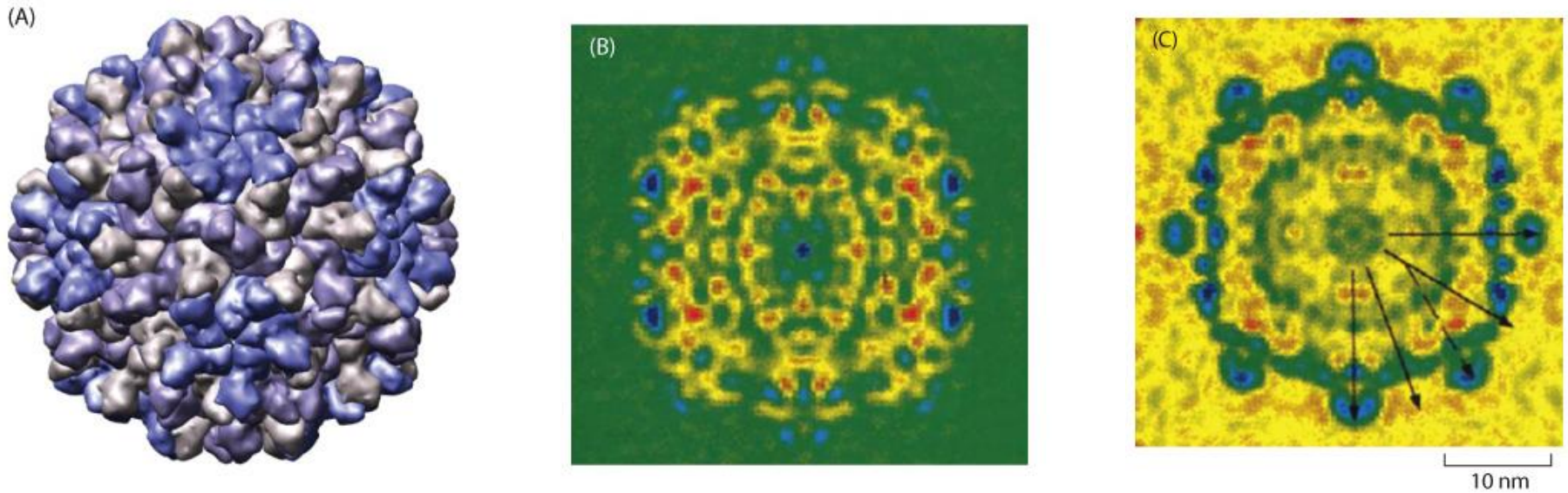
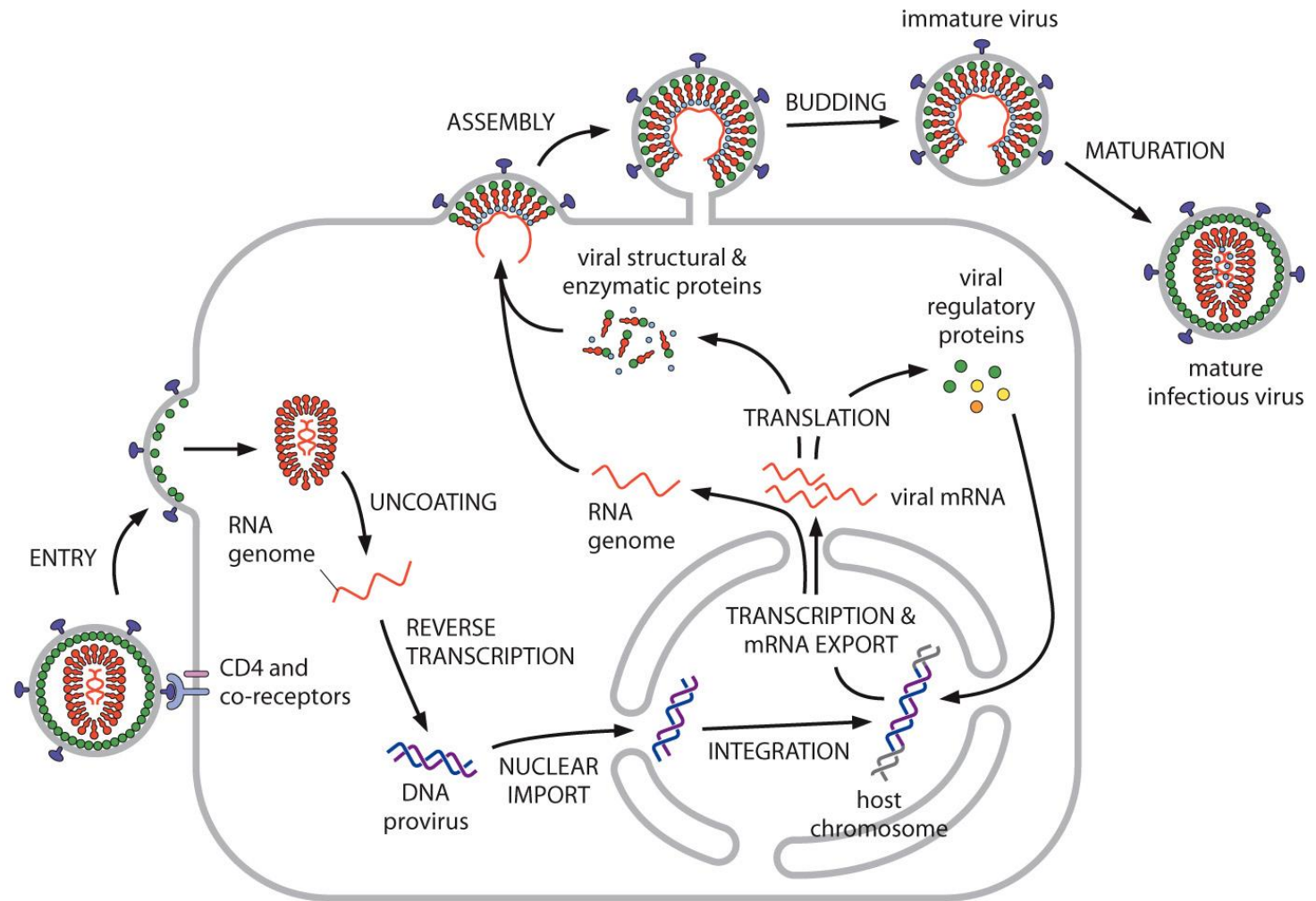
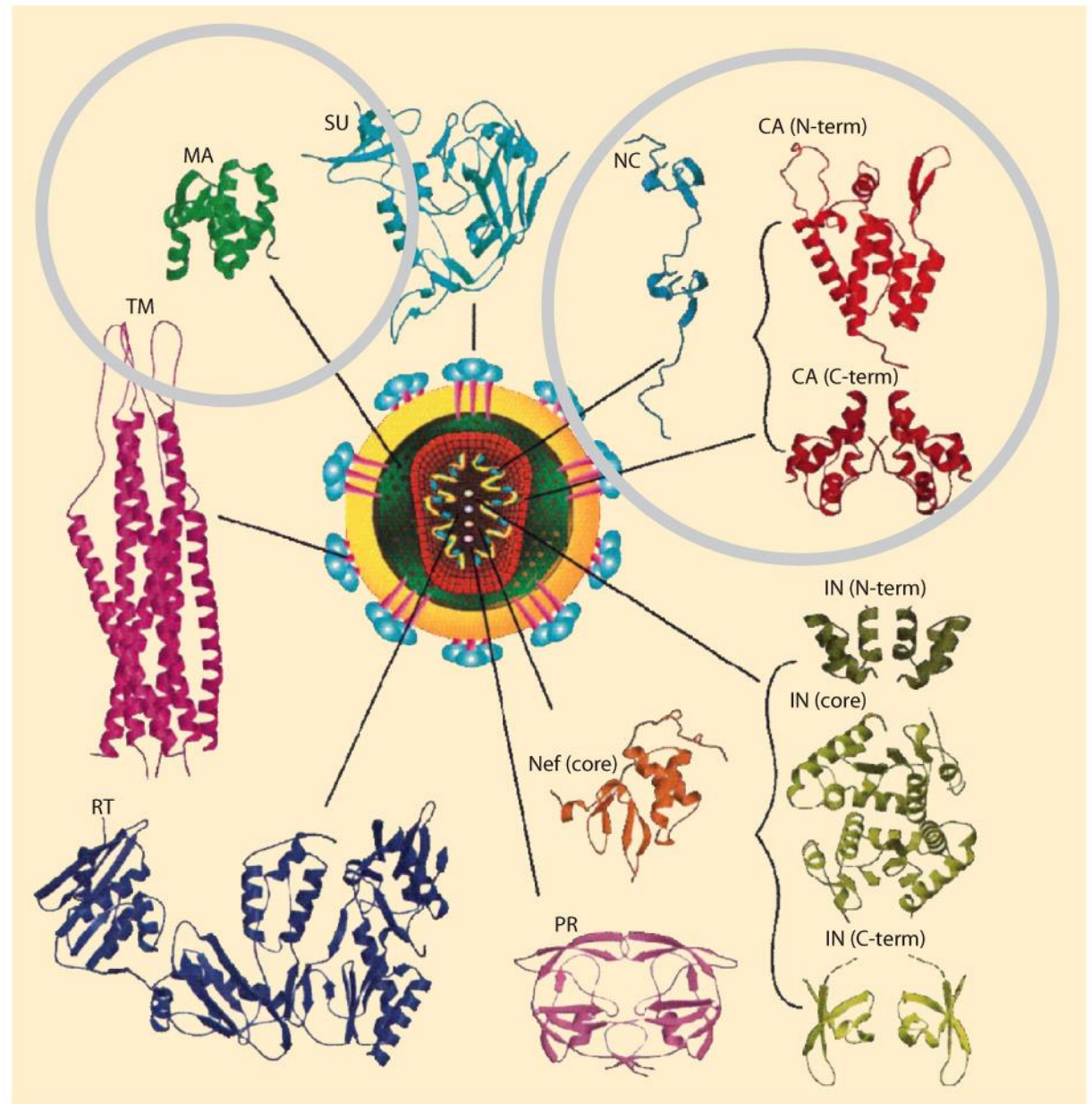


Figure 8.28 Molecular Biology of Assemblies and

tomato bushy stunt virus (TBSV)

assembly and maturation of human immunodeficiency virus (HIV)





Box 8.1 Figure 8.1.2 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Influenza virus

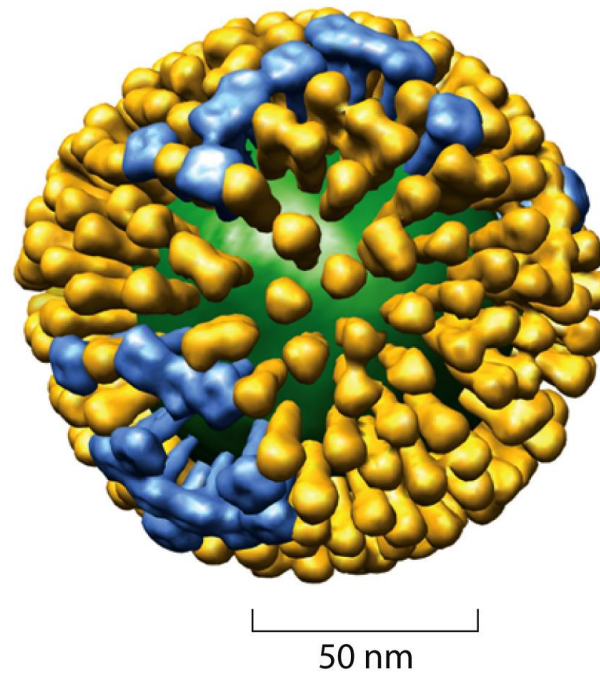


Figure 8.60b Molecular Biology of Assemblies and Machines (© Garland Science 2016)

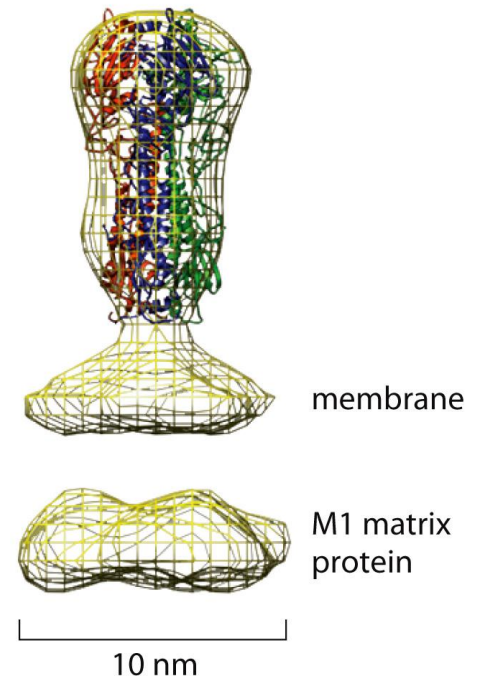
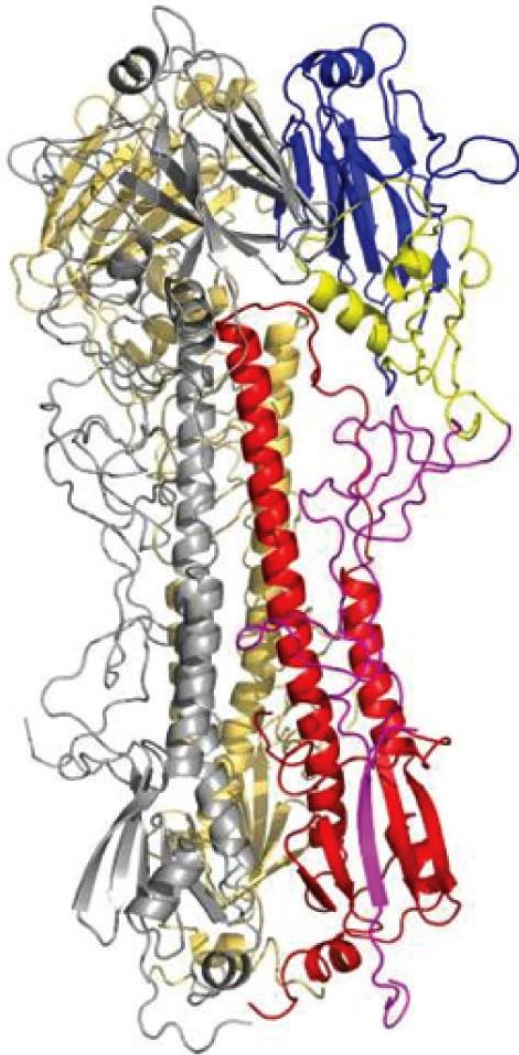
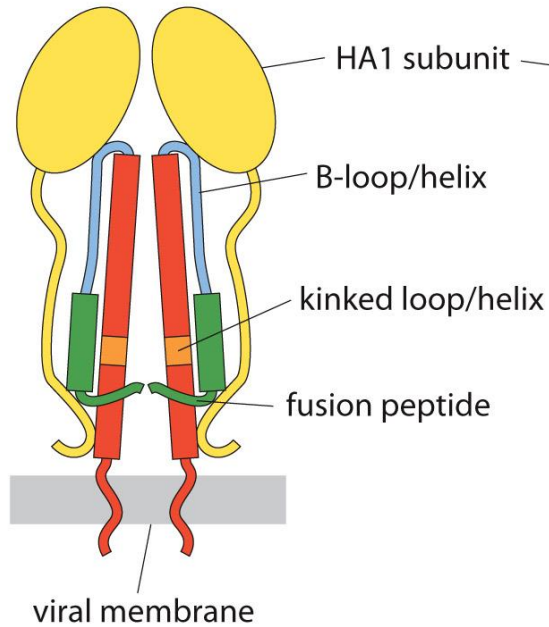


Figure 8.60c Molecular Biology of Assemblies and Machines (© Garland Science 2016)

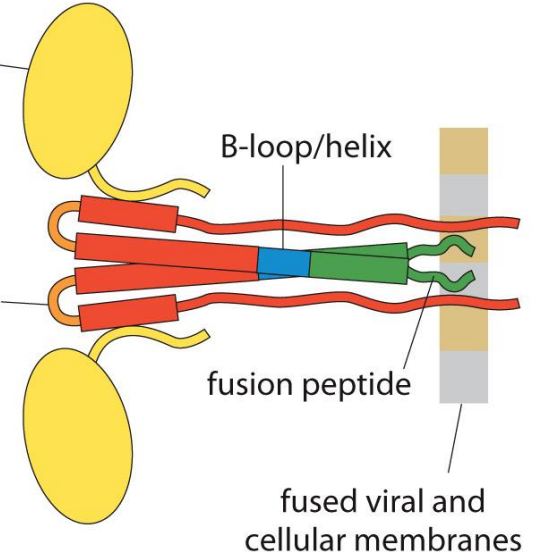


neutral pH/pre-fusion

target membrane



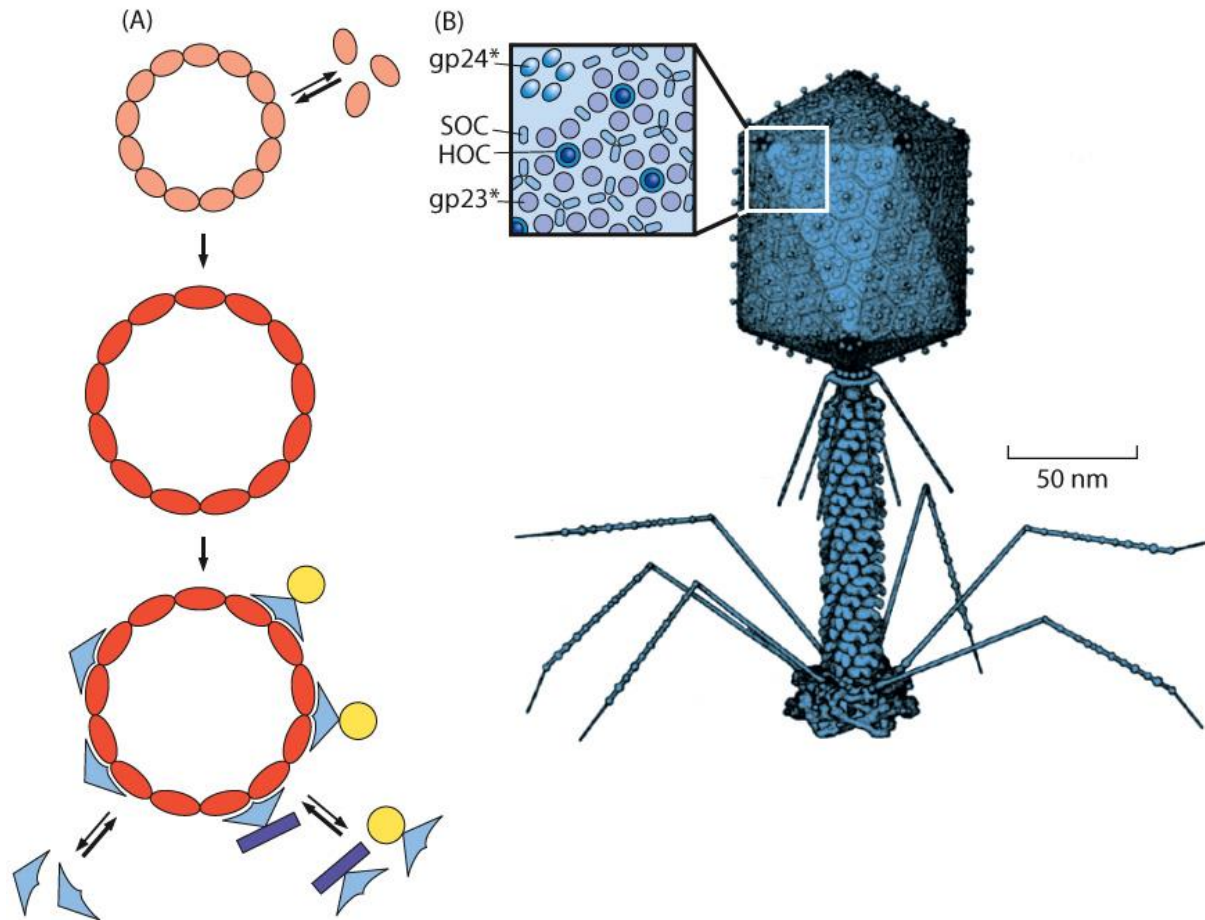
(F) low pH/post-fusion



.60ef Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Figure 8.60d Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Display of proteins on accessory proteins of dsDNA bacteriophages



Display of proteins on accessory proteins of dsDNA bacteriophages

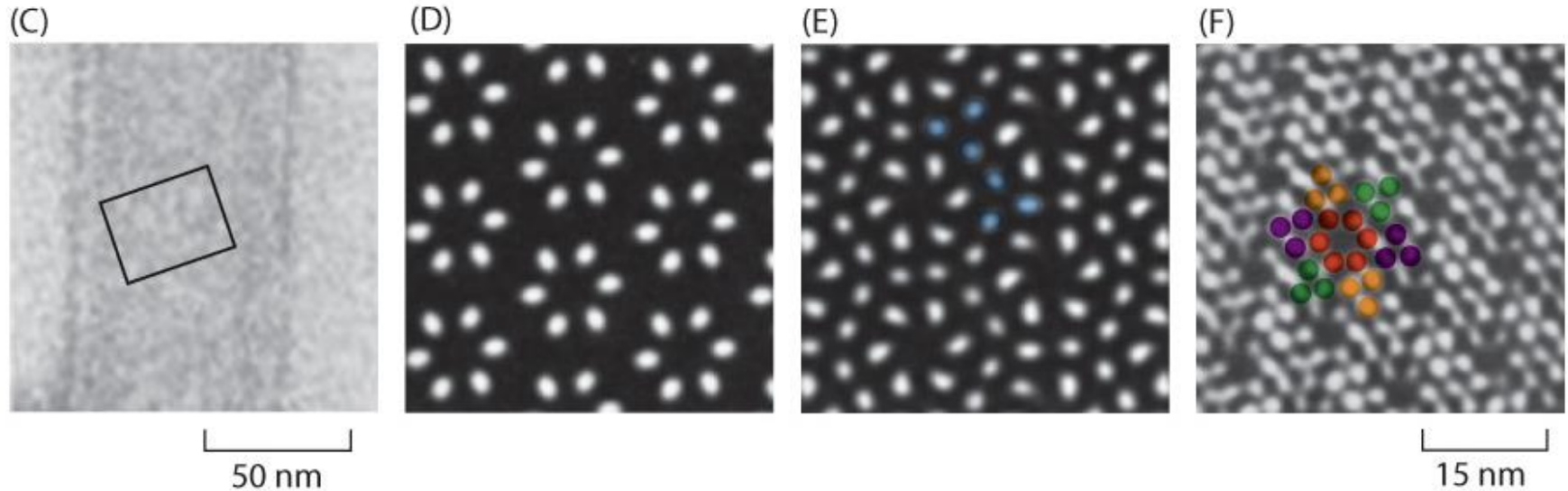


Figure 8.67 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Display of an Ig domain

flock house virus

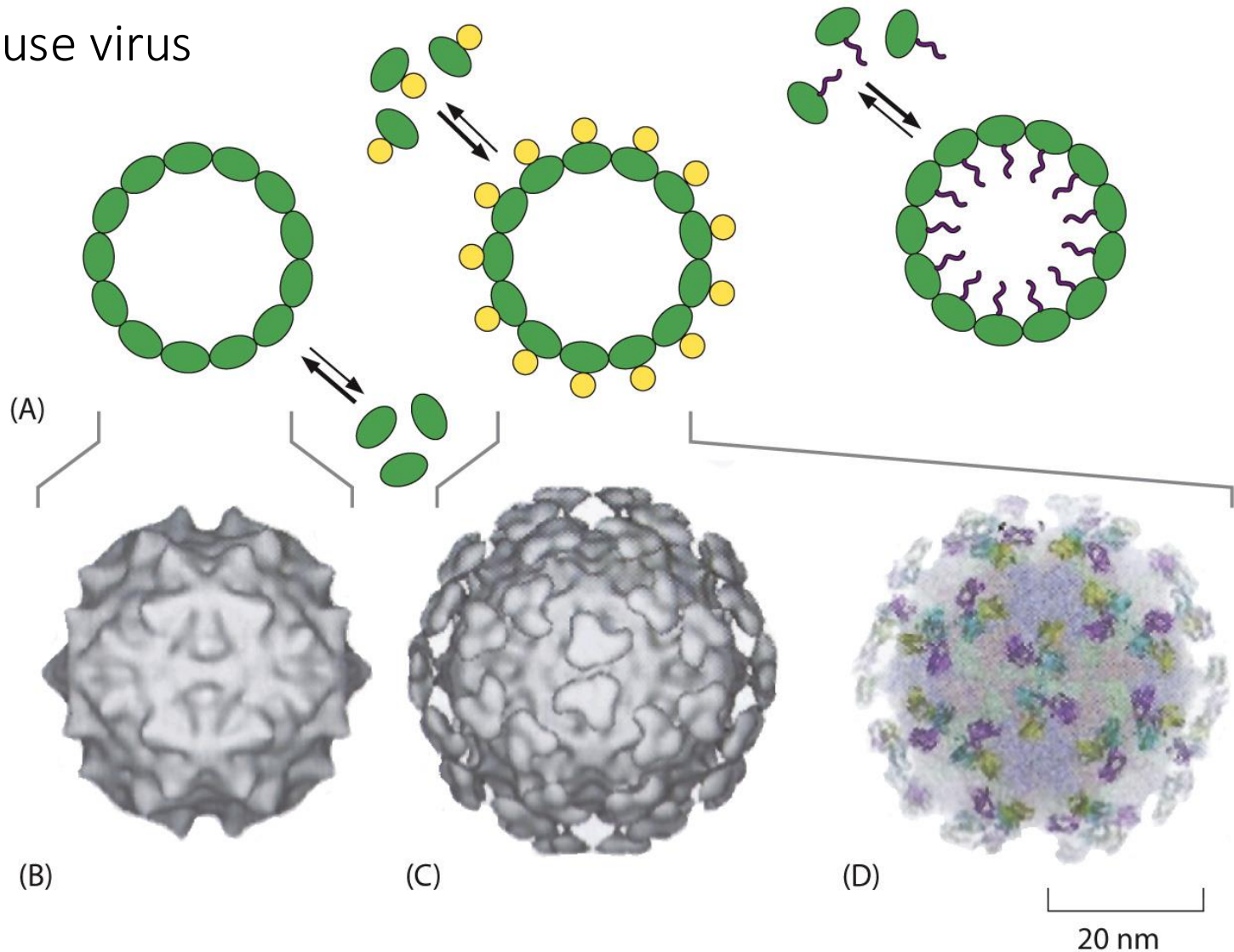


Figure 8.68 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Display of green fluorescent protein at the tips of HBV capsid spikes

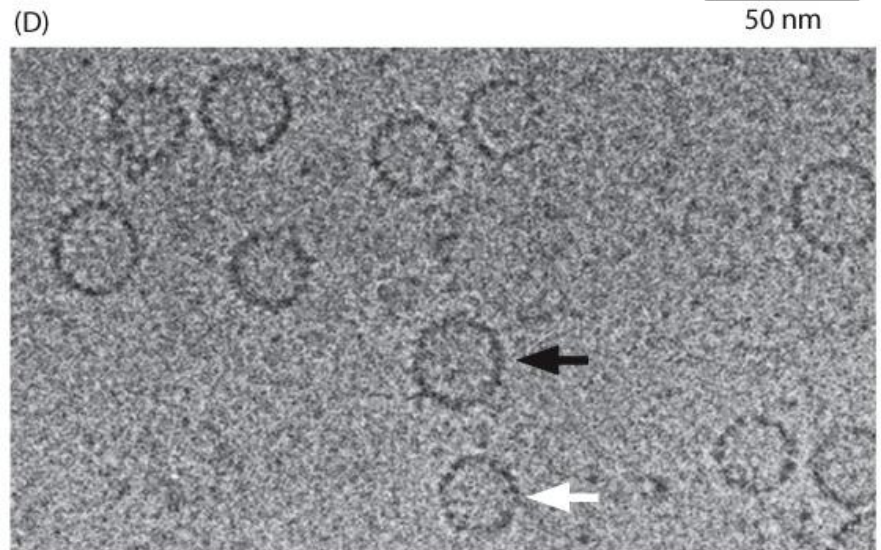
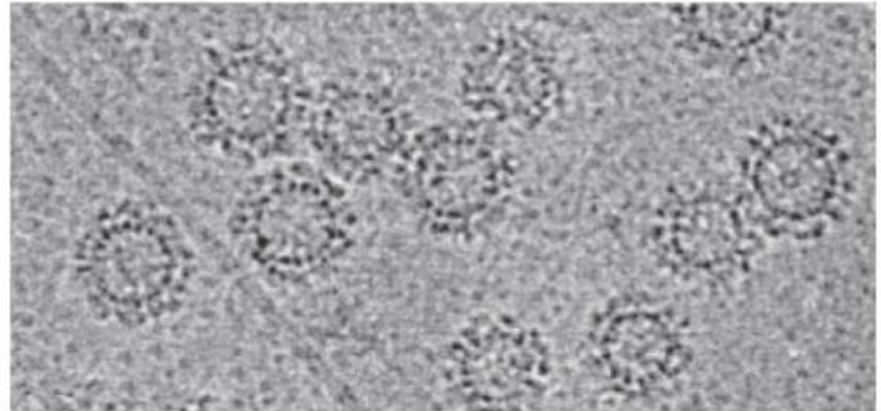
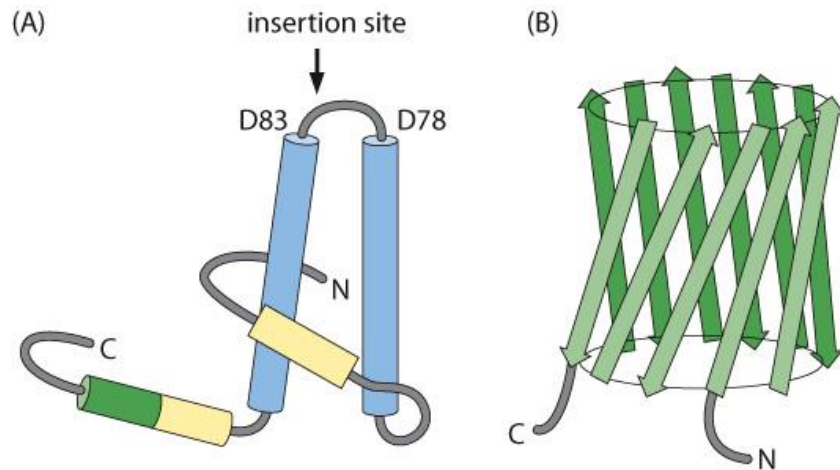


Figure 8.69 Molecular Biology of Assemblies and Machines (© Garland Science 2016)

Generation of protective vaccines

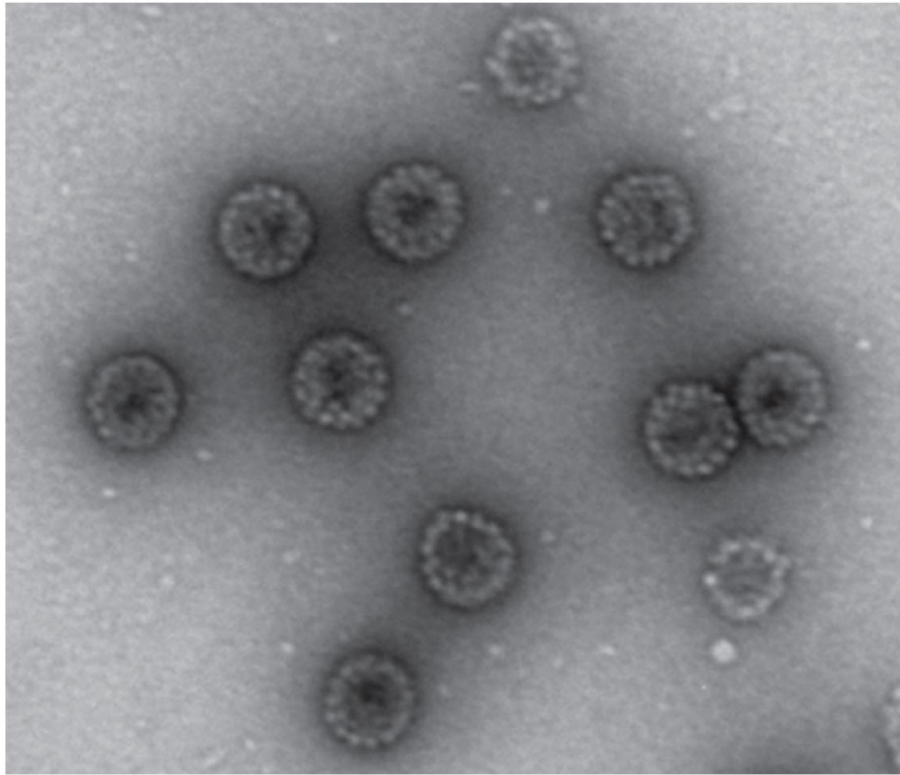


Figure 8.70a Molecular Biology of Assemblies and Machines (© Garland Science 2016)

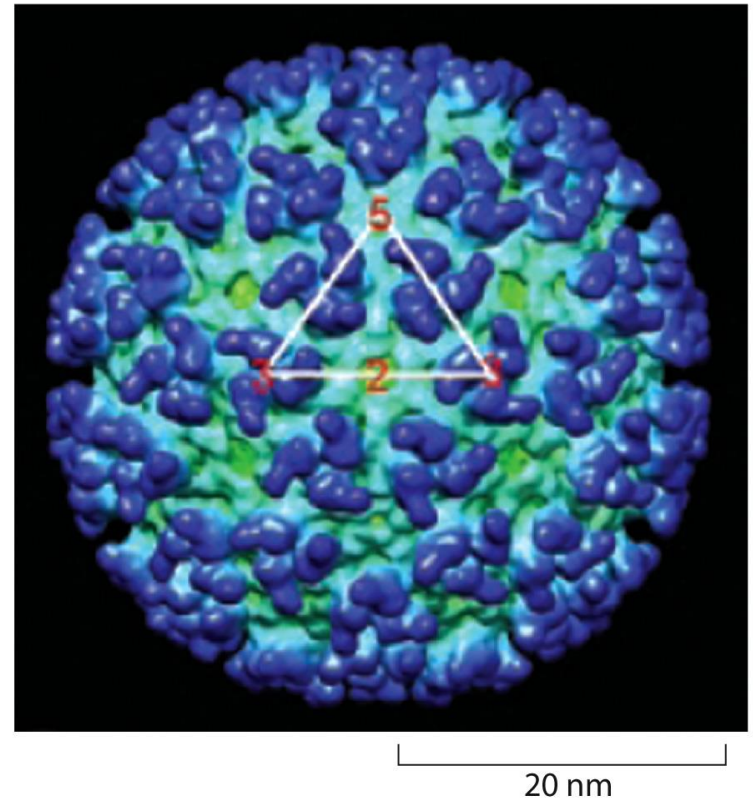


Figure 8.70b Molecular Biology of Assemblies and Machines (© Garland Science 2016)

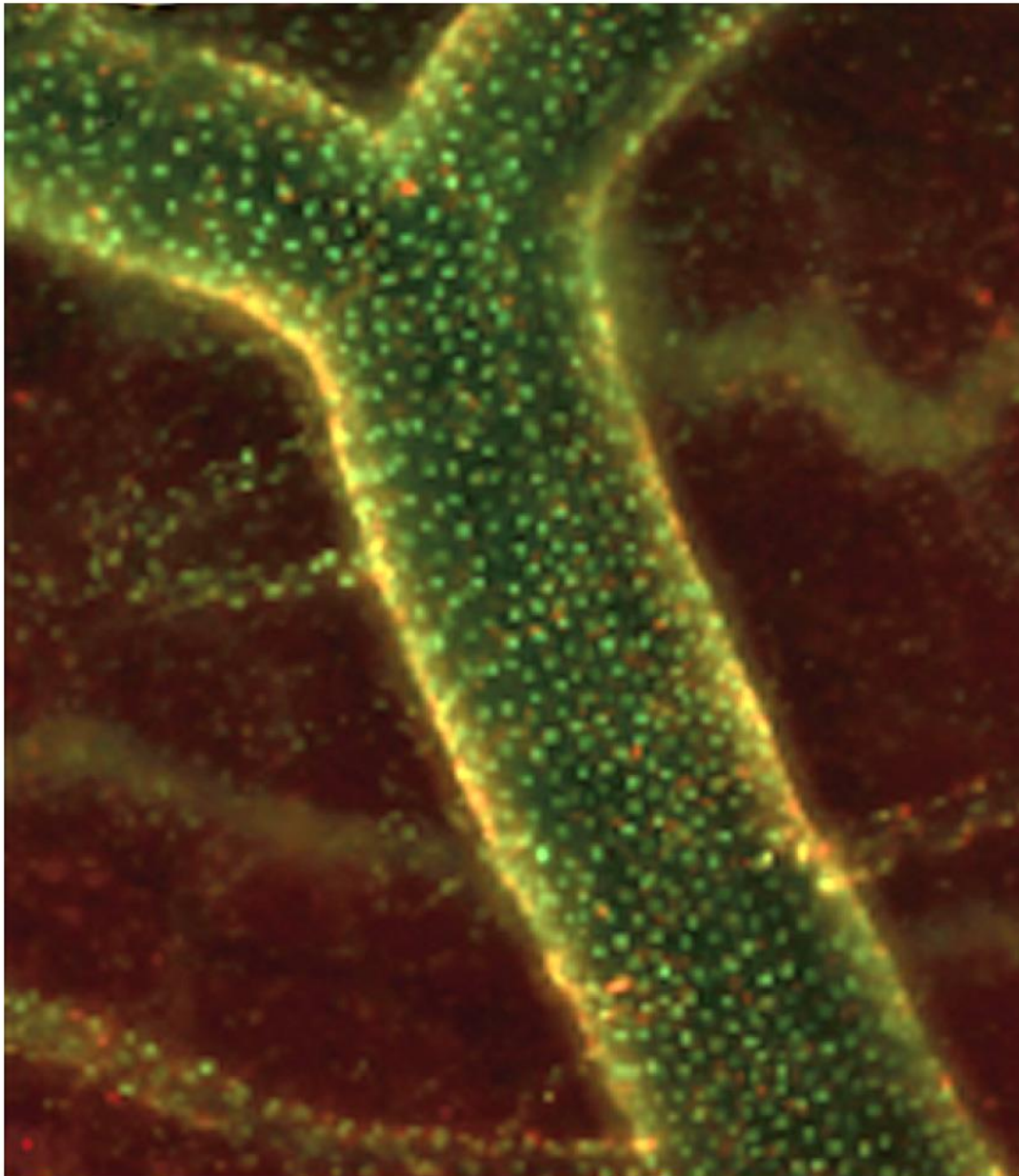


Figure 8.71 Molecular Biology of Assemblies and Machines (© Garland Science 2016)