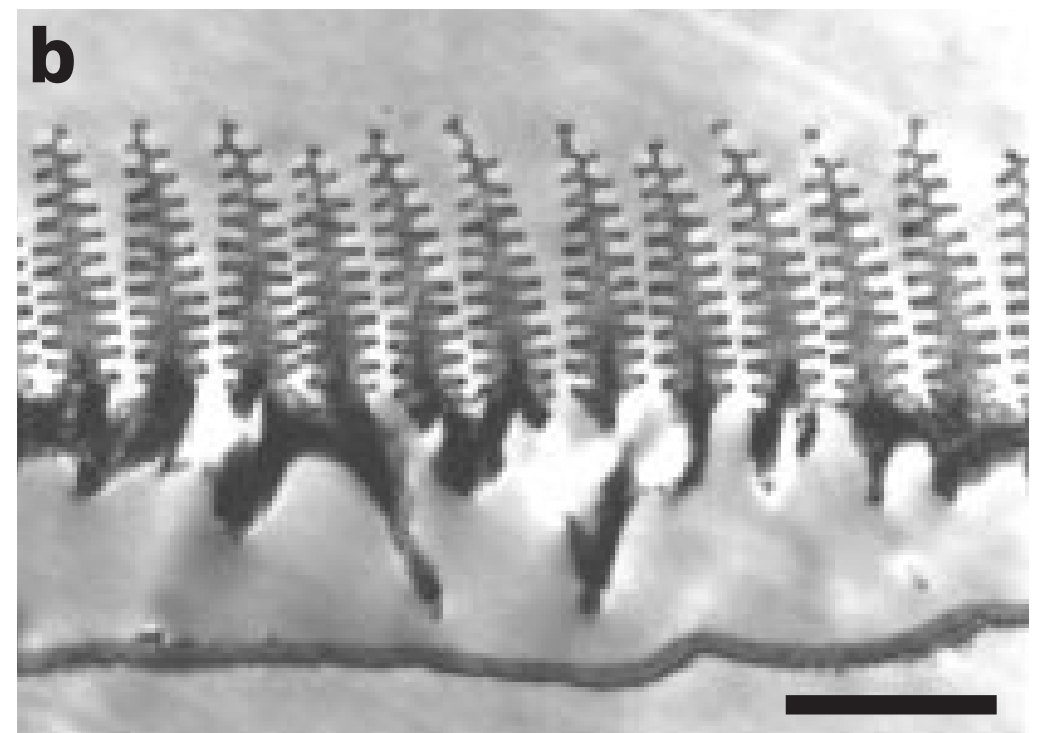
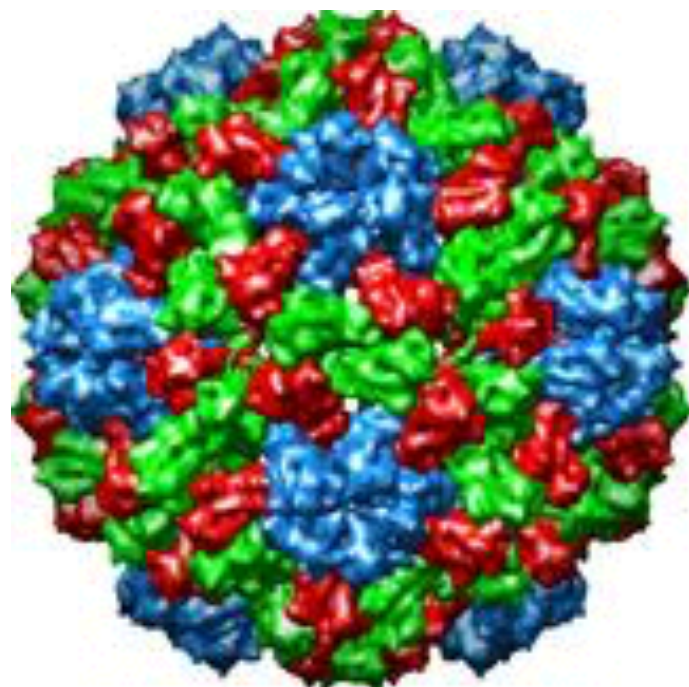
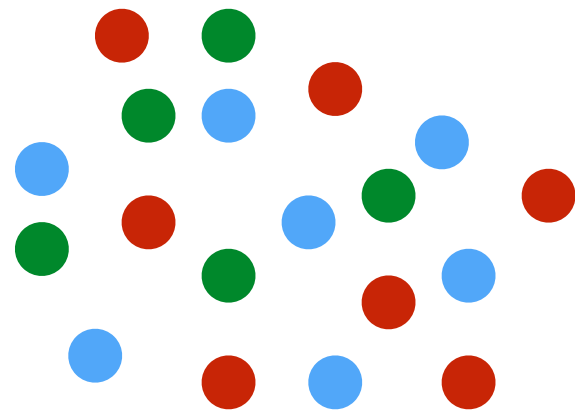


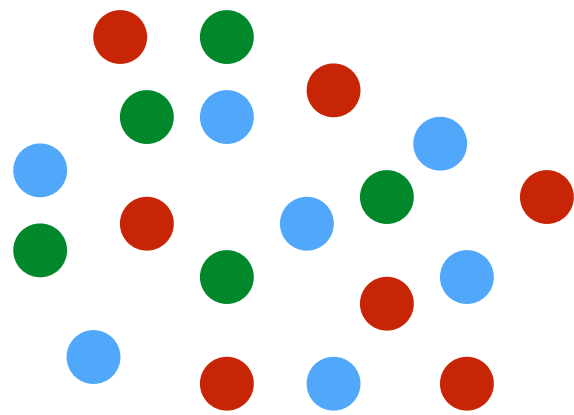
Self assembly and structural colors



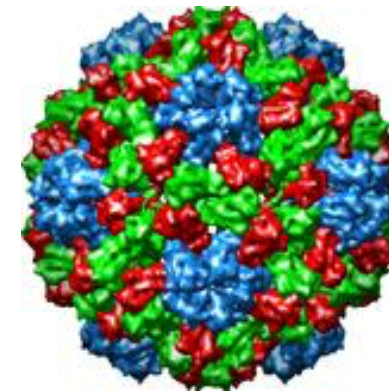
1.7 μm

Self-assembly of viral capsids

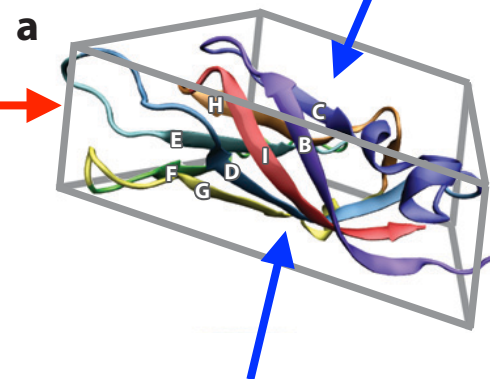
capsid proteins
in solution



Cowpea Chlorotic
Mottle virus

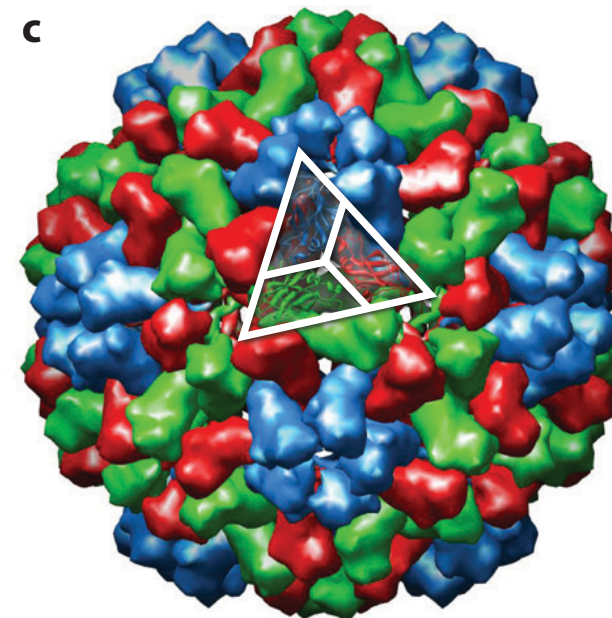
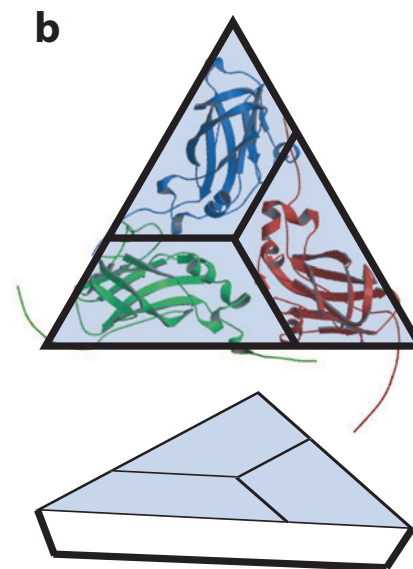


top side
is hydrophilic



all sides are
hydrophobic

bottom side
is hydrophilic

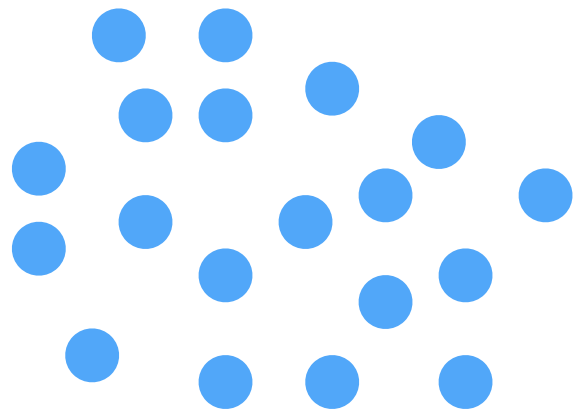


Hydrophilic parts
are on the outside
and on the inside of
assembled capsid.

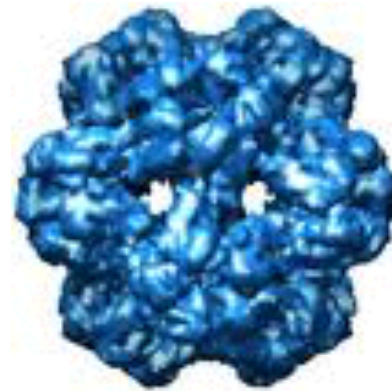
Hydrophobic parts
are at protein
junctions and are
hidden from water.

Self-assembly of viral capsids

capsid proteins
in solution



Brome mosaic
virus

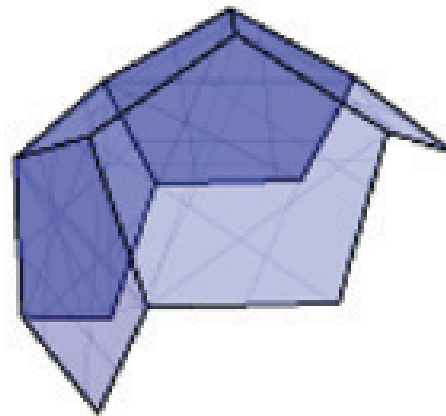


Note: we only present thermodynamics of self-assembly. Kinetics of self-assembly can be analyzed with master equations.



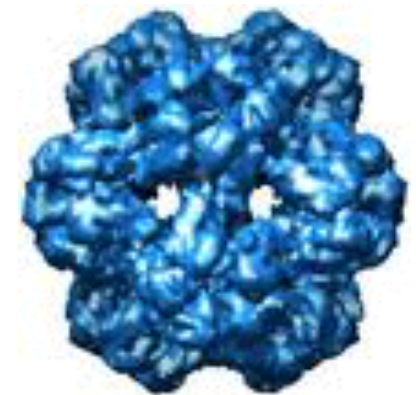
$$E(1) = 0 \quad C(1)$$

energy and concentration
of protein monomers



$$E(n) \quad C(n)$$

energy and concentration of
partially assembled capsids
containing n proteins

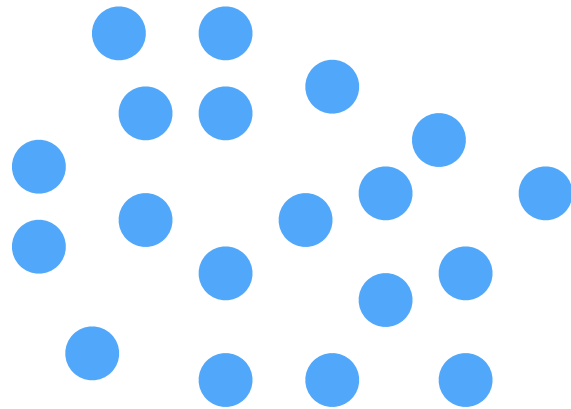


$$E(N) \quad C(N)$$

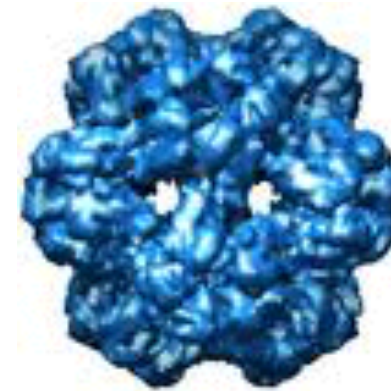
energy and concentration
of fully assembled capsids

Self-assembly of viral capsids

capsid proteins
in solution



Brome mosaic
virus



$E(n)$ $C(n)$
energy and concentration of
partially assembled capsids
containing n proteins

$$E(1) = 0 \quad C(1)$$

energy and concentration
of protein monomers

$$E(N) \quad C(N)$$

energy and concentration
of fully assembled capsids

Total concentration of capsid proteins

$$C_{\text{tot}} = \sum_{n=1}^N nC(n)$$

System free energy

$$G \sim \sum_{n=1}^N [C(n)E(n) + k_B T C(n) (\ln(C(n)/C_0) - 1)]$$

energy

mixing entropy

Self-assembly of viral capsids

Total concentration of capsid proteins

$$C_{\text{tot}} = \sum_{n=1}^N nC(n)$$

System free energy

$$G \sim \sum_{n=1}^N [C(n)E(n) + k_B T C(n) (\ln(C(n)/C_0) - 1)]$$

Minimize free energy with respect to concentrations $C(n)$ subject to the fixed total concentration C_{tot} constraint.

Minimize functional

$$H = G + \mu \left[C_{\text{tot}} - \sum_n nC(n) \right]$$

Afterwards set the Lagrange multiplier μ to fix the total concentration C_{tot} .

$$C(n) = C_0 e^{-(E(n) - \mu n)/k_B T}$$

$$C(1) = C_0 e^{\mu/k_B T}$$

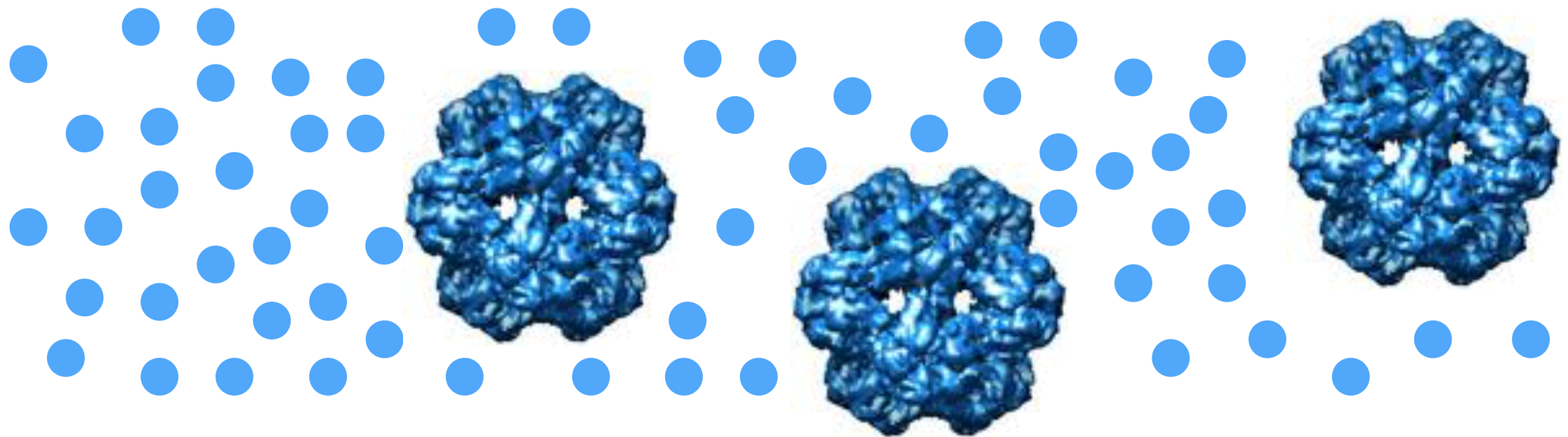
Parameter μ plays a role of chemical potential!

Law of mass action

$$\frac{C(n)}{C_0} = \left(\frac{C(1)}{C_0} \right)^n e^{-E(n)/k_B T}$$

$C(1)$ is determined by fixing the total concentration!

Self-assembly of viral capsids



$$\frac{C(n)}{C_0} = \left(\frac{C(1)}{C_0} \right)^n e^{-E(n)/k_B T}$$

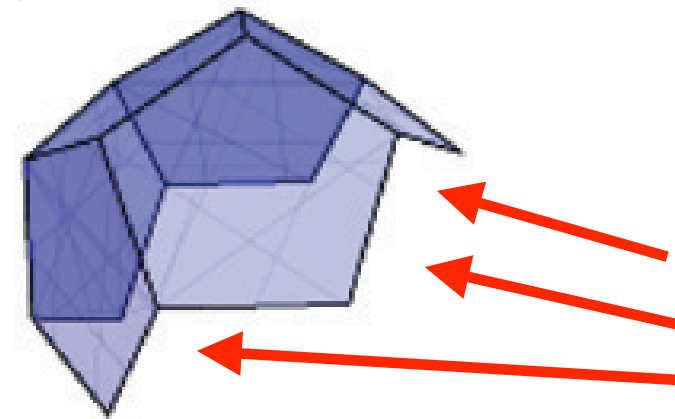
Neglect concentration of partially assembled capsids

$$C(n) \approx 0$$

Total protein concentration

$$C_{\text{tot}} \approx C(1) + NC(N)$$

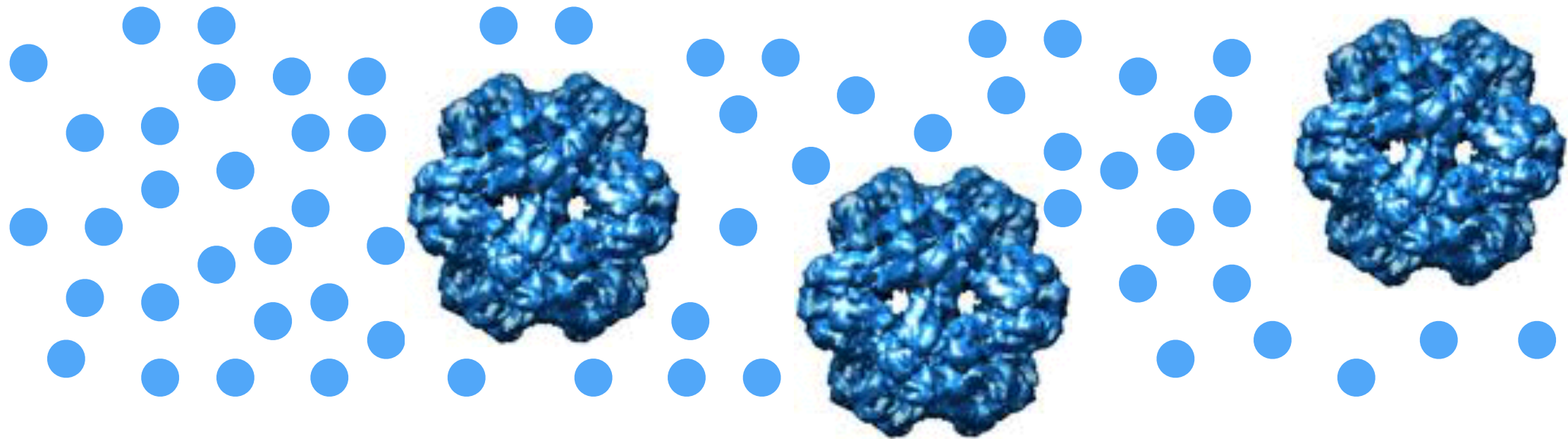
$$\frac{C_{\text{tot}}}{C_0} \approx \frac{C(1)}{C_0} + N \left(\frac{C(1)}{C_0} e^{-E(N)/(Nk_B T)} \right)^N$$



Exposed hydrophobic regions

$$C^* = C_0 e^{E(N)/(Nk_B T)}$$

Self-assembly of viral capsids



$$\frac{C_{\text{tot}}}{C_0} \approx \frac{C(1)}{C_0} + N \left(\frac{C(1)}{C^*} \right)^N$$

$$C^* = C_0 e^{E(N)/(Nk_B T)}$$

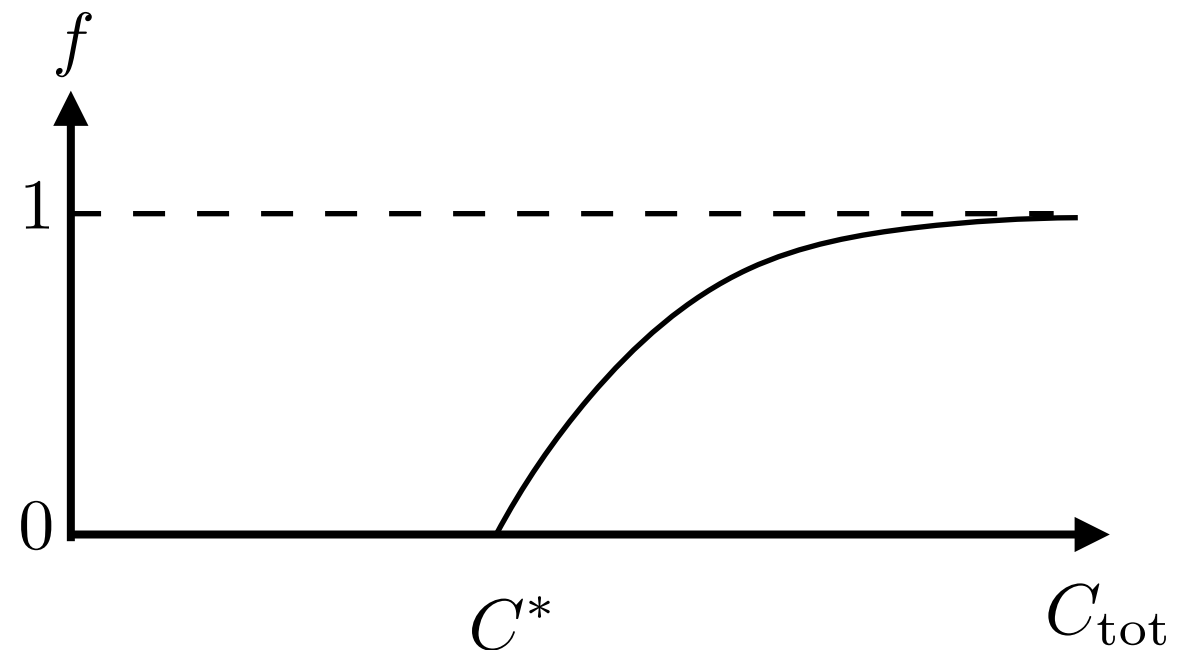
At low concentrations $C_{\text{tot}} \ll C^*$

$$C(1) \approx C_{\text{tot}}$$

At large concentrations $C_{\text{tot}} \gg C^*$

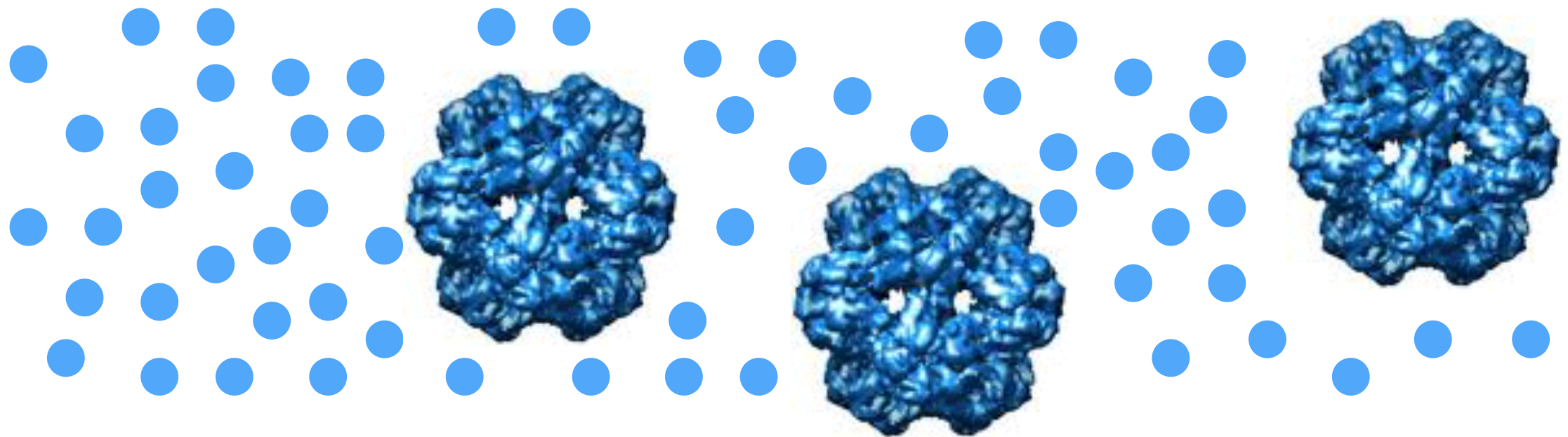
$$C(1) \approx C^* \left(\frac{C_{\text{tot}}}{NC_0} \right)^{1/N} \approx C^*$$

Fraction of proteins assembled in capsids $f = 1 - \frac{C(1)}{C_{\text{tot}}}$



This generic profile is also observed for assembly of more complex viral capsids!

Self-assembly of viral capsids

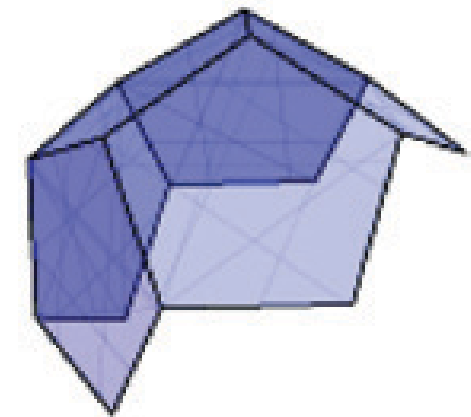


$$\frac{C(n)}{C_0} = \left(\frac{C(1)}{C_0} \right)^n e^{-E(n)/k_B T}$$

Can we really neglect partially assembled capsids at large protein concentrations?

$$\frac{C(N/2)}{C(N)} = \left(\frac{C(1)}{C_0} \right)^{-N/2} e^{-[E(N/2) - E(N)]/k_B T}$$

$$C(1) \approx C^* = C_0 e^{E(N)/(Nk_B T)}$$



For Cowpea Chlorotic Mottle Virus the scission energy is

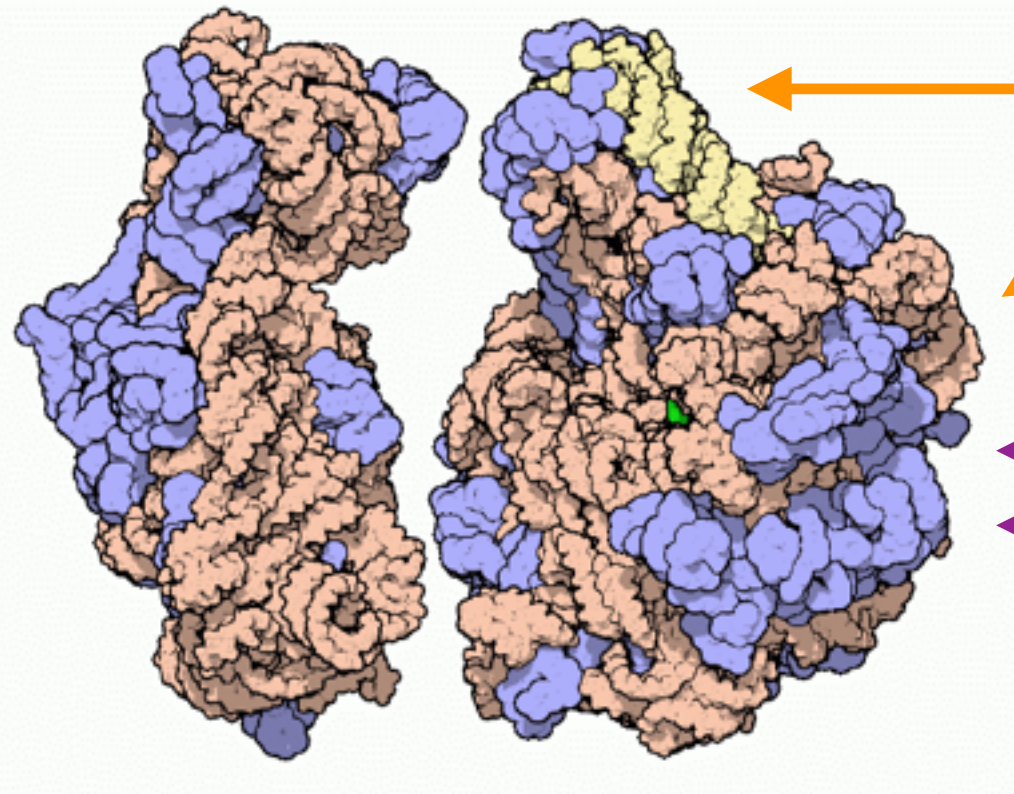
$$2E(N/2) - E(N) \sim 100k_B T$$

$$\frac{C(N/2)}{C(N)} \approx e^{-[E(N/2) - E(N)/2]/k_B T} \ll 1$$

Complex self-assembly

Ribosomes are huge multi-protein complexes that are important for the synthesis of new proteins.

25 – 30nm



RNA strands

dozens of
different
proteins

Multiple proteins fit together like a puzzle to make the desired structure.

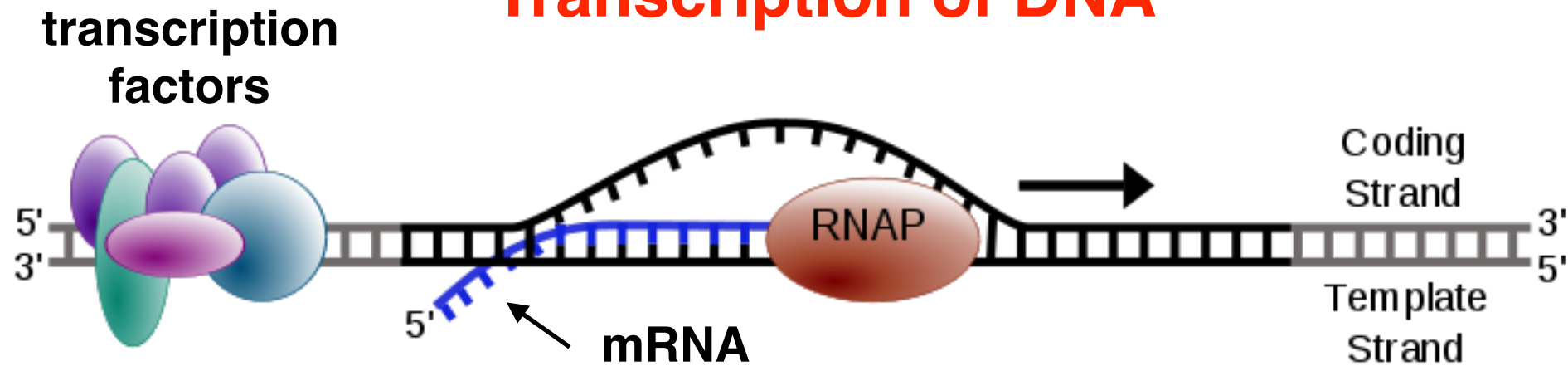


Matching pieces are characterized with strong (specific) binding due to the shape complementarity.

Non-matching pieces bind weakly (non-specifically).

Production of new proteins

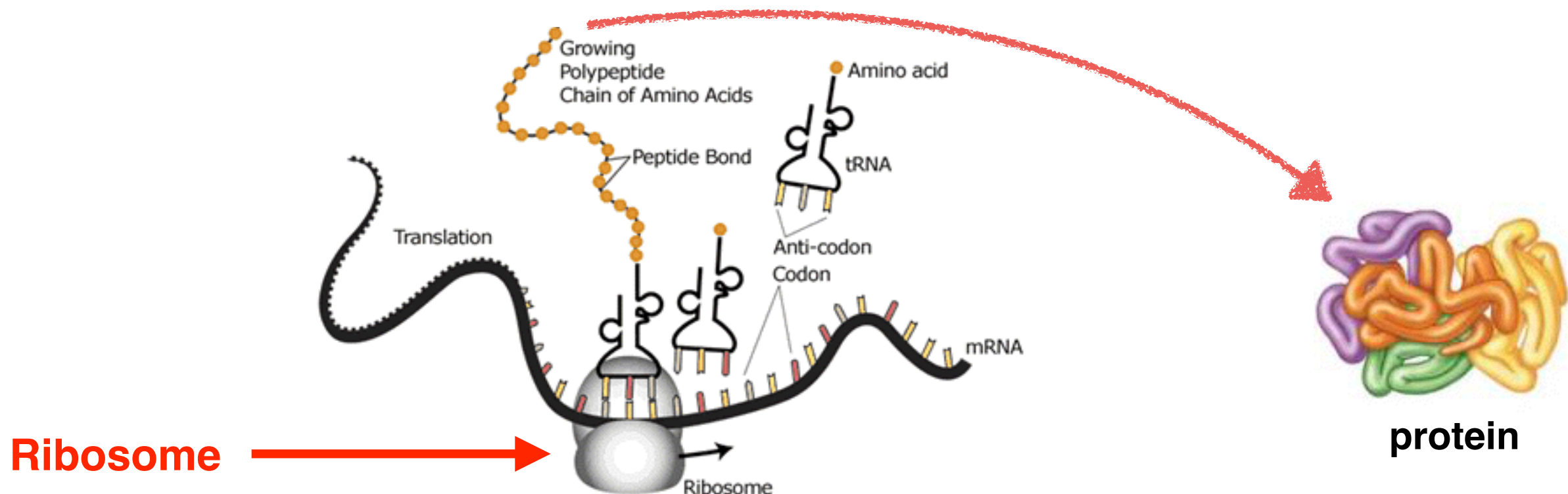
Transcription of DNA



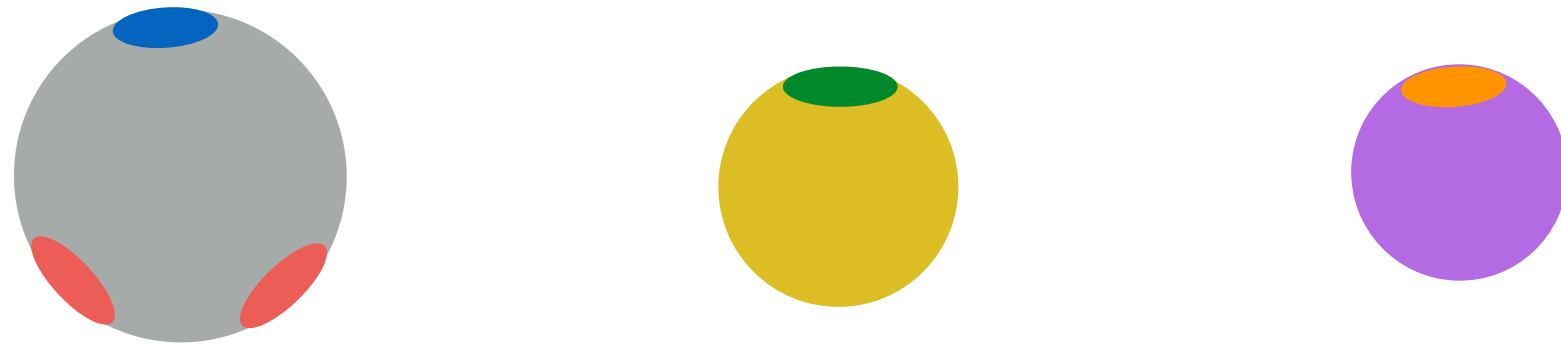
Transcription factors are proteins, which bind to specific locations on DNA, and they help recruiting RNA polymerase (RNAP) that makes a messenger RNA (mRNA) copy of certain DNA segment.

Note: some transcription factors (repressors) also prevent transcription.

Translation of mRNA

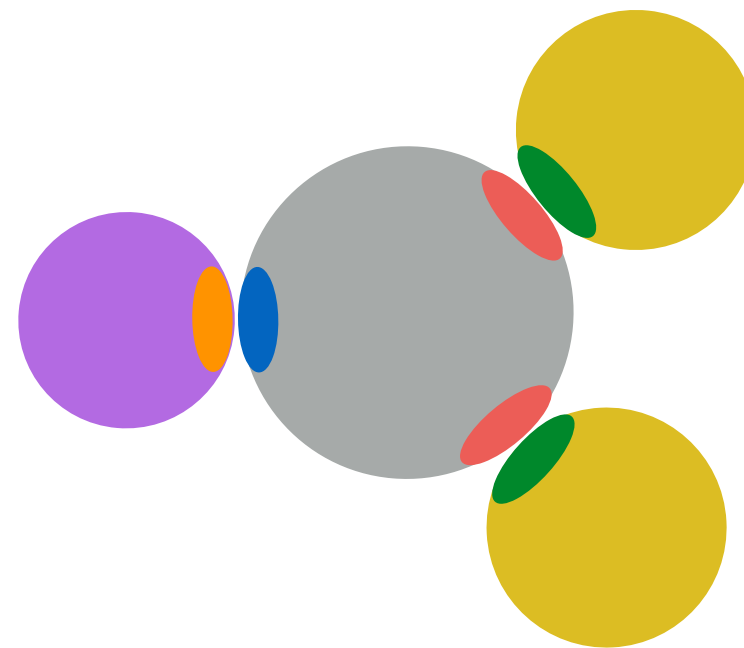


Patchy particles

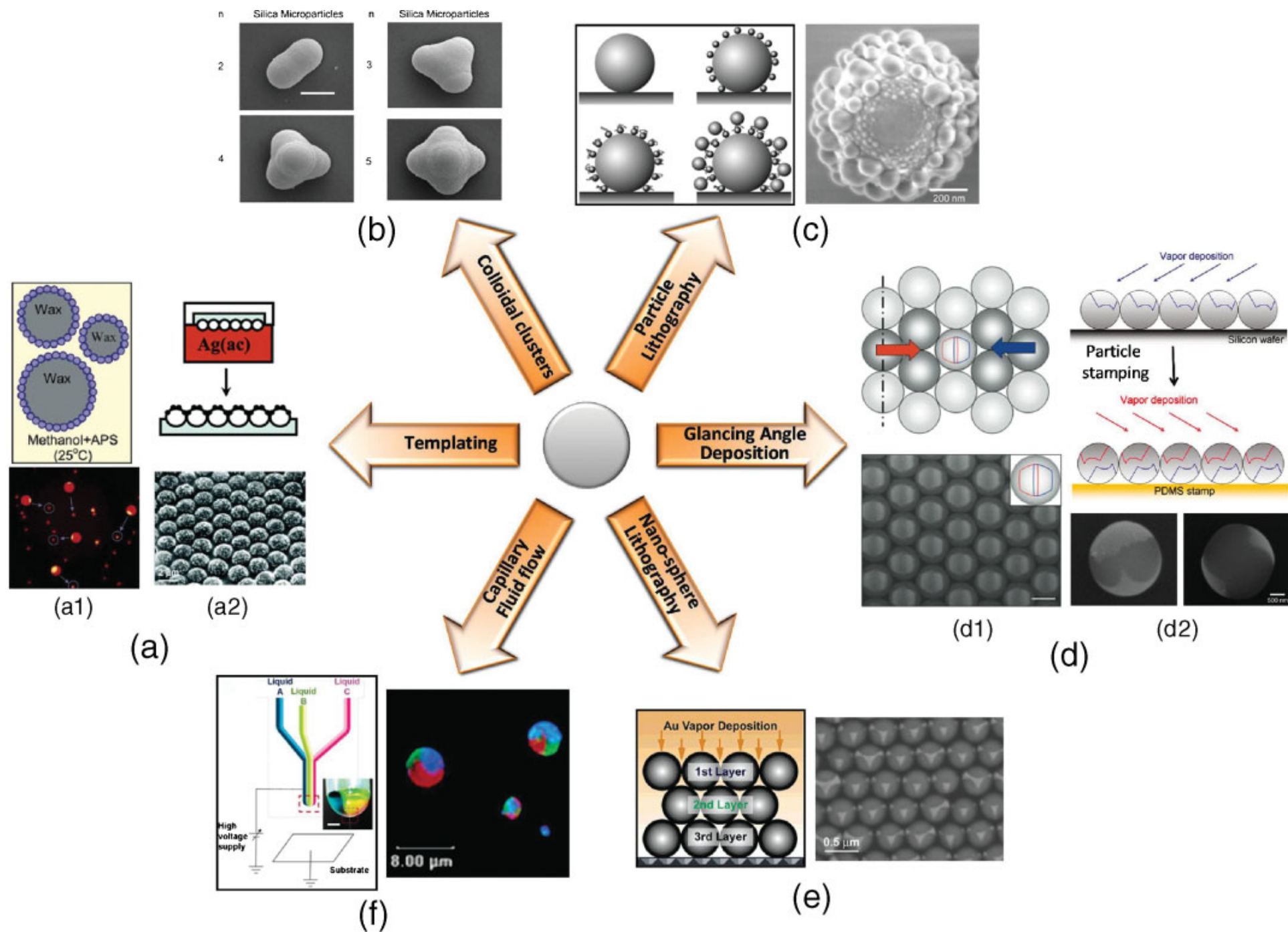


Particles with patches of different chemical/physical properties.

Patches can be designed to bind strongly only with certain partners.

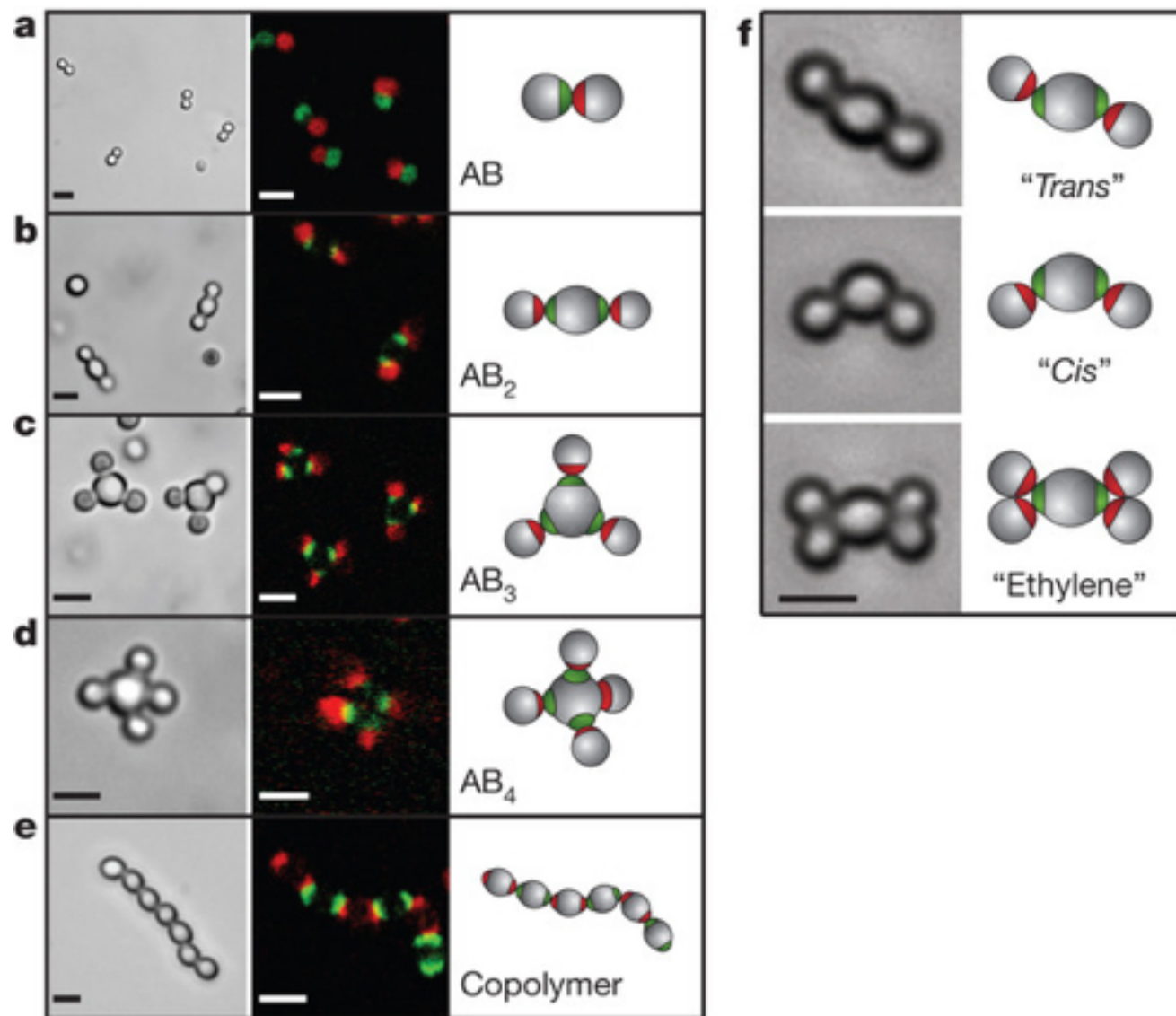


Experimental approaches for making patchy particles



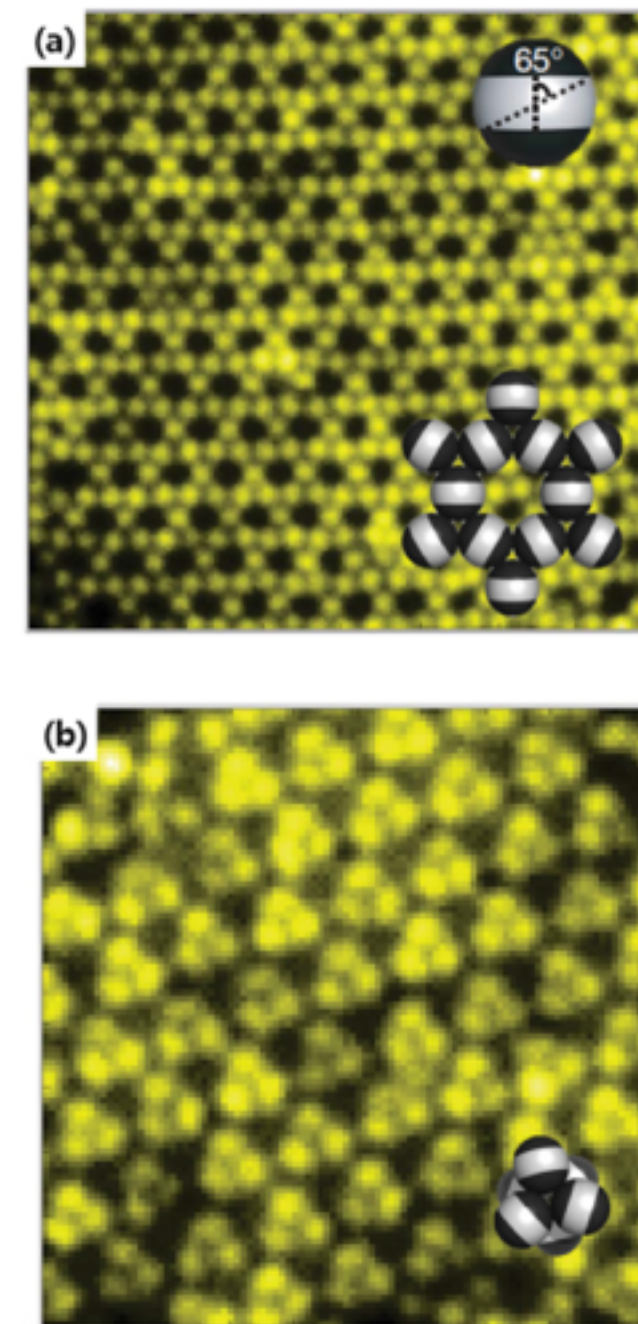
Self-assembly of patchy particles

simple molecule-like structures



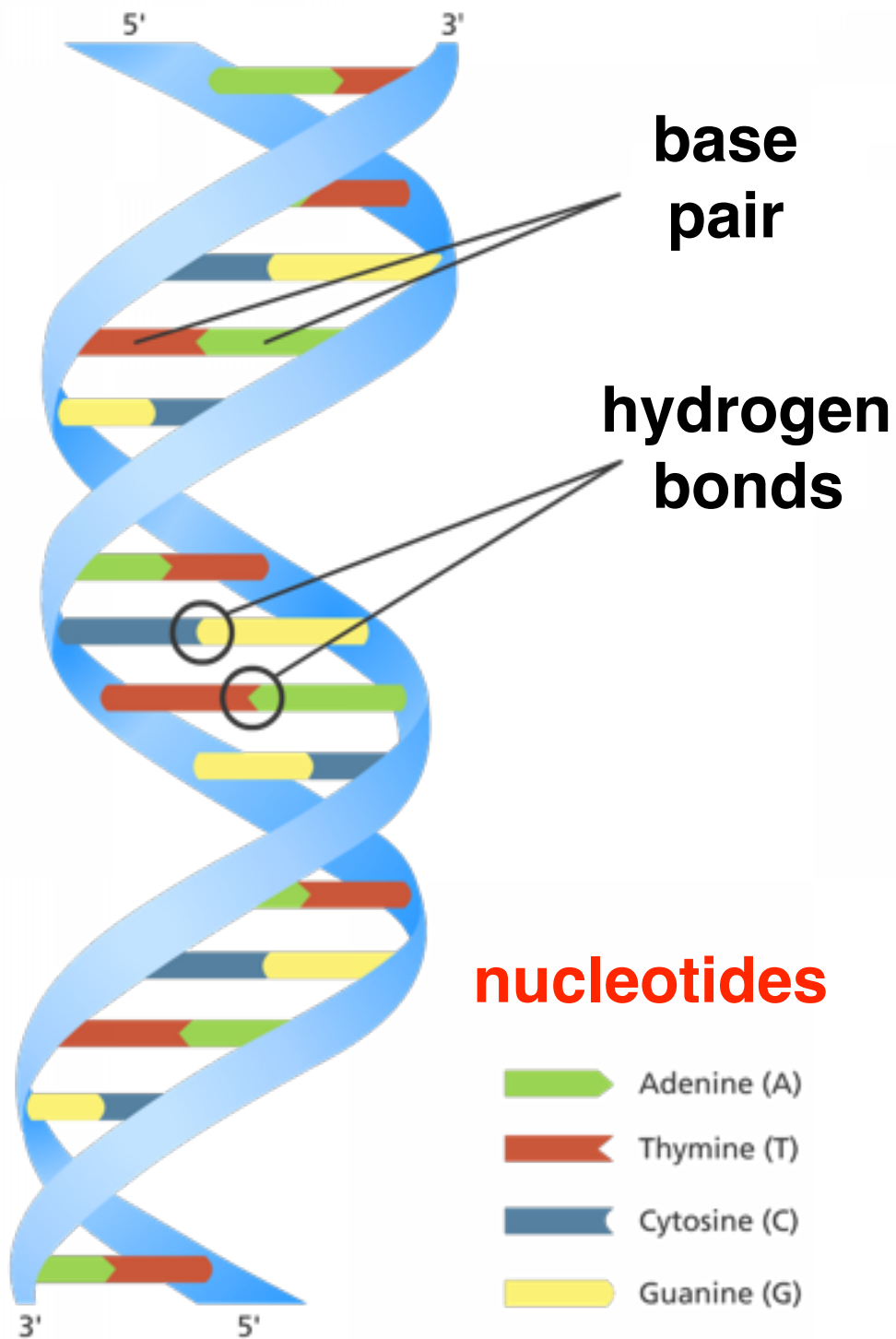
Y. Wang et al., Nature 491, 51 (2012)

crystal structures



G.-R. Yi et al., J. Phys.: Condens. Mat. 25, 193101 (2013)

Double stranded DNA forms, when the opposite strands are complementary (A-T, G-C)



DNA

Binding energy between two DNA strands a and b with sequences s of length N .

$$E_{\text{int}}(\{s_i^a\}, \{s_i^b\}) \approx \sum_{i=1}^N M(s_i^a, s_i^b)$$

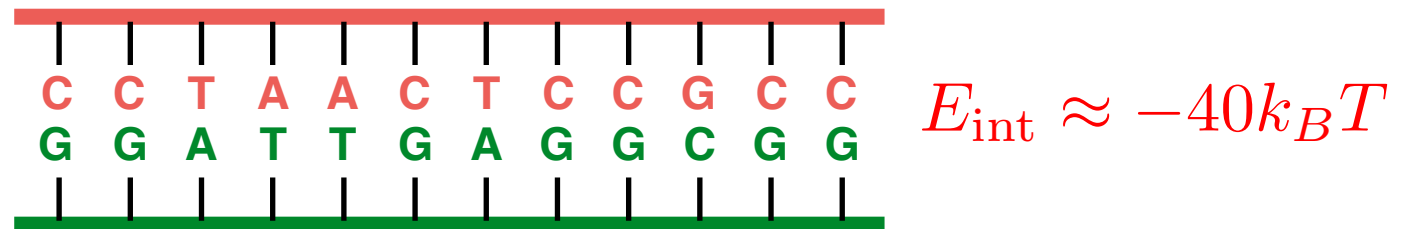
$$M(C, G) = M(G, C) \approx -4k_B T \quad \text{room temperature}$$

$$M(A, T) = M(T, A) \approx -2k_B T$$

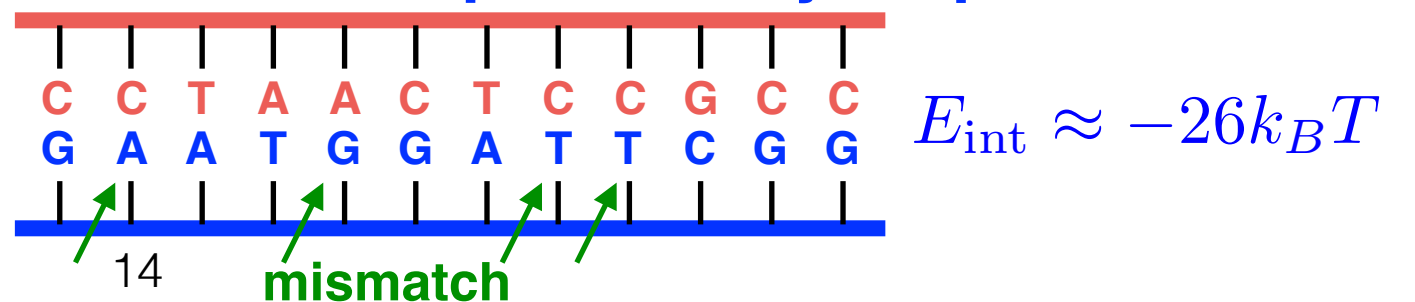
$$M(A, C) = M(C, A) \approx 0$$

$$M(G, T) = M(T, G) \approx 0$$

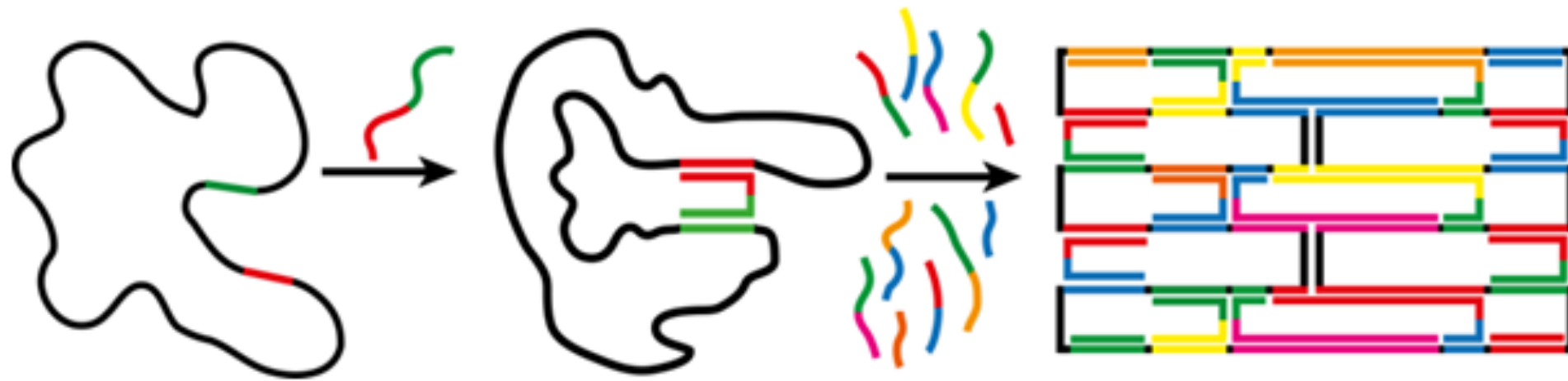
Strong binding between complementary sequences



Weaker binding between non-complementary sequences

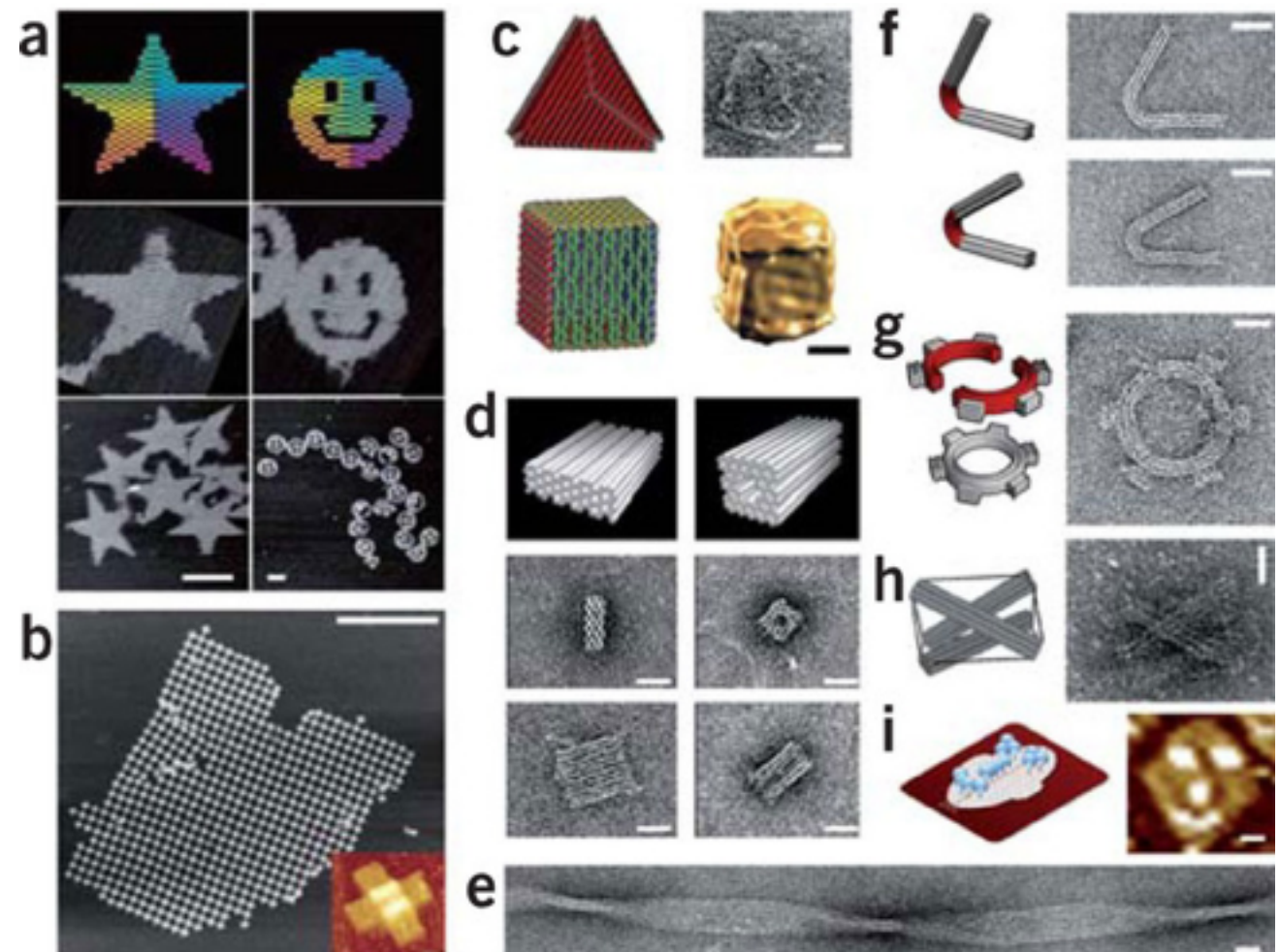


Scaffold DNA origami



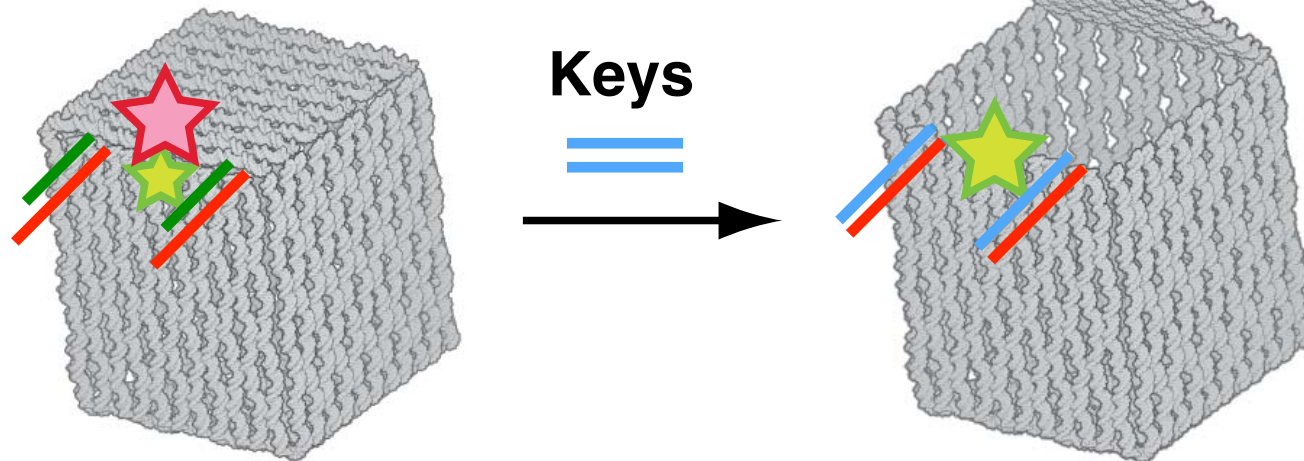
Short strands (synthetic DNA) act like staples that fold the scaffold (virus DNA) into desired structure.

Different colors of staples correspond to different complementary sequences.



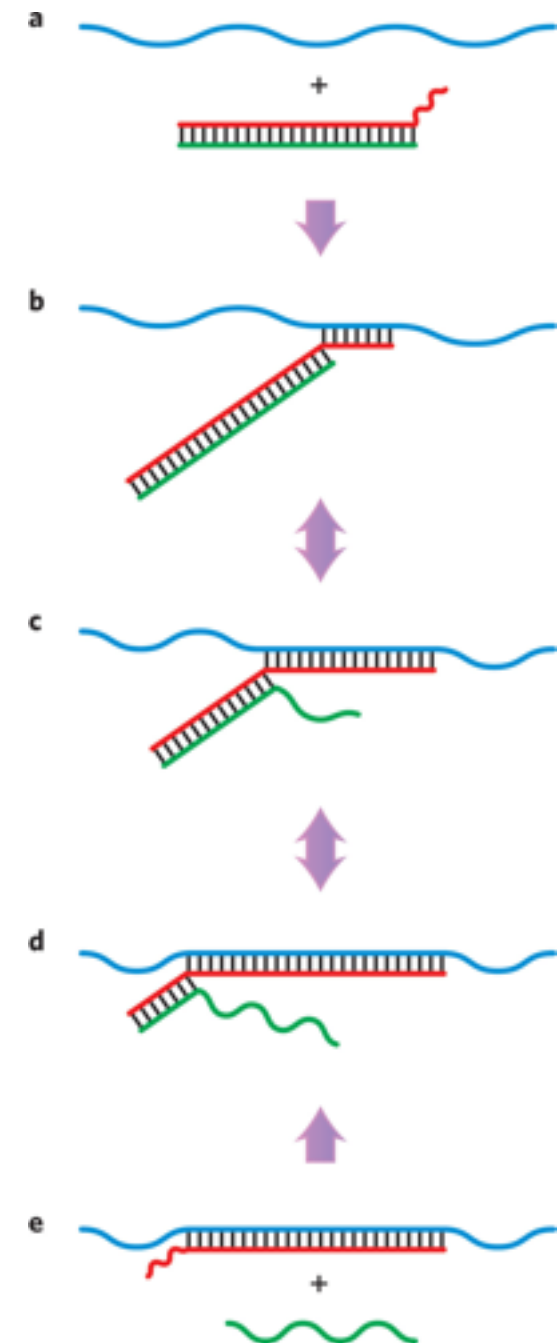
Actuation of DNA origami with a toehold exchange of DNA strands

Box is closed by binding
of complementary DNA
strands between the
cover and the side



Longer strands (keys) bind
to their complementary DNA
strands on the side of the
box to release the cover.

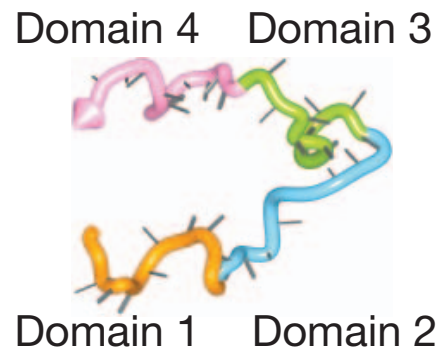
Toe-hold exchange



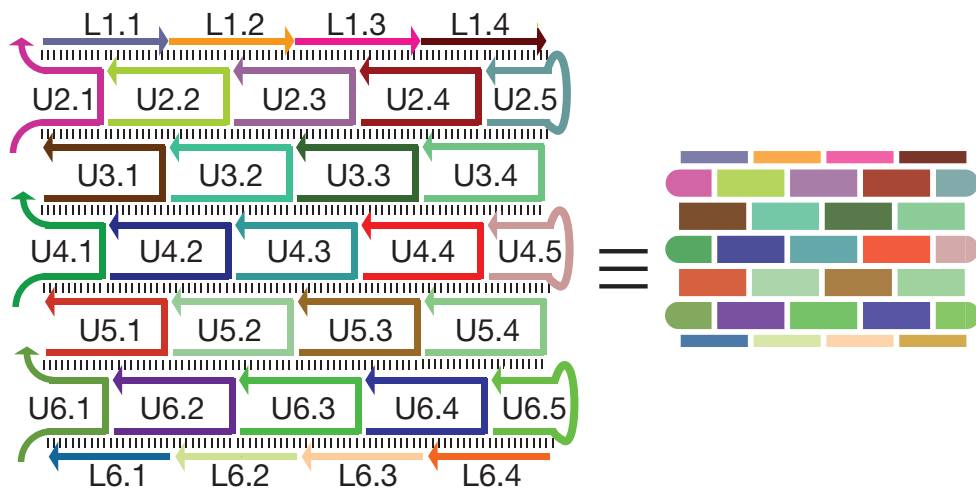
DNA brick origami

Short staple DNA strands are designed to fit like bricks in a wall. Sequence of DNA strands determine, which “bricks fit together”.

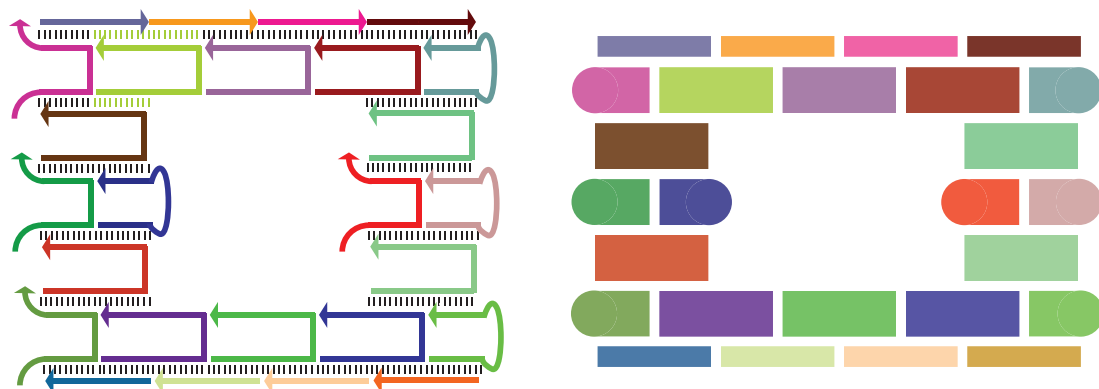
Single stranded DNA building brick (42 bases)



“Brick-wall” diagram



Design of arbitrary structure by removal of certain DNA strands (bricks) from mixture.

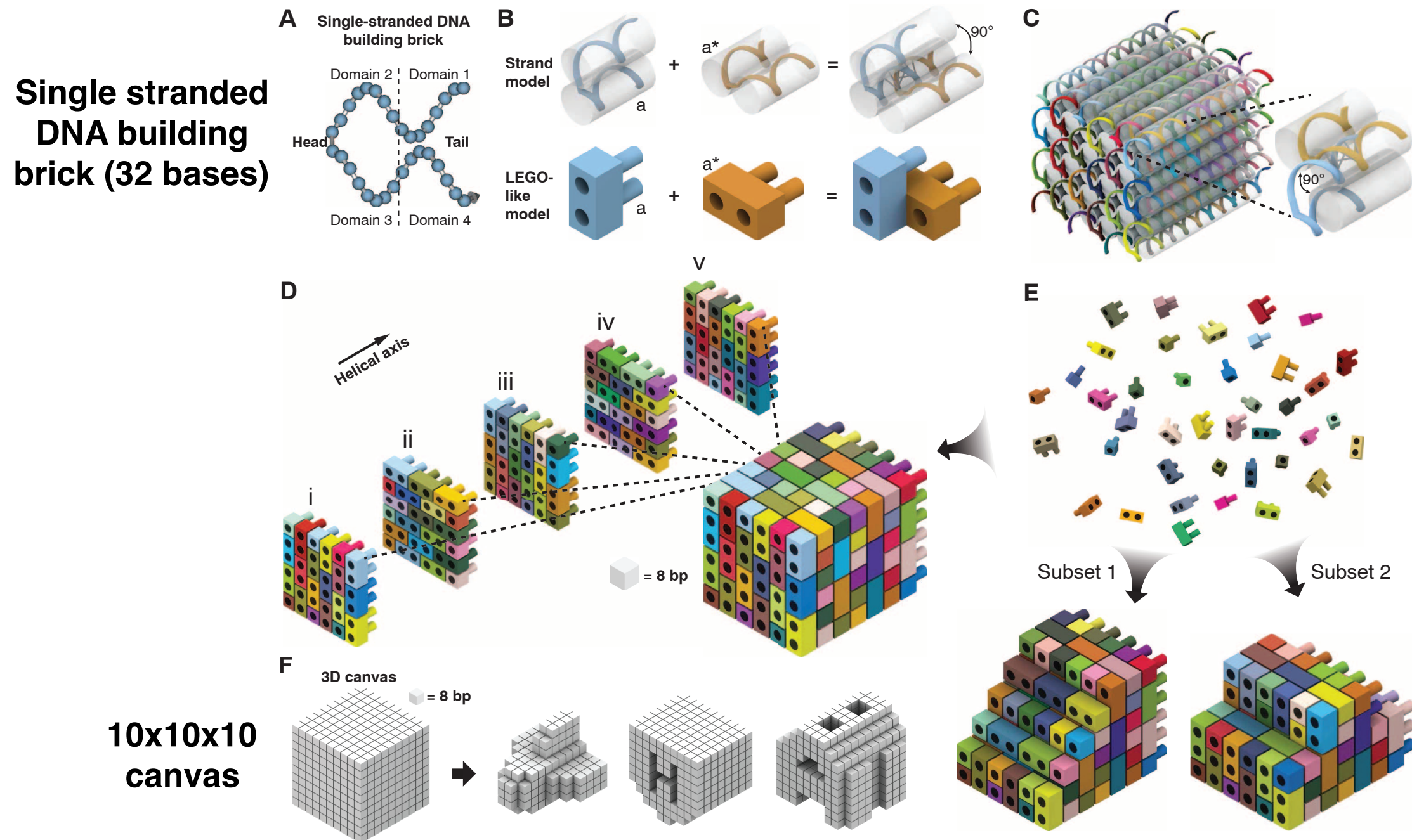


Example of generated structures



DNA brick origami

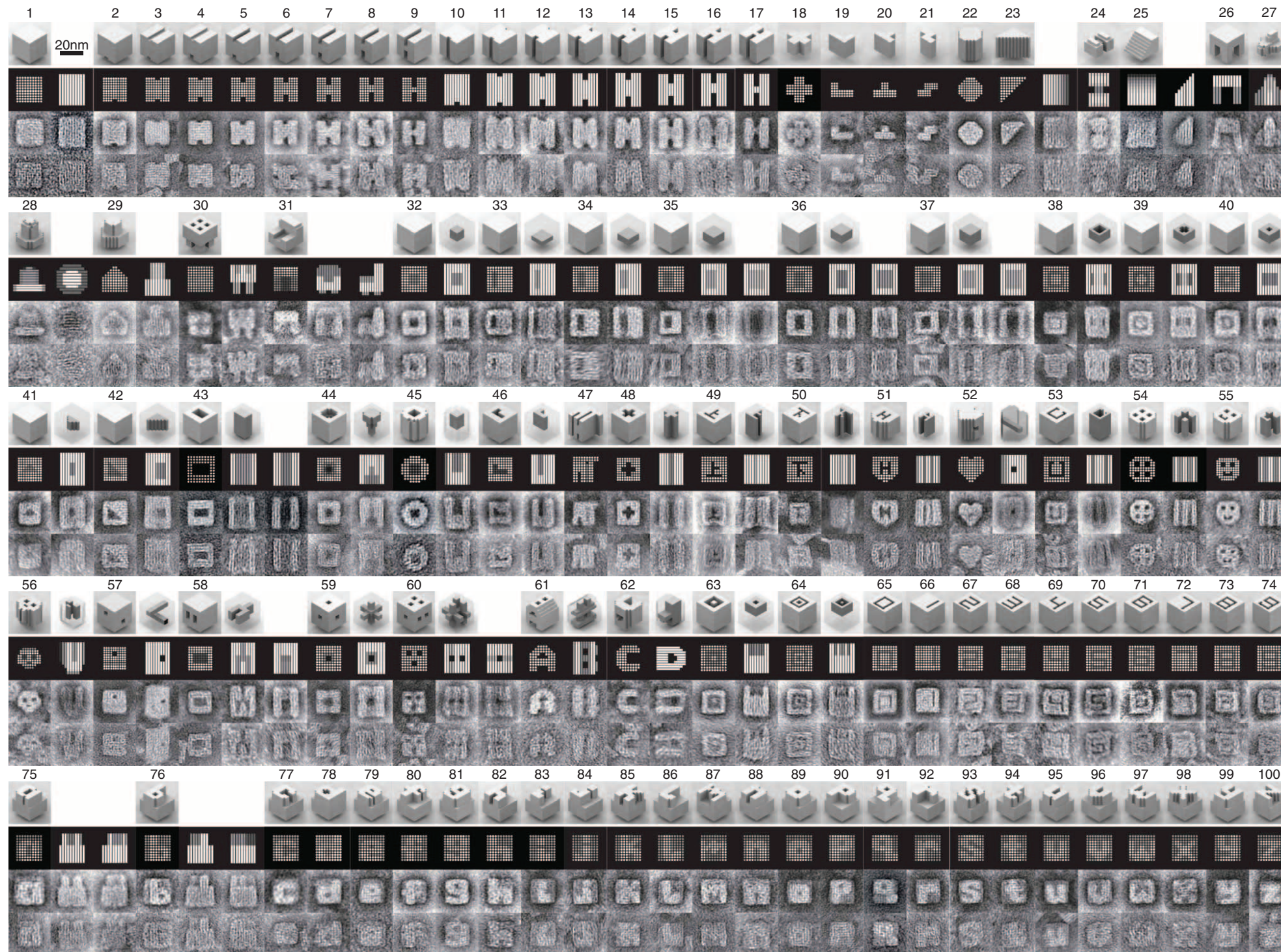
Short staple DNA strands are designed to fit together like lego blocks. Sequence of DNA strands determine, which “lego blocks fit together”.



Design of arbitrary structure by removal of certain DNA strands (bricks) from mixture.

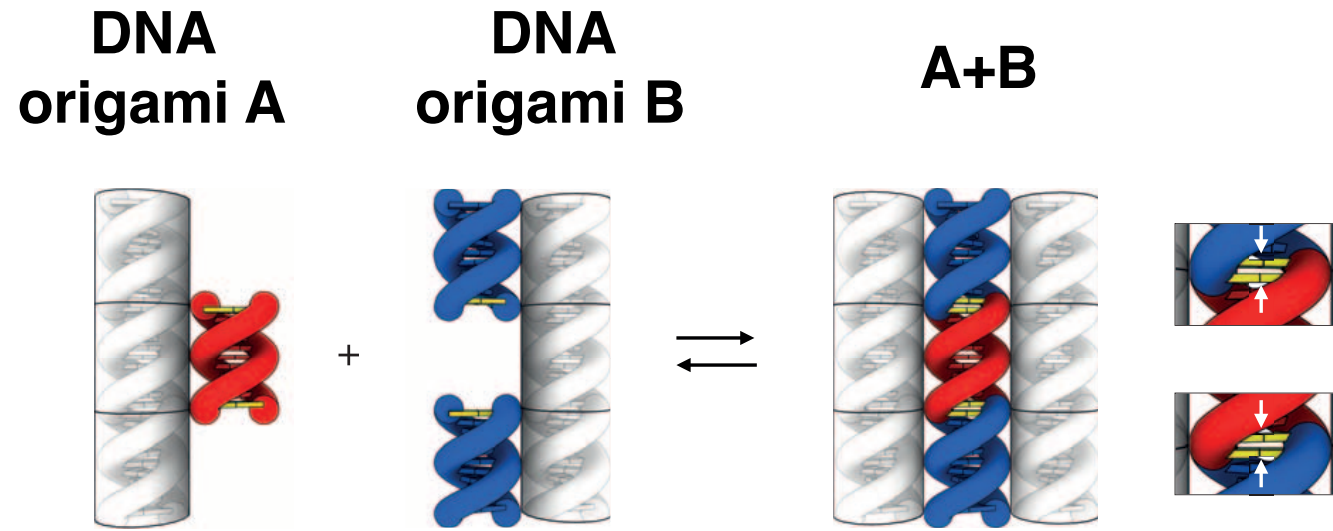
DNA brick origami

Example of generated 3D structures

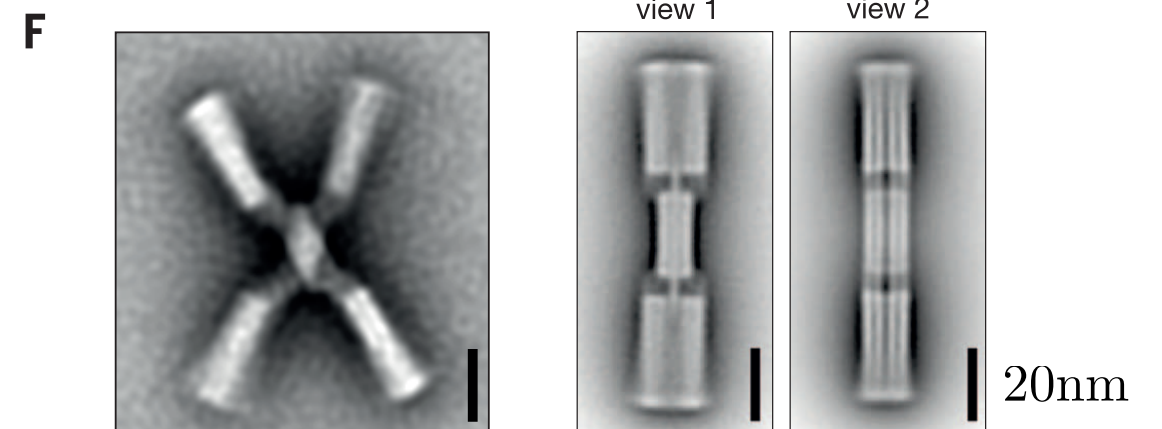
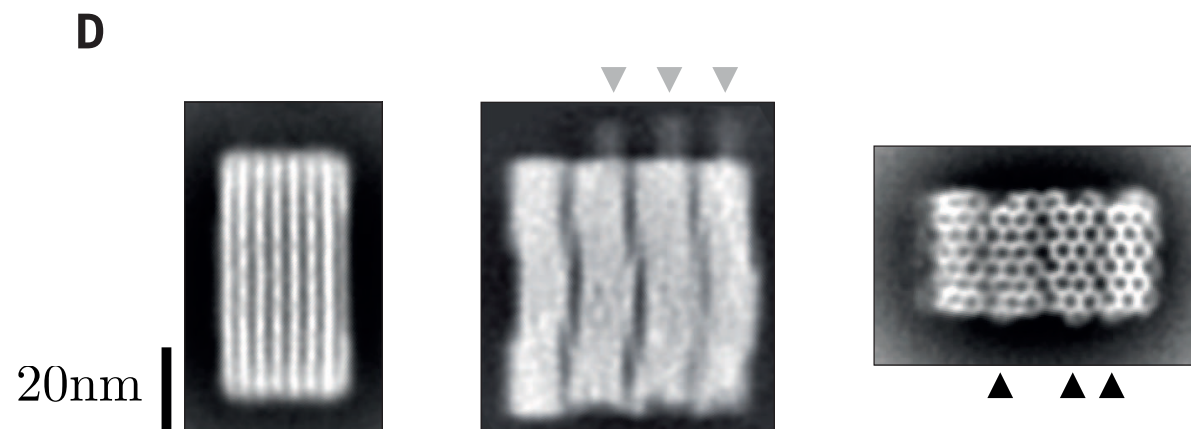
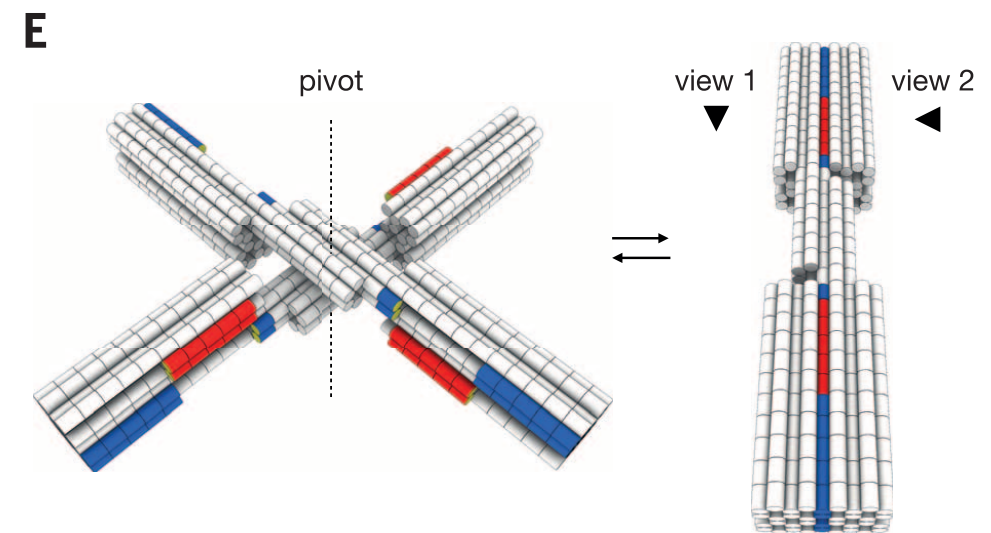
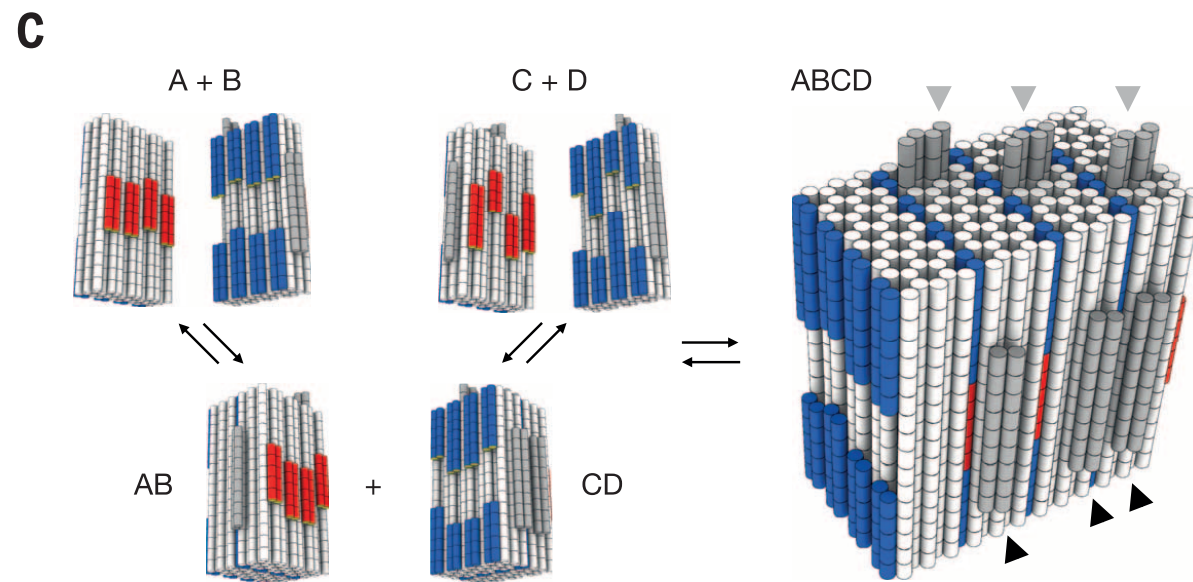


20nm

Shape complementarity with DNA origami



binding can be strengthened by additional complementary nucleotides (yellow)



Actuation of DNA origami

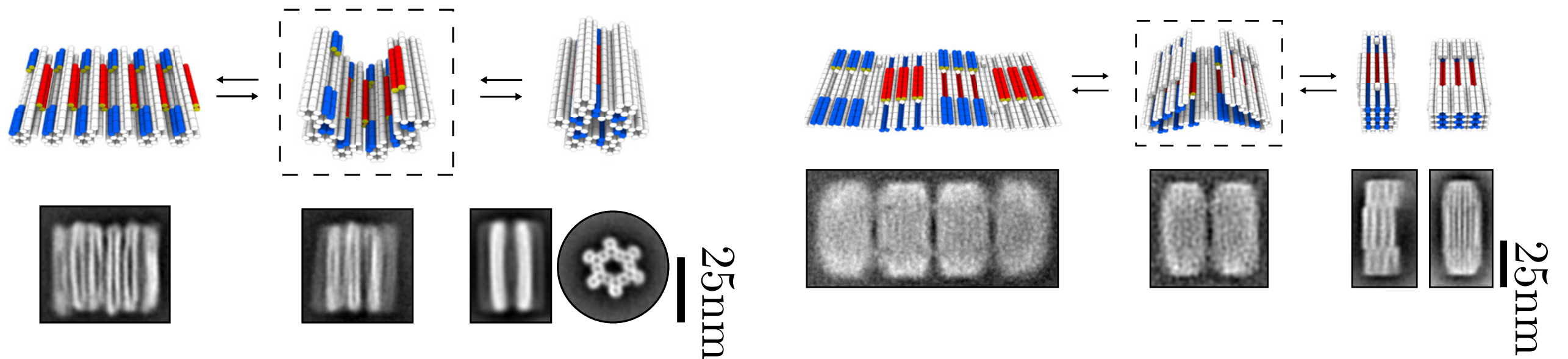
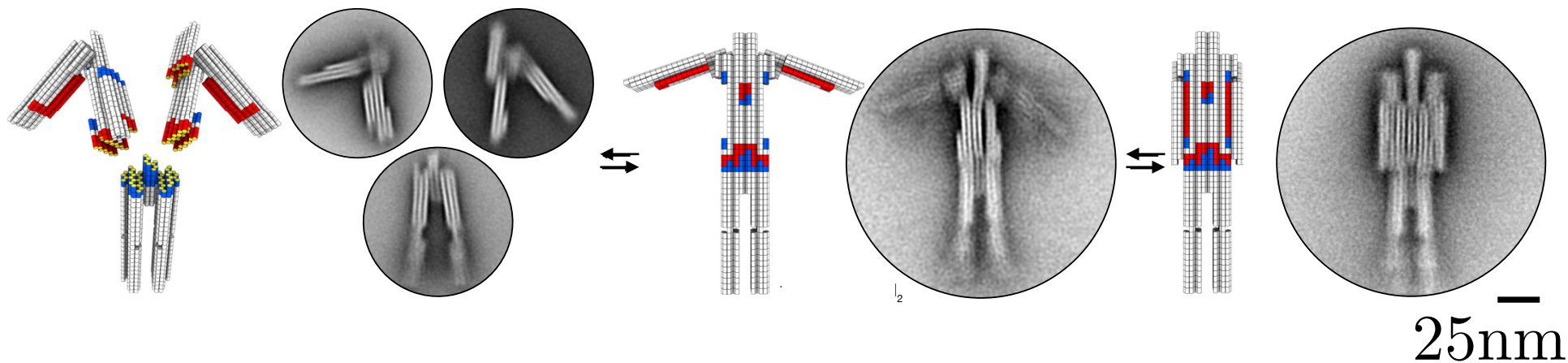
Assembly of structures is controlled by temperature and external salt, which screens the electrostatic interaction between charged DNA strands.

5 mM MgCl₂

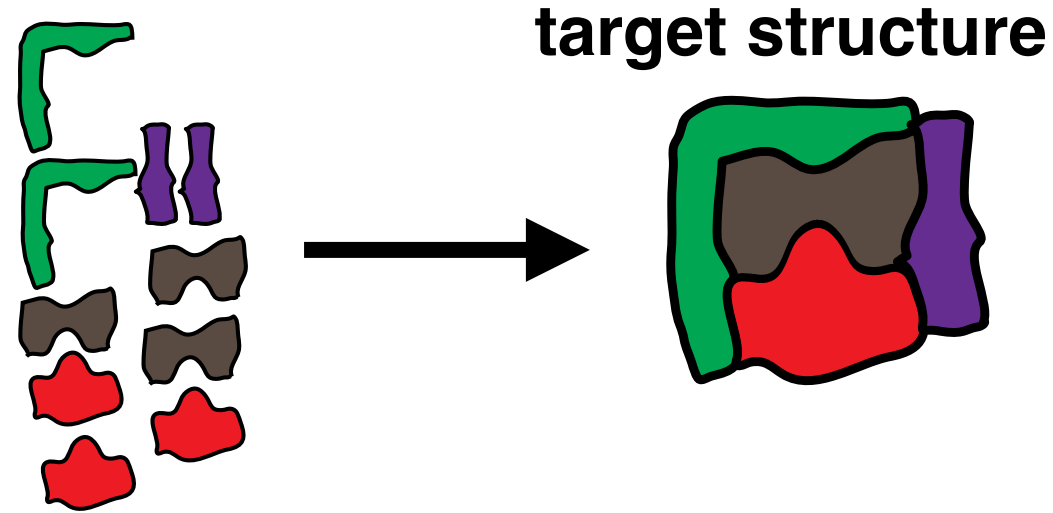
12.5 mM MgCl₂

30 mM MgCl₂

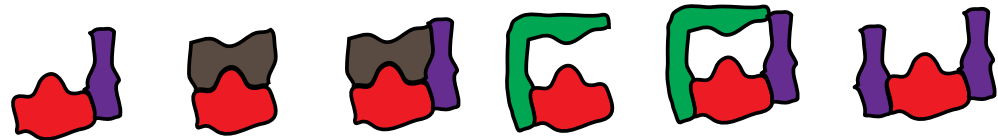
Vitruvian man
by da Vinci



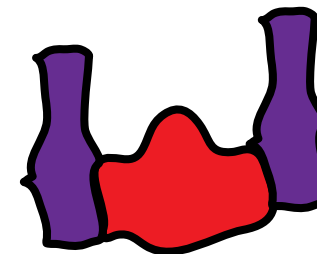
Potential issues with self-assembly



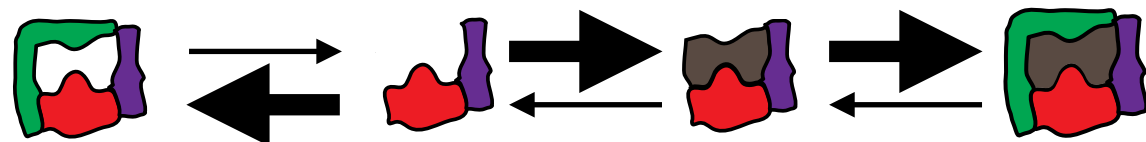
There are exponentially many competing structures. Entropic effects may dominate for large structures!



If non-specific interactions are too strong, we may get incorrectly bound structures.

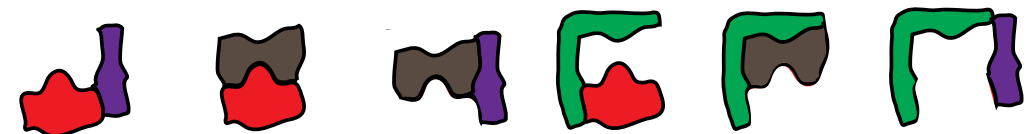


If specific interactions are too strong, we may get trapped in incomplete structures. E.g. green piece has to unbind, before the brown piece can bind correctly, but this unbinding is exponentially slow!



Kinetic arrest: target structure can be self-assembled in many different ways. All components may be used up before generating target structures! This may result in many incomplete structures.

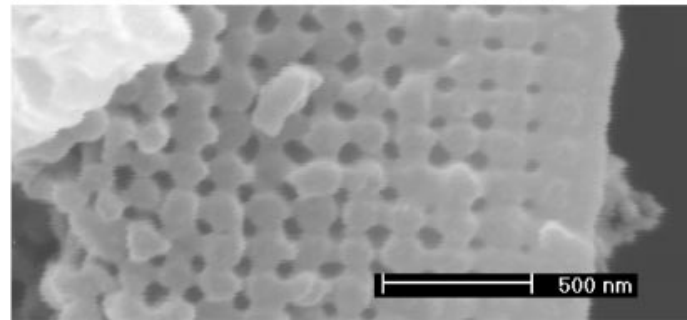
Solution: nonuniform concentrations of components may guide certain assembly pathways.



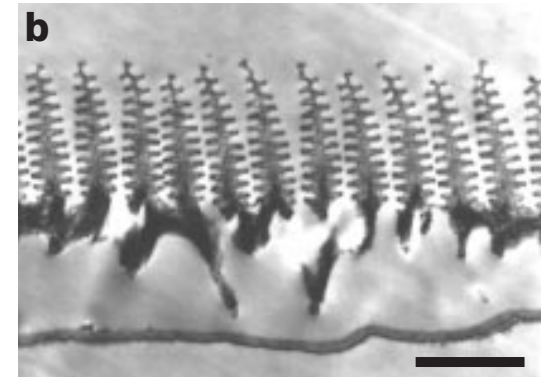
Structural colors

Structural colors of animals and plants appear due to the selective reflection of ambient light on structural features underneath the surface.

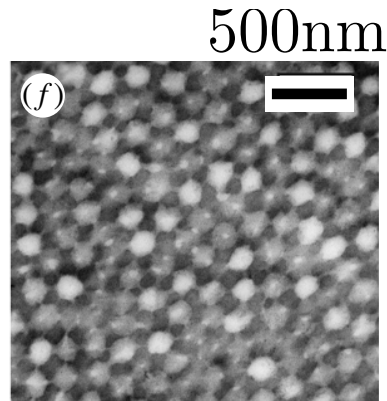
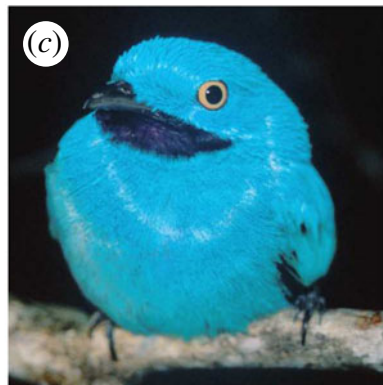
Peacock feather eyes



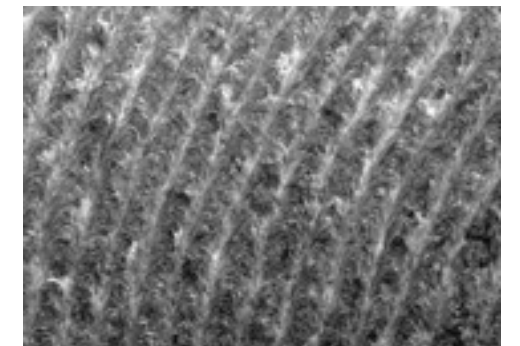
Morpho butterfly



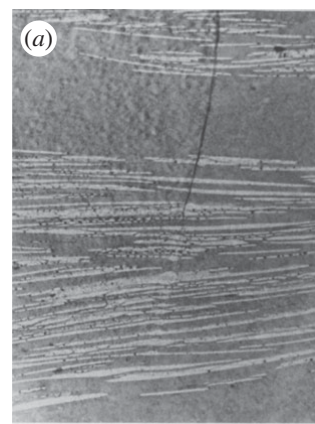
Plum-throated Cotinga



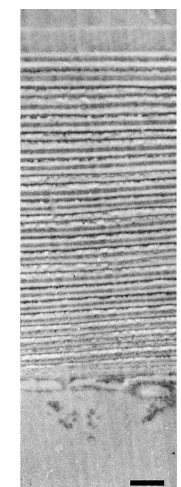
Marble berry



bleak fish



Chrysina aurigans beetle



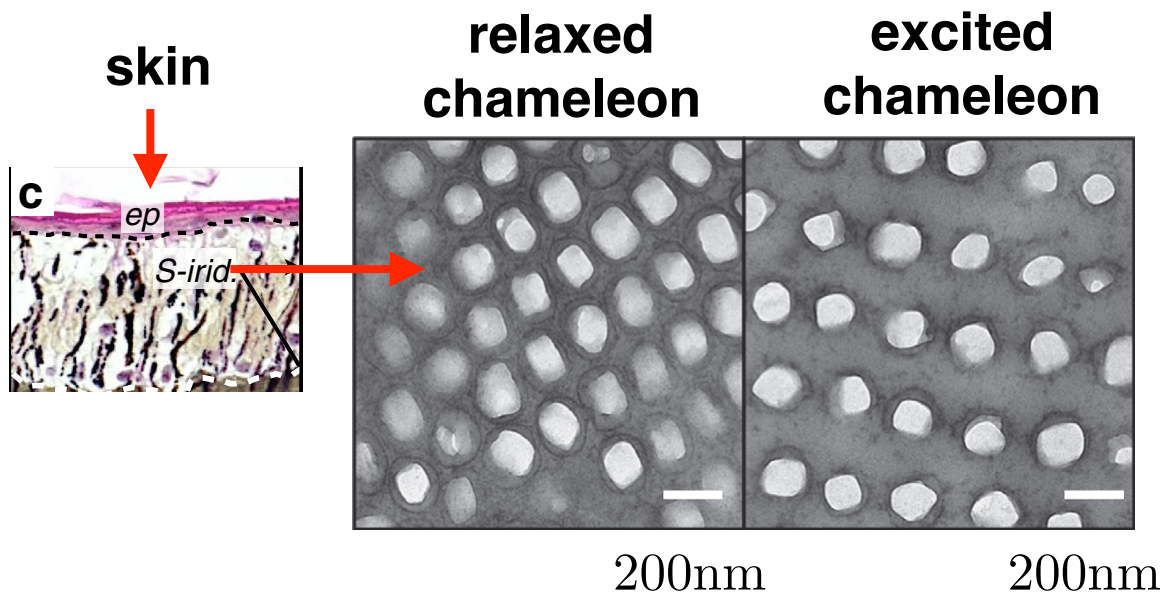
Dynamic structural colors

Chameleon (speed 8x)



J. Teyssier et al., Nat. Comm. 6, 6368 (2015)

Changes in osmotic concentration lead to the swelling of cells in excited chameleon. This changes the spacing of periodic structure from which the ambient light is reflected.

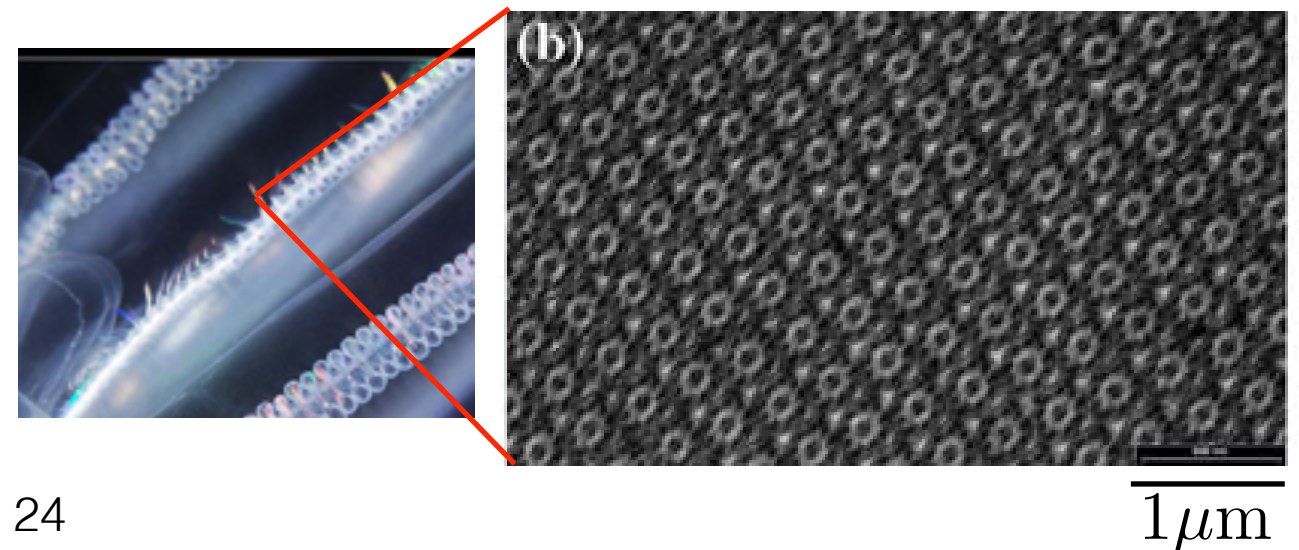


Comb Jelly (real time)



<https://www.youtube.com/watch?v=Qy90d0XvJIE>

Rainbow color waves are produced by the beating of cilia, which change the orientation of periodic structure from which the ambient light is reflected.



Dynamic colors in cephalopods

octopus

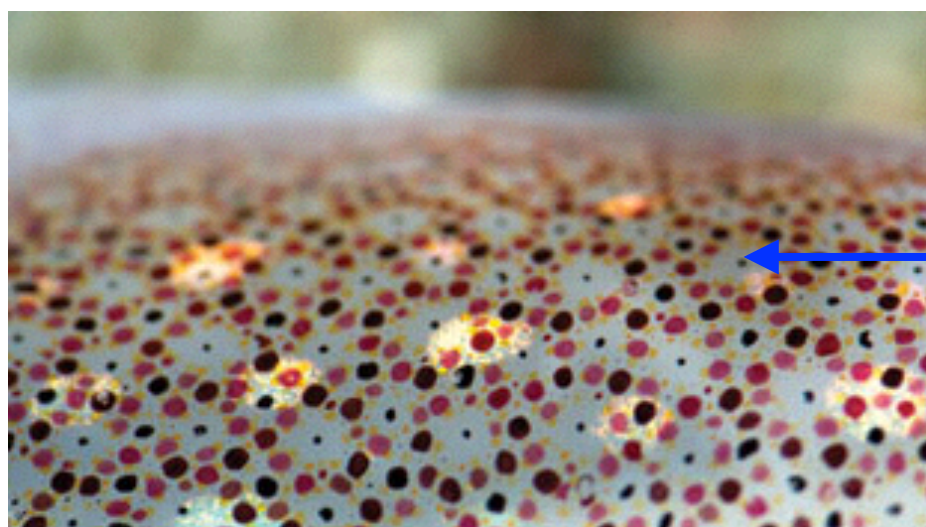


squid



<https://www.youtube.com/watch?v=9MB2ItsAPnQ>

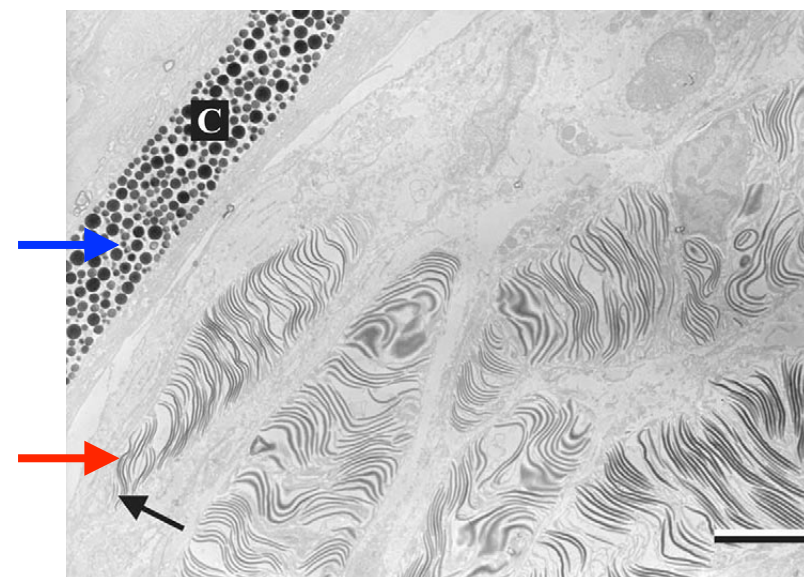
Dynamical color change in cephalopod is achieved by modulation of size and spacing of both the pigment cells and the cells reflecting light.



squid skin surface

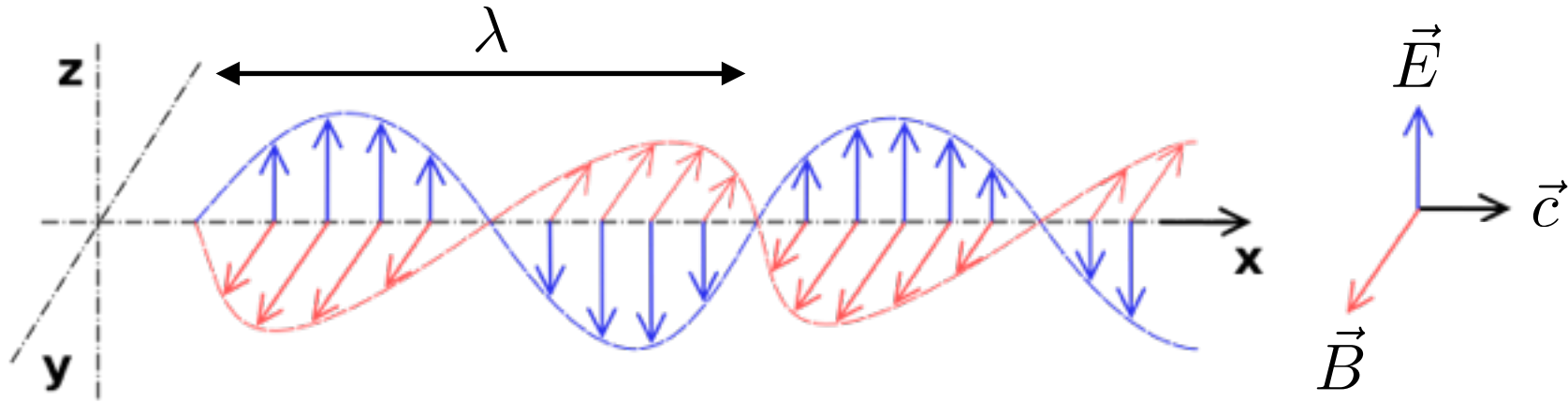
chromatophores
(pigment cells)

iridophores
(reflecting light)



7.5 μ m

Electromagnetic waves



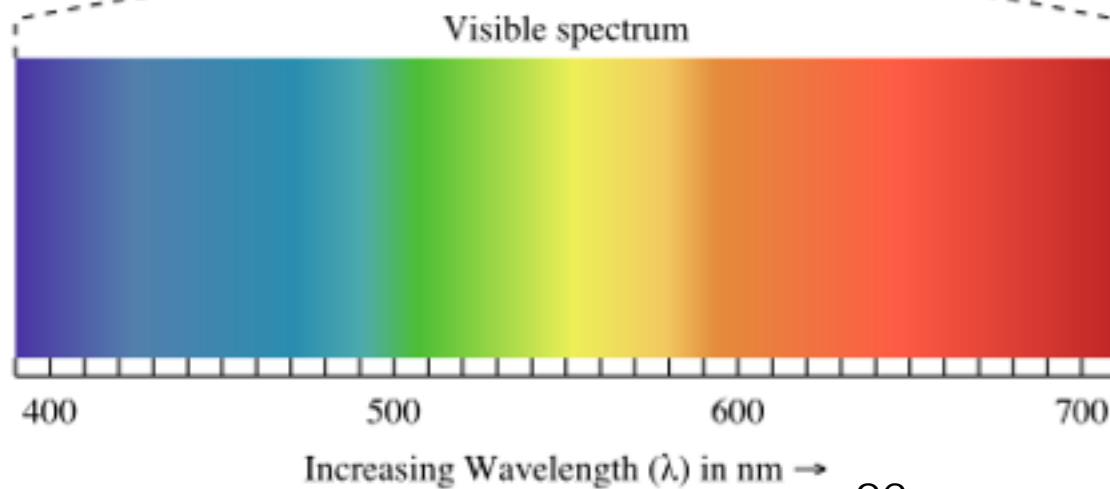
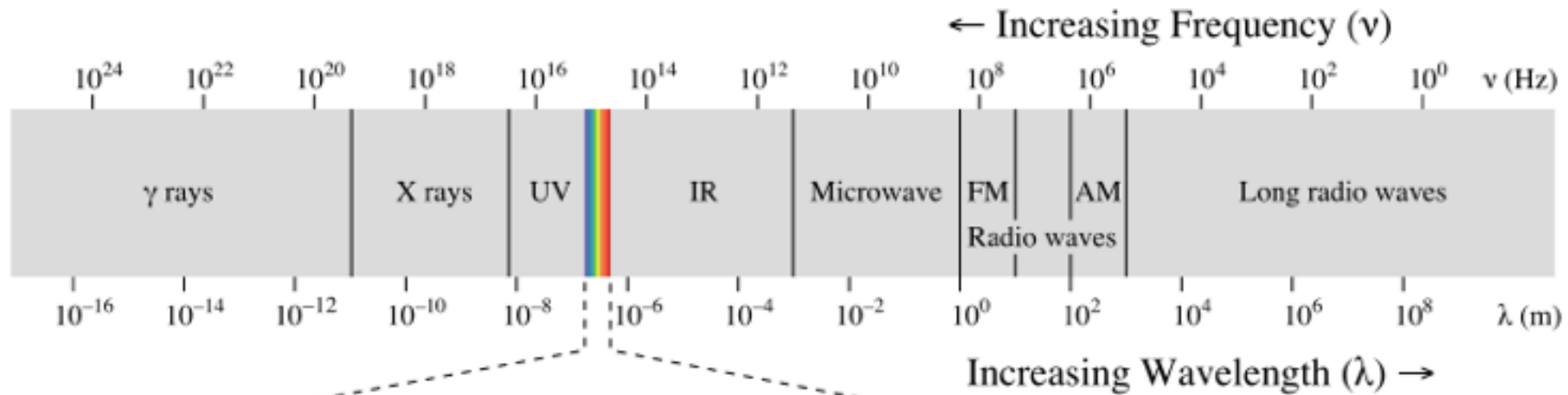
electric field
magnetic field

$$\vec{E}(x, t) = \vec{E}_0 e^{2\pi i(\nu t - x/\lambda)}$$

$$\vec{B}(x, t) = \vec{B}_0 e^{2\pi i(\nu t - x/\lambda)}$$

$$c^2 \vec{B}_0 = \vec{c} \times \vec{E}_0$$

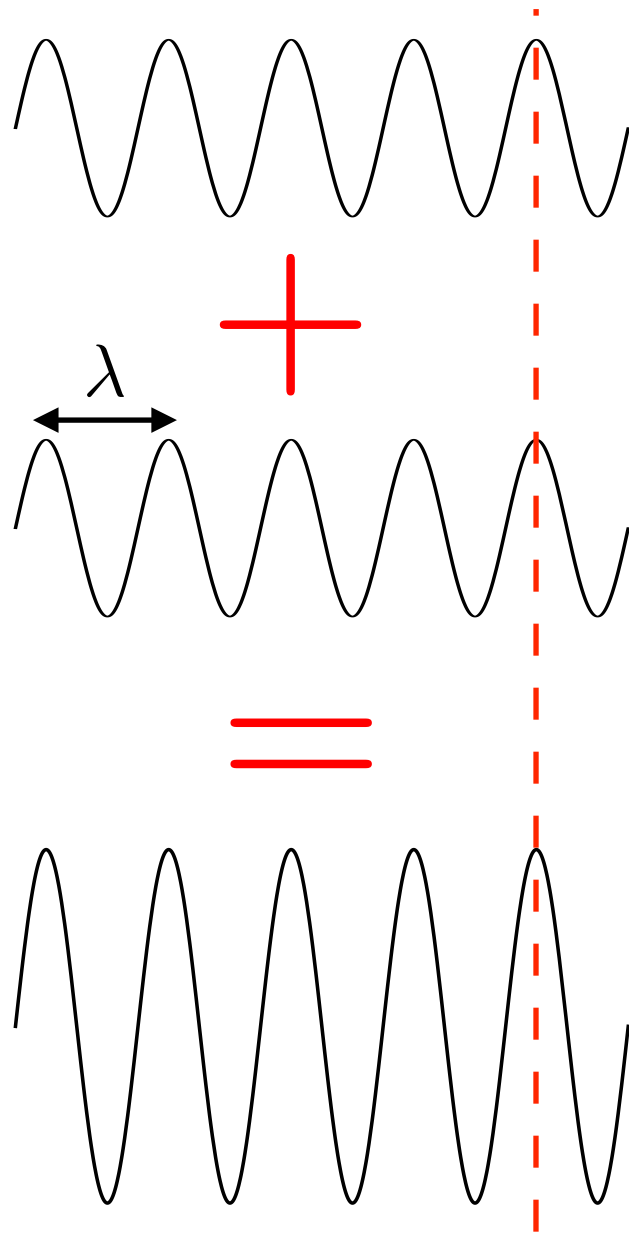
speed of light
 $c = \lambda\nu = 3 \times 10^8 \text{ m/s}$



White light coming from the sun contains electromagnetic waves of all wavelengths!

Interference

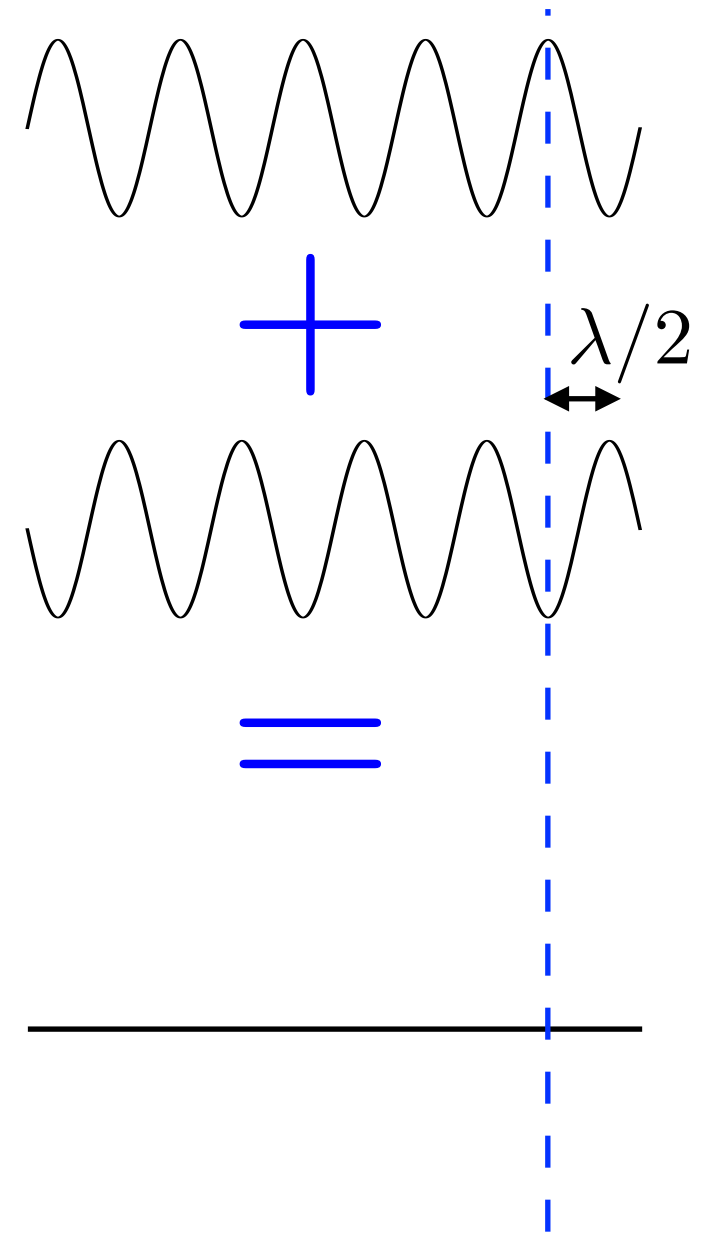
**constructive
interference**



Constructive interference occurs when the two waves are in phase: waves offset by $m\lambda$,

$$m = 0, \pm 1, \pm 2, \dots$$

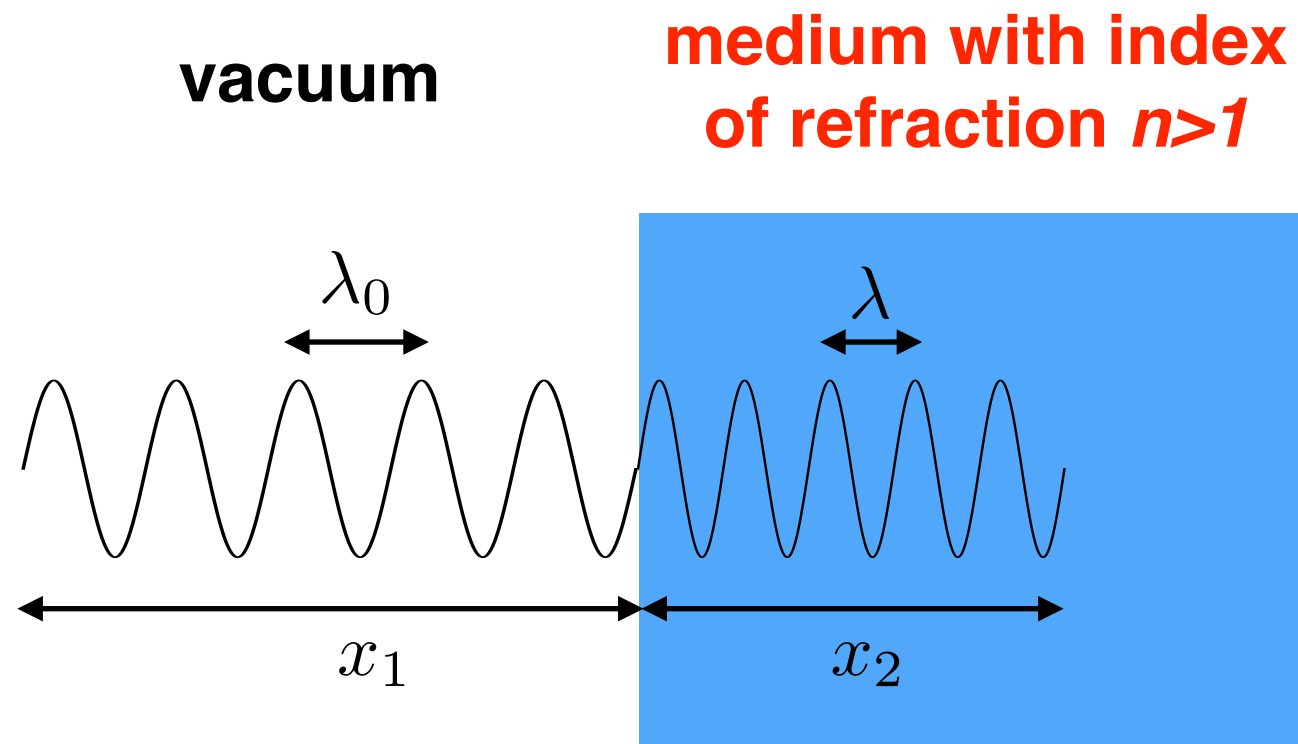
**destructive
interference**



Destructive interference occurs when the two waves are out of phase: waves offset by $(m + 1/2)\lambda$,

$$m = 0, \pm 1, \pm 2, \dots$$

Propagation of light in medium



speed of light

$$c_0 = 3 \times 10^8 \text{ m/s}$$

$$c = c_0/n$$

frequency

$$\nu_0$$

$$\nu = \nu_0$$

wavelength

$$\lambda_0$$

$$\lambda = \lambda_0/n$$

$$c_0 = \nu_0 \lambda_0$$

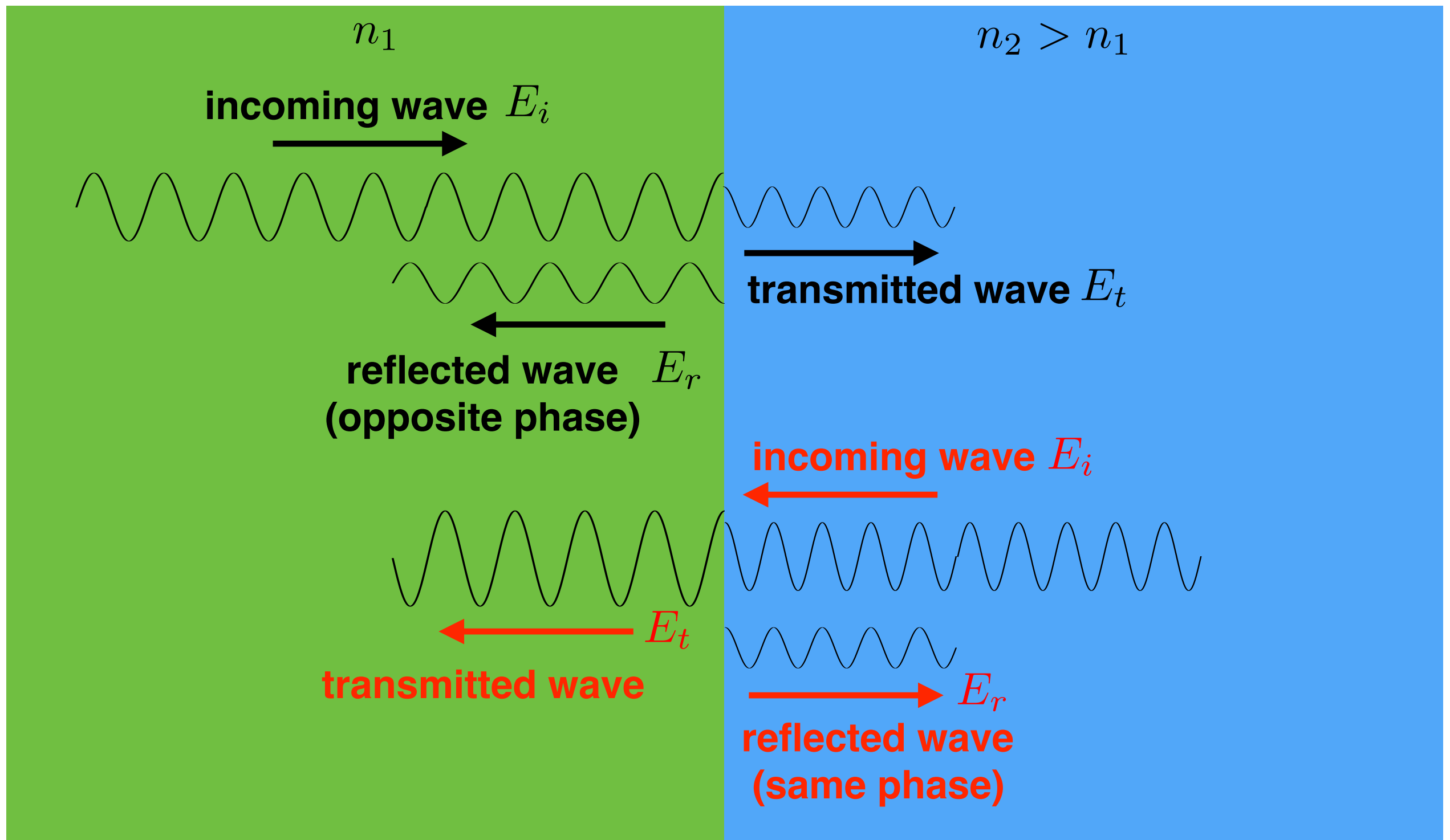
$$c = \nu \lambda$$

total number of cycles

$$\frac{x_1}{\lambda_0} + \frac{x_2}{\lambda} = \frac{x_1 + n x_2}{\lambda_0}$$

Optical path length is geometric distance multiplied by the index of refraction!

Reflection of light at the interface between two media



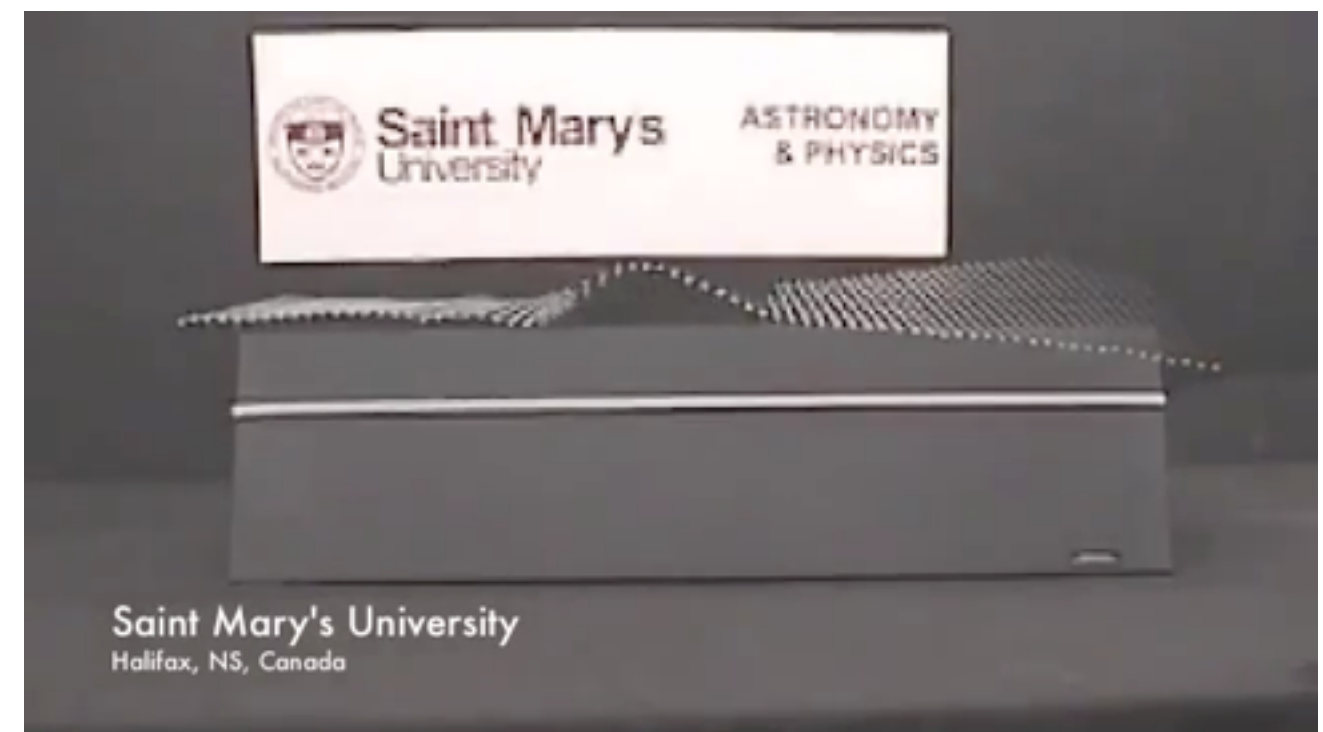
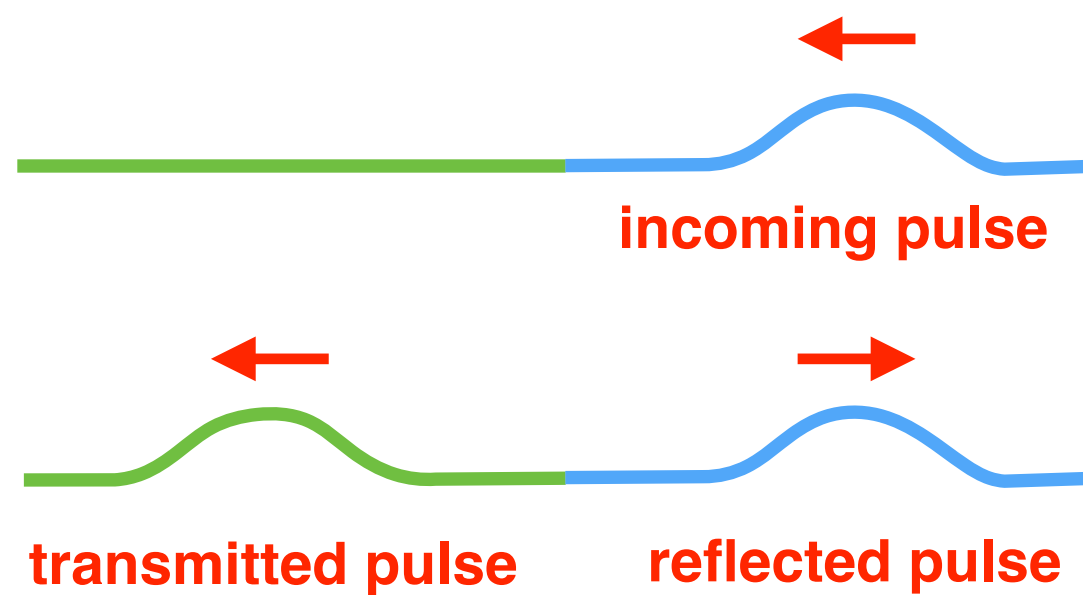
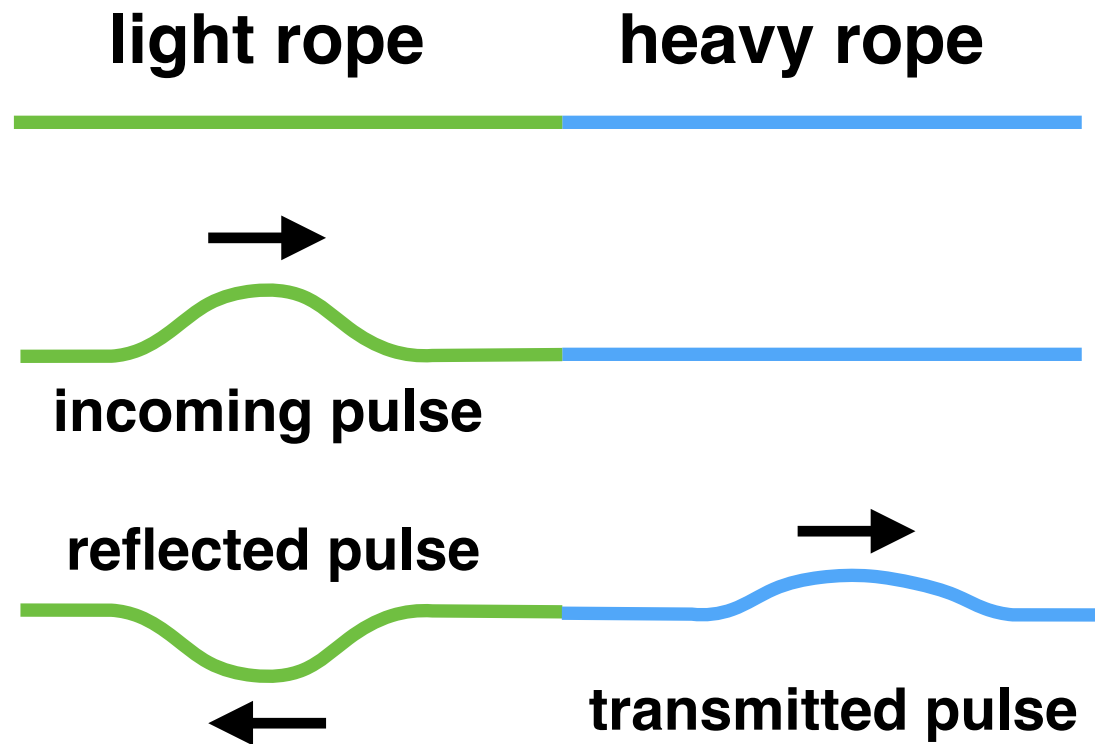
amplitude of reflected electric field

$$\frac{E_r}{E_i} = \frac{n_1 - n_2}{n_1 + n_2}$$

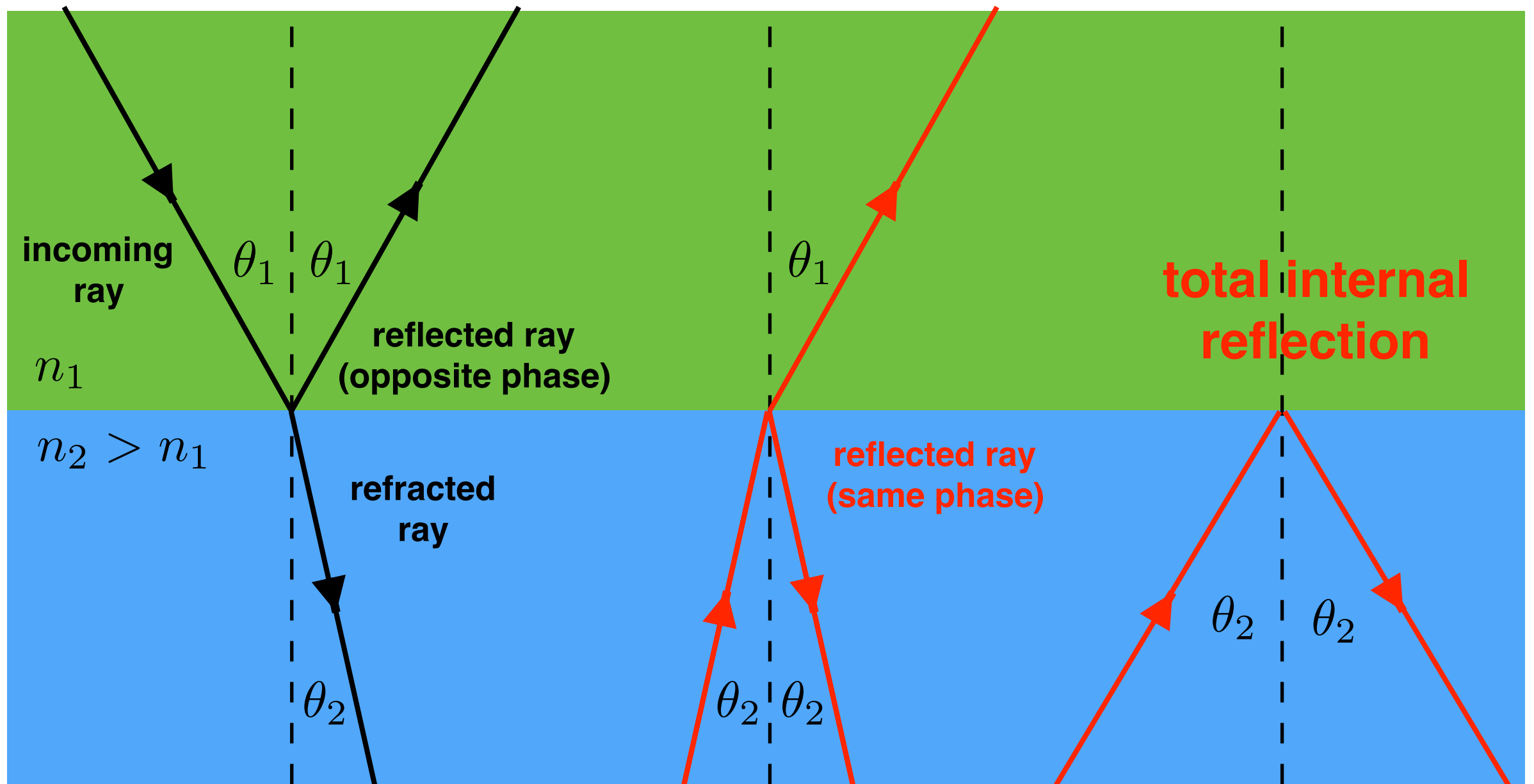
amplitude of transmitted electric field

$$\frac{E_t}{E_i} = \frac{2n_1}{n_1 + n_2}$$

Reflection of elastic waves



Refraction of light



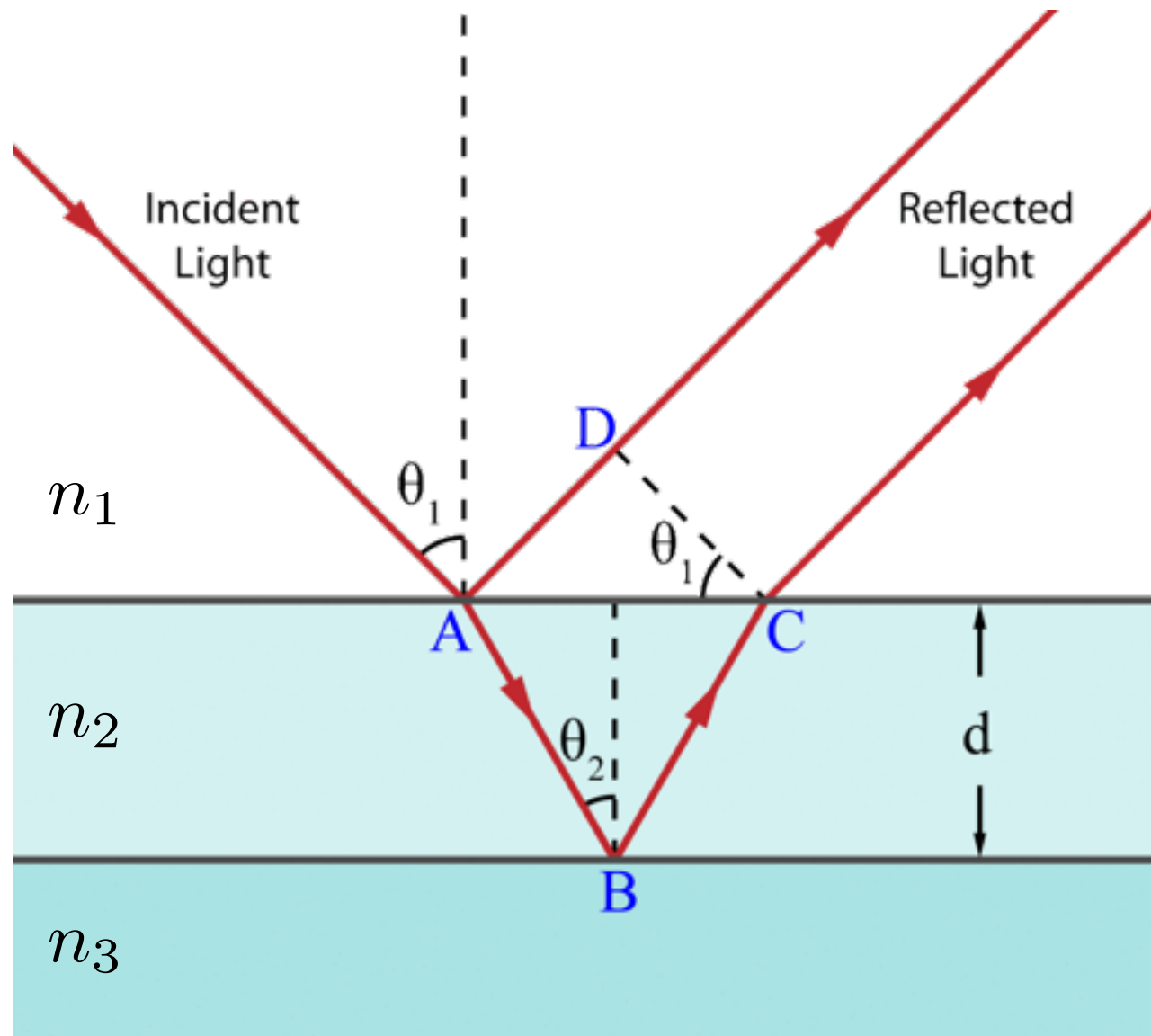
Snell's law

$$n_1 \sin \theta_1 = n_2 \sin \theta_2$$

Total internal reflection

$$\theta_2 > \arcsin(n_1/n_2)$$

Interference on thin films



difference between optical path lengths of the two reflected rays

$$OPD = n_2 (\overline{AB} + \overline{BC}) - n_1 \overline{AD}$$

$$OPD = 2n_2 d \cos(\theta_2)$$

no additional phase difference due to reflections

$$n_1 < n_2 < n_3 \quad n_1 > n_2 > n_3$$

constructive interference

$$OPD = m\lambda$$

destructive interference

$$OPD = (m + 1/2)\lambda$$

$$m = 0, \pm 1, \pm 2, \dots$$

additional π phase difference due to reflections

$$n_1 < n_2 > n_3 \quad n_1 > n_2 < n_3$$

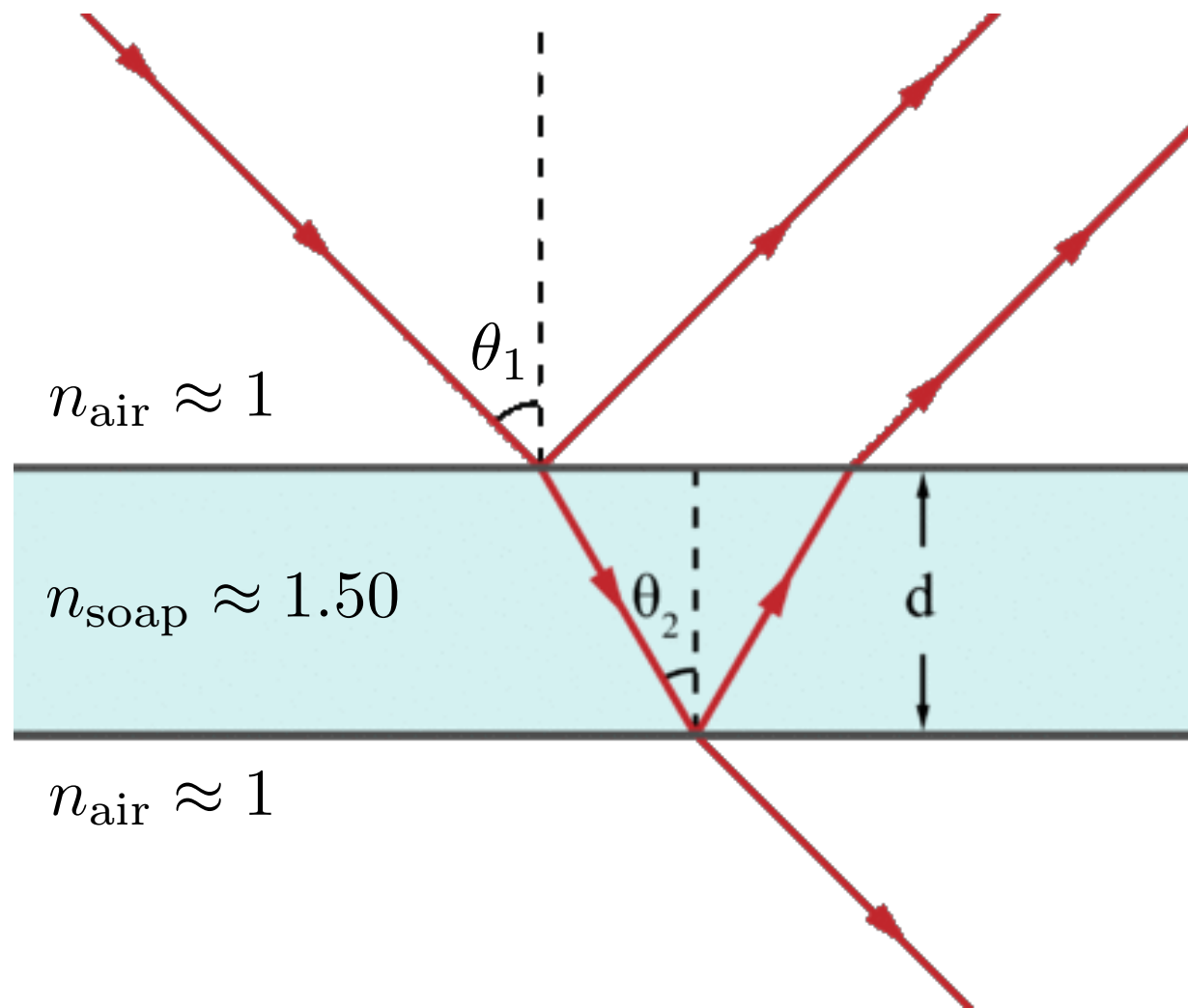
constructive interference

$$OPD = (m + 1/2)\lambda$$

destructive interference

$$OPD = m\lambda$$

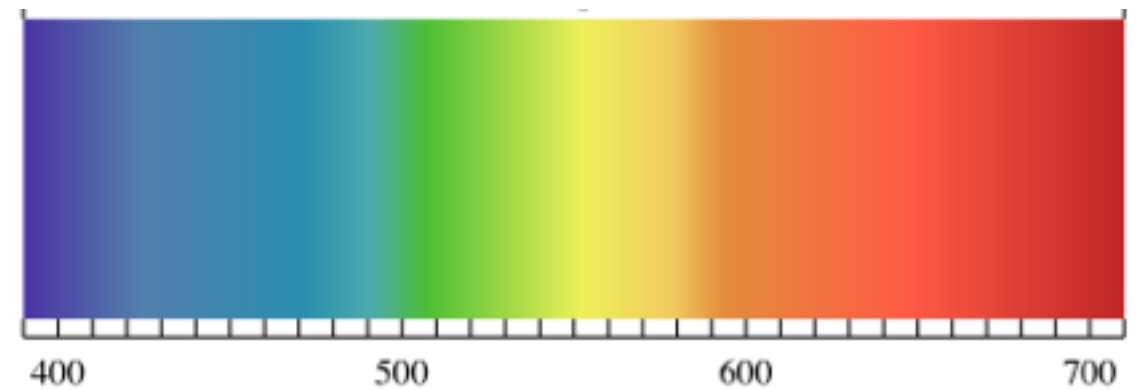
Interference on soap bubbles



soap bubble



visible spectrum



wavelength λ [nm]

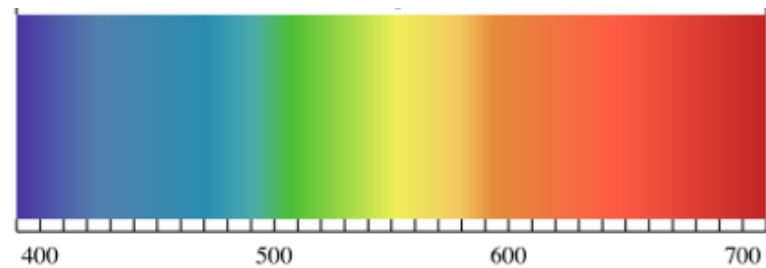
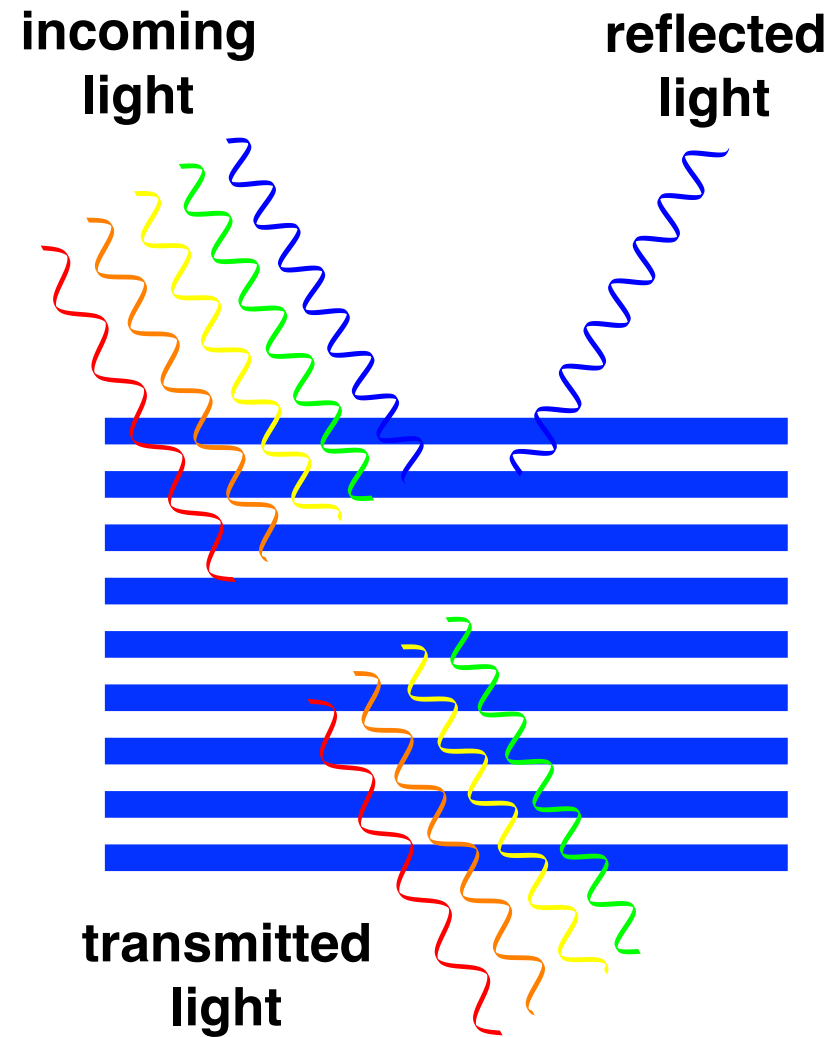
**constructive interference
for different colors happens
at different angles**

$$2dn_{\text{soap}} \cos(\theta_2) = (m + 1/2)\lambda$$

$$m = 0, \pm 1, \pm 2, \dots$$

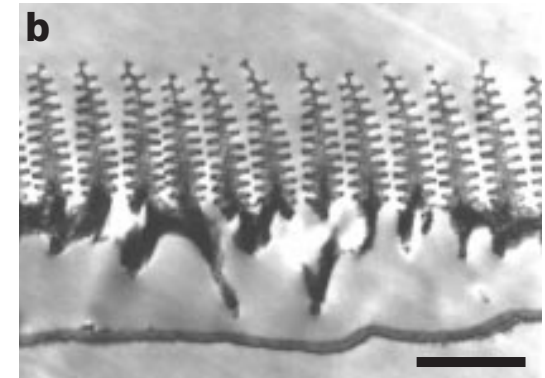
Single structural color

Single reflected color on structures with uniform spacing



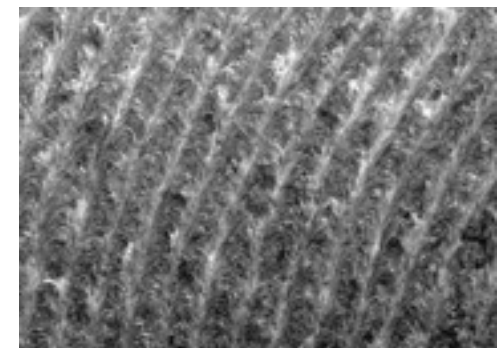
wavelength λ [nm]

Morpho butterfly



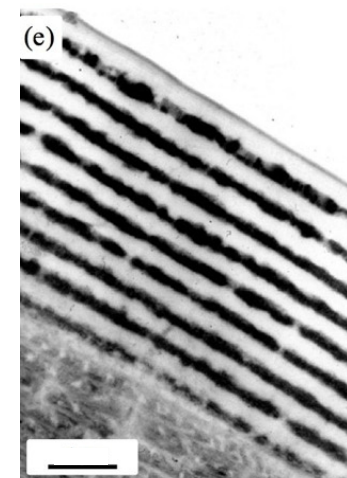
1.7 μm

Marble berry



250nm

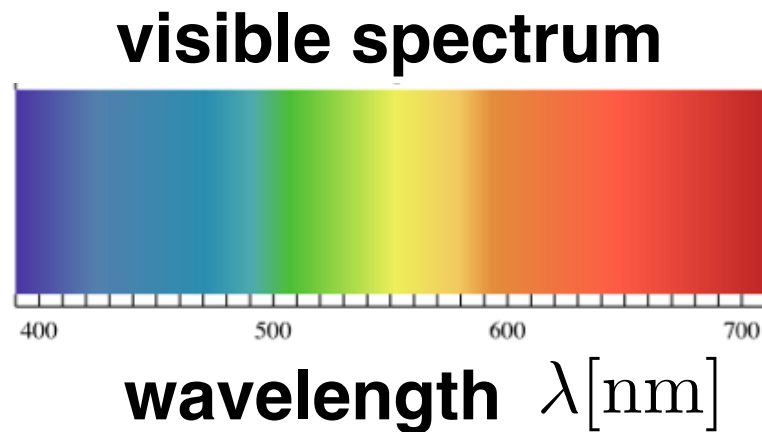
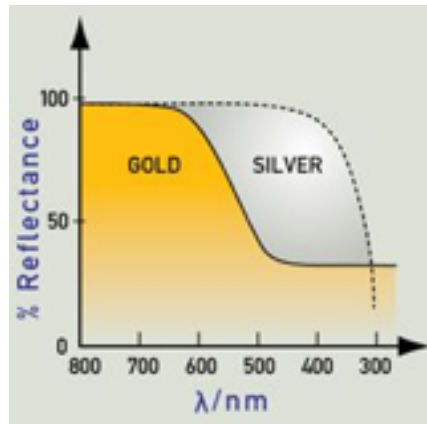
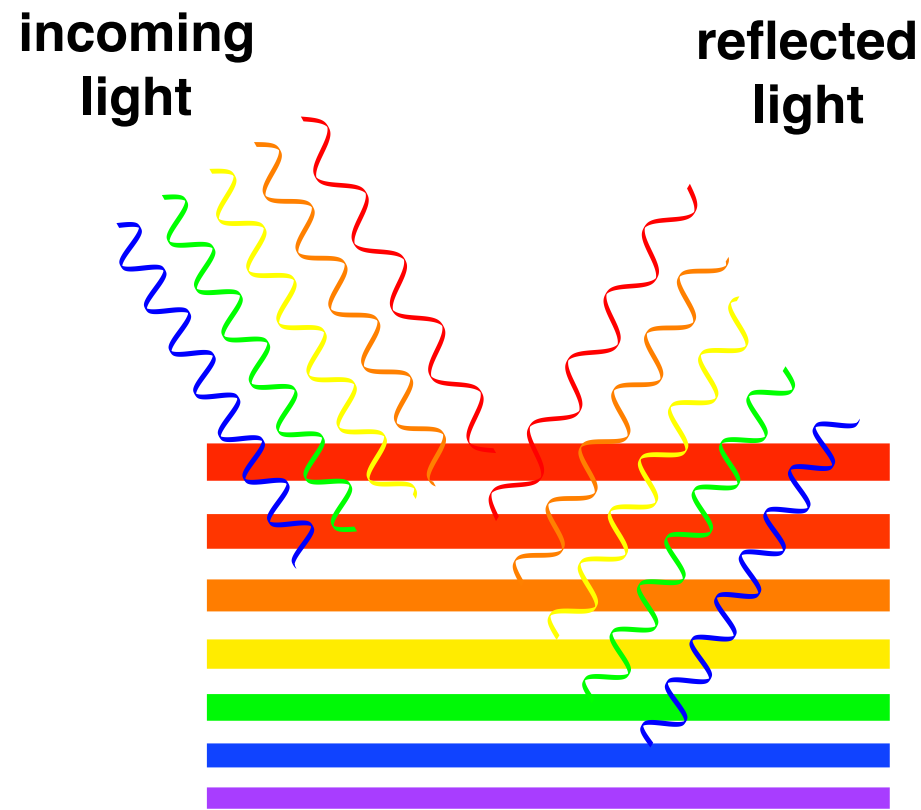
Chrysochroa raja beetle



1 μm

Silver and gold structural colors

Many colors reflected on structures with varying spacing

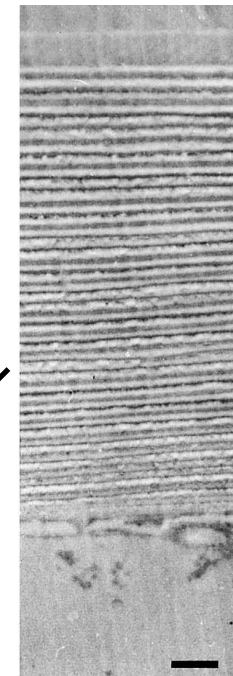


chirped structure

Chrysina limbata beetle



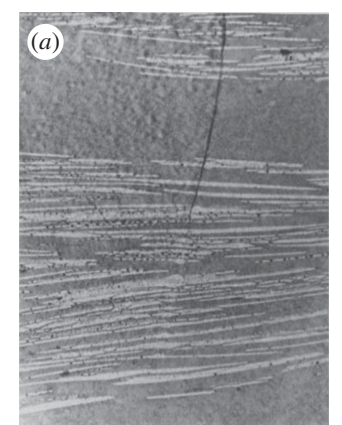
Chrysina aurigans beetle



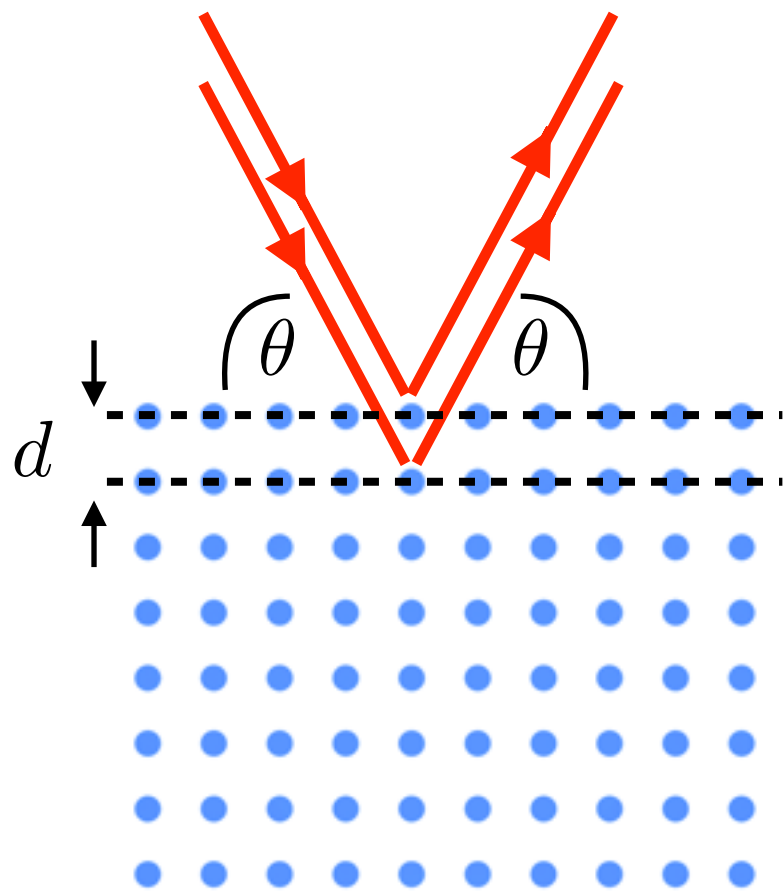
thicker
↓
thinner

disordered layer spacing

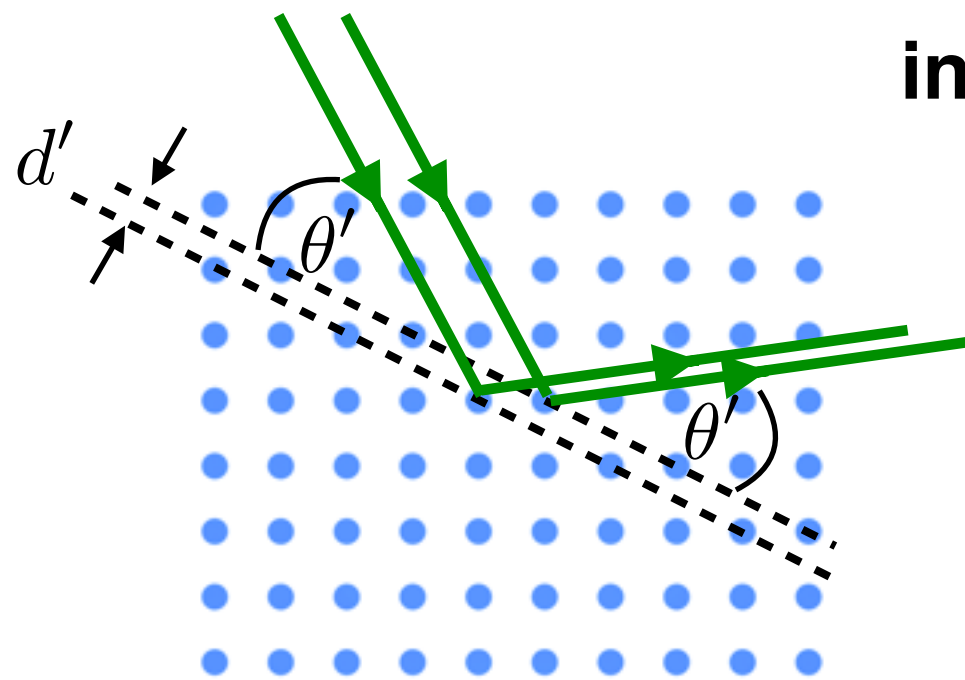
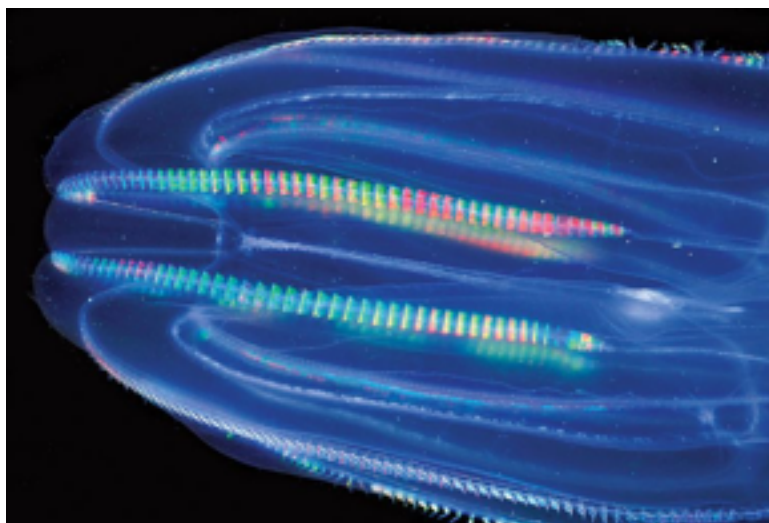
bleak fish



Bragg scattering on crystal layers



Comb jelly



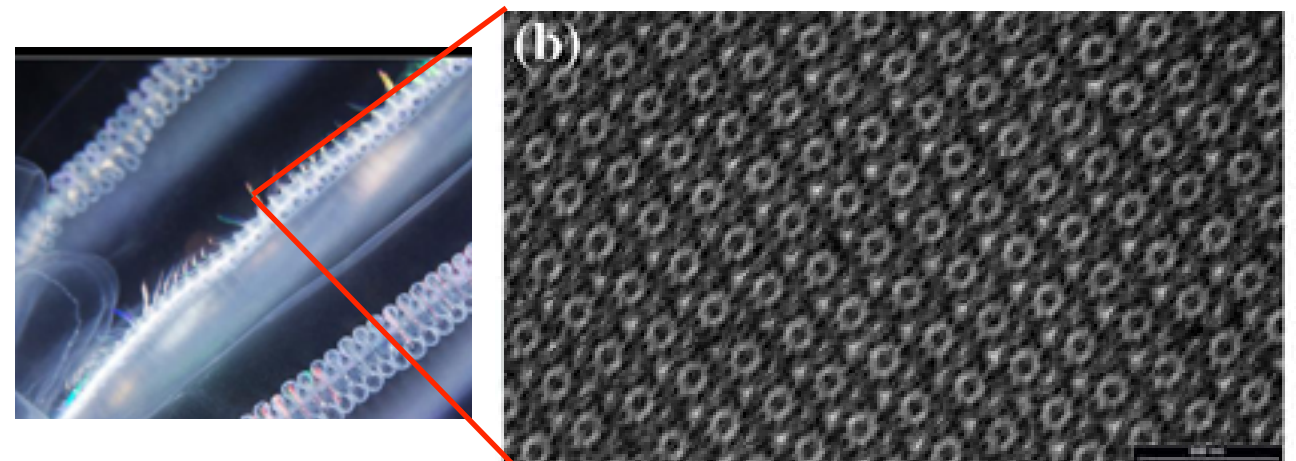
**constructive
interference condition**

$$2d \sin \theta = m\lambda$$

$$2d' \sin \theta' = m\lambda'$$

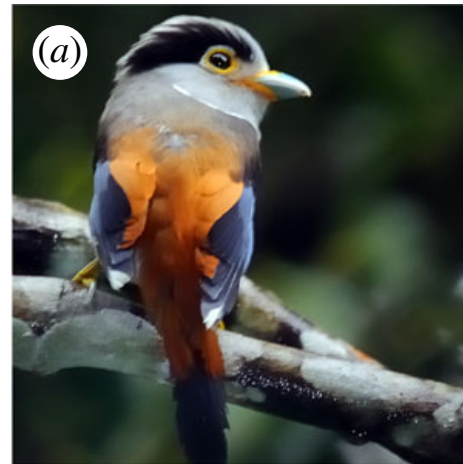
$$m = 0, \pm 1, \pm 2, \dots$$

Beating cilia are changing crystal orientation



Scattering on disordered structures

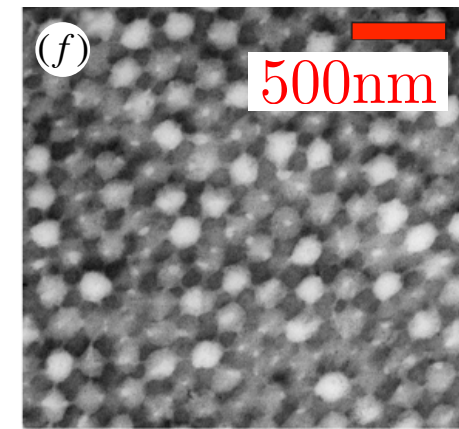
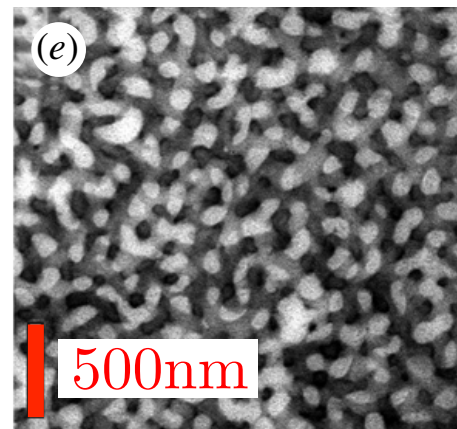
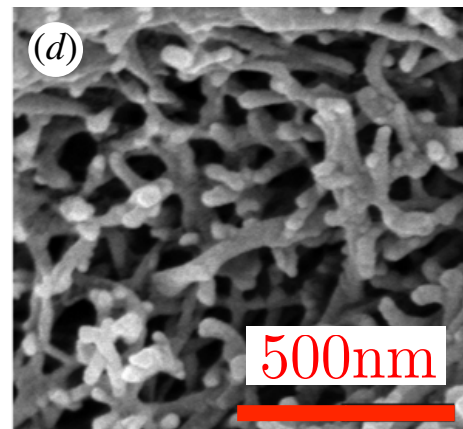
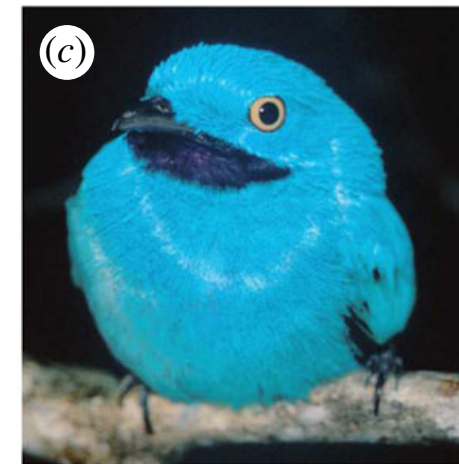
**Silver-breasted
Broadbill**



**Eastern
bluebird**



**Plum-throated
Cotinga**



**Disordered structures that are locally order
and have a characteristic length scale.**

**This length scale determines what light
wavelengths are preferentially scattered.**

This gives rise to blue colors in birds above.

Noise barriers around the Amsterdam airport



Sound from airplanes that are landing and taking off is reflected from artificial barriers into the atmosphere.