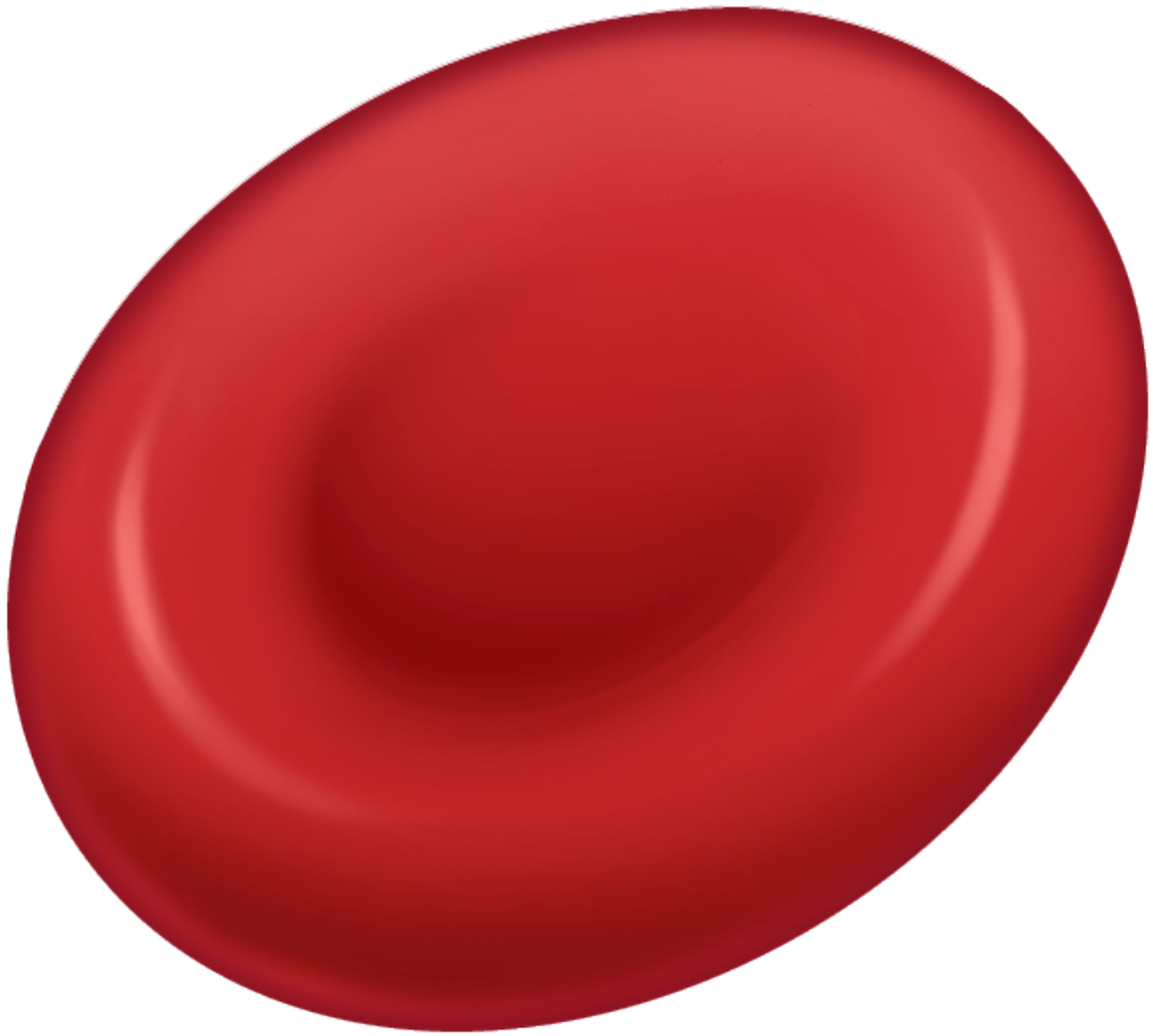
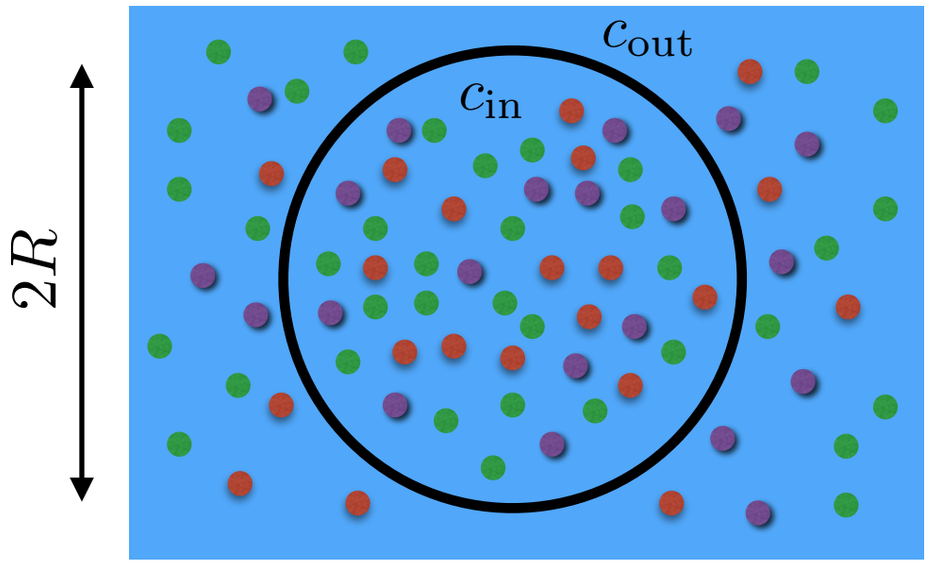
MAE 545: Lecture 14 (3/29)

Shapes of vesicles and cells



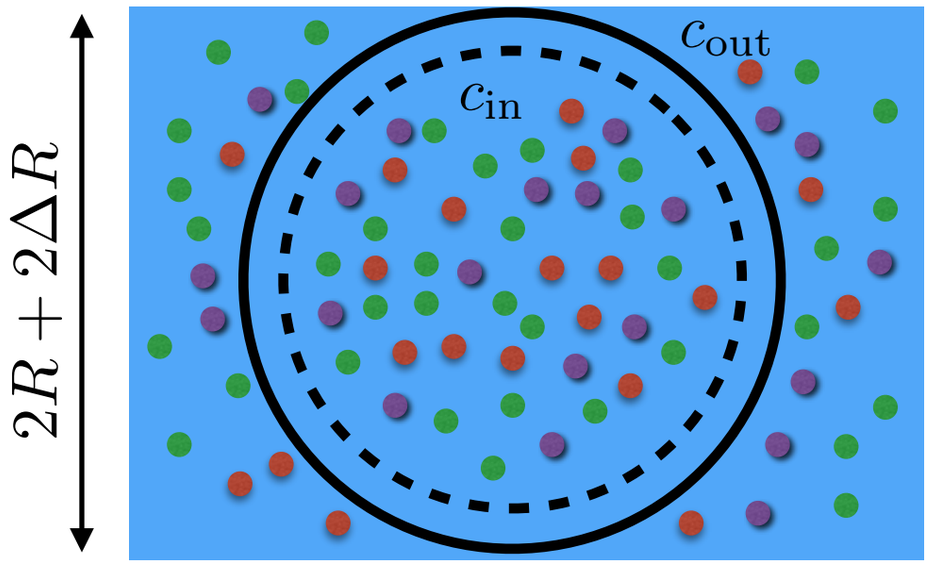
Cells in hypotonic and hypertonic solutions

$c_{\text{in}} > c_{\text{out}}$ **hypotonic solution**



Water flows in the cell until the mechanical equilibrium is reached.

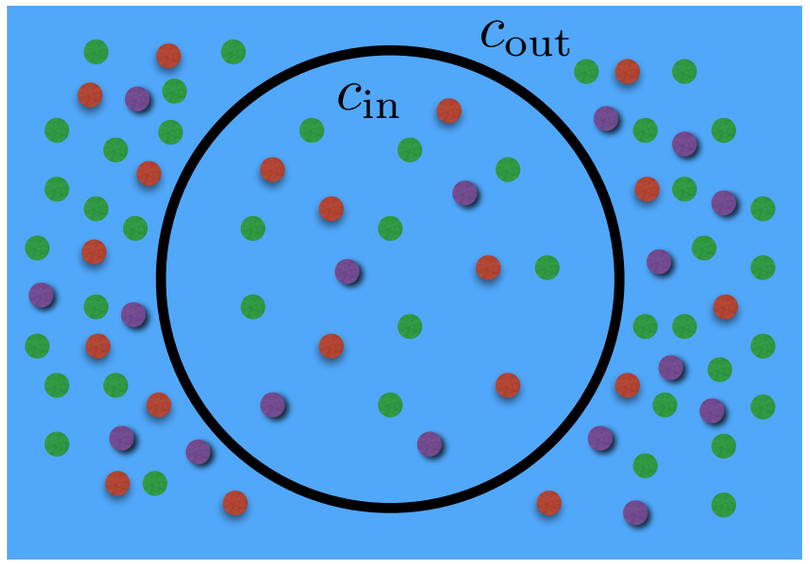
$c_{\text{in}} > c_{\text{out}}$



$$\frac{\Delta R}{R} = \frac{R\Delta p}{4B} = \frac{R}{4B} k_B T \left(c_{\text{in}} - c_{\text{out}}\right)$$

2

$c_{\text{in}} < c_{\text{out}}$ **hypertonic solution**

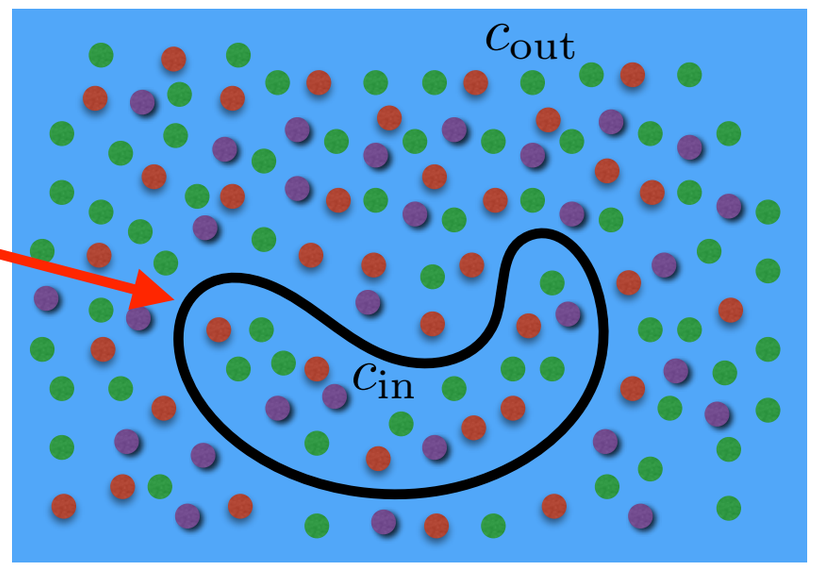


Water flows out of the cell until concentrations become equal.

$c_{\text{in}} = c_{\text{out}}$

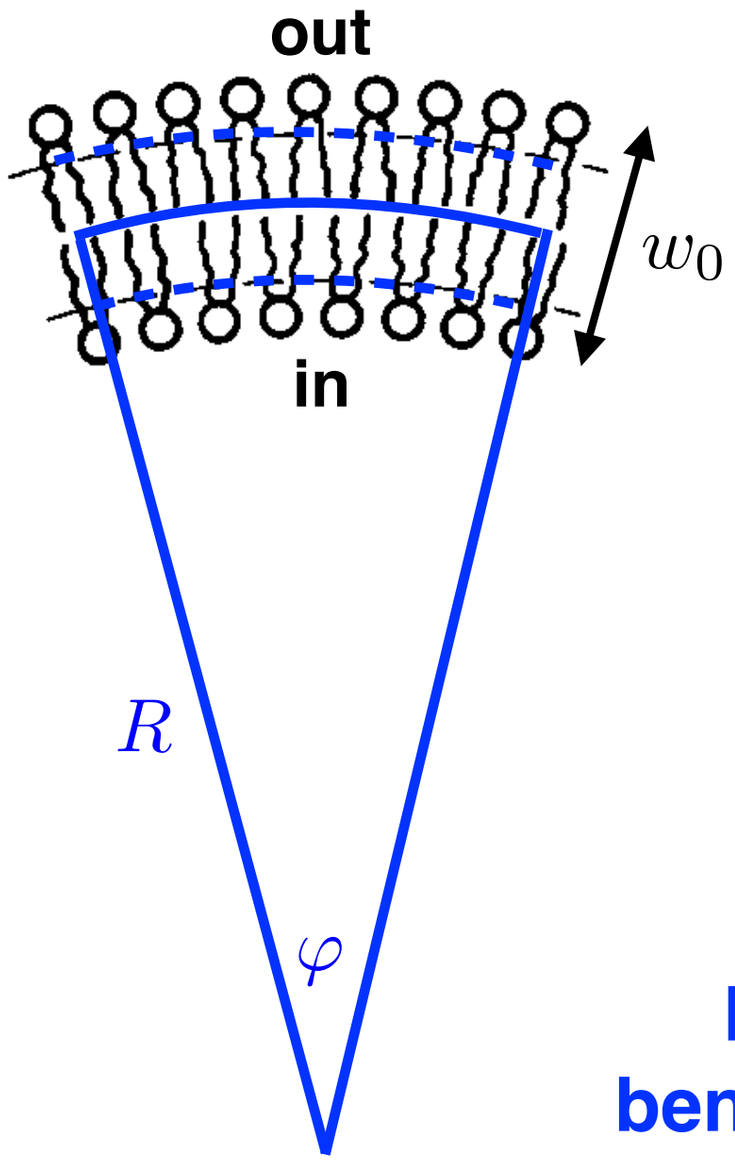
Thin cell membrane prefers to bend rather than compress

How can we estimate the shape of "deflated" cells?



$$V_0 = \frac{N}{c_{\text{out}}}$$

Area difference between lipid layers



Length difference for 2D example on the left

$$\Delta\ell = \ell_{\text{out}} - \ell_{\text{in}} = (R + w_0/2)\varphi - (R - w_0/2)\varphi$$

$$\Delta\ell = w_0\varphi = \frac{w_0\ell}{R}$$

Area difference between lipid layers in 3D

$$\Delta A = A_{\text{out}} - A_{\text{in}} = w_0 \int dA \left(\frac{1}{R_1} + \frac{1}{R_2}\right)$$

Lipids can move within a given layer, but flipping between layers is unlikely. This sets a preferred area difference ΔA_0 .

Non-local bending energy

$$E = \frac{k_r}{2Aw_0^2}\left(\Delta A - \Delta A_0\right)^2$$

$$k_r \approx 3\kappa \approx 60 k_B T$$

Total elastic energy for cells (vesicles)

Shape of cells (vesicles) can be obtained by minimizing the total elastic energy

this term is constant for a given topology

$$E = \int dA \left[\frac{1}{2}(B-\mu)u_{ii}^2 + \mu u_{ij}^2 + \frac{\kappa}{2}\left(\frac{1}{R_1}+\frac{1}{R_2}-C_0\right)^2 + \frac{\kappa_G}{R_1 R_2}\right]$$

$$+\frac{k_r}{2A_0 w_0^2}\left(\Delta A - \Delta A_0\right)^2 + \frac{1}{2}k_B T c_{\text{out}} V_0 \left(\frac{V-V_0}{V_0}\right)^2$$

Energetically it is very costly to change the cell volume V_0 and the membrane area A_0 (large bulk modulus B)!

Introduce dimensionless quantities that would be equal to 1 for sphere

definition for sphere radius	dimensionless area	dimensionless volume	dimensionless curvature	dimensionless area difference between layers	dimensionless energy
$R_0 = \sqrt{\frac{A_0}{4\pi}}$	$a = \frac{A_0}{4\pi R_0^2} = 1$	$v = \frac{V_0}{4\pi R_0^3/3}$	$c_0 = C_0 R_0$	$\Delta a = \frac{\Delta A}{8\pi w_0 R_0}$	$e = \frac{E}{8\pi\kappa}$

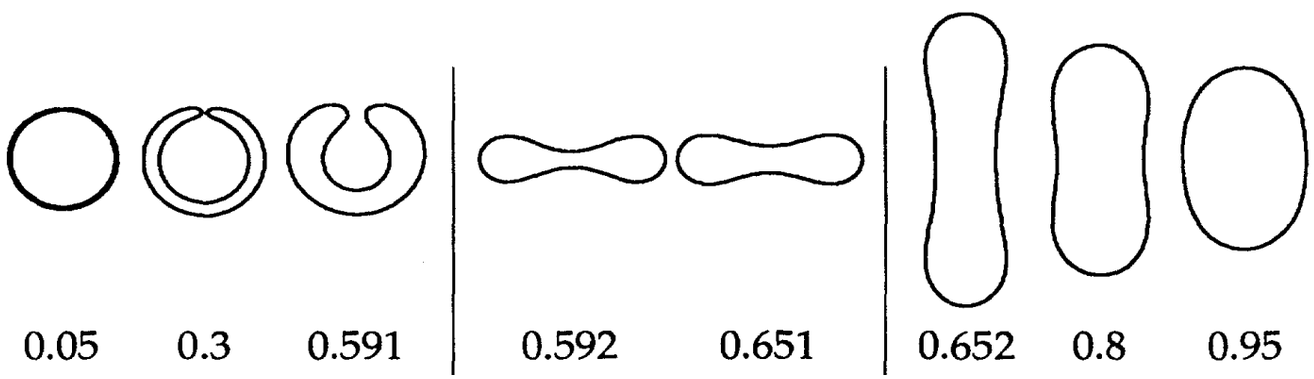
Minimal model: minimization of bending energy for lipid vesicles

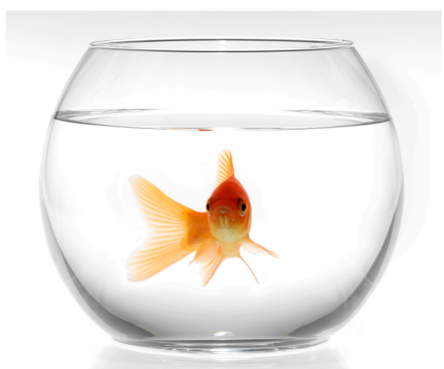
Find the shape of vesicles that minimize bending energy by constraining the volume to *v*<1.

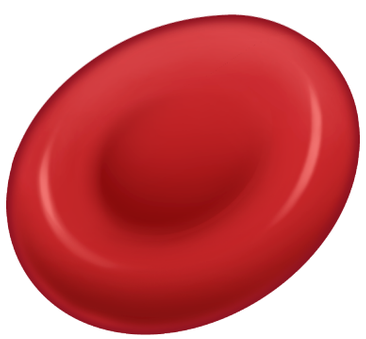
$$e = \int \frac{da}{4} \left(\frac{1}{r_1} + \frac{1}{r_2} \right)^2$$

Minimum energy configurations

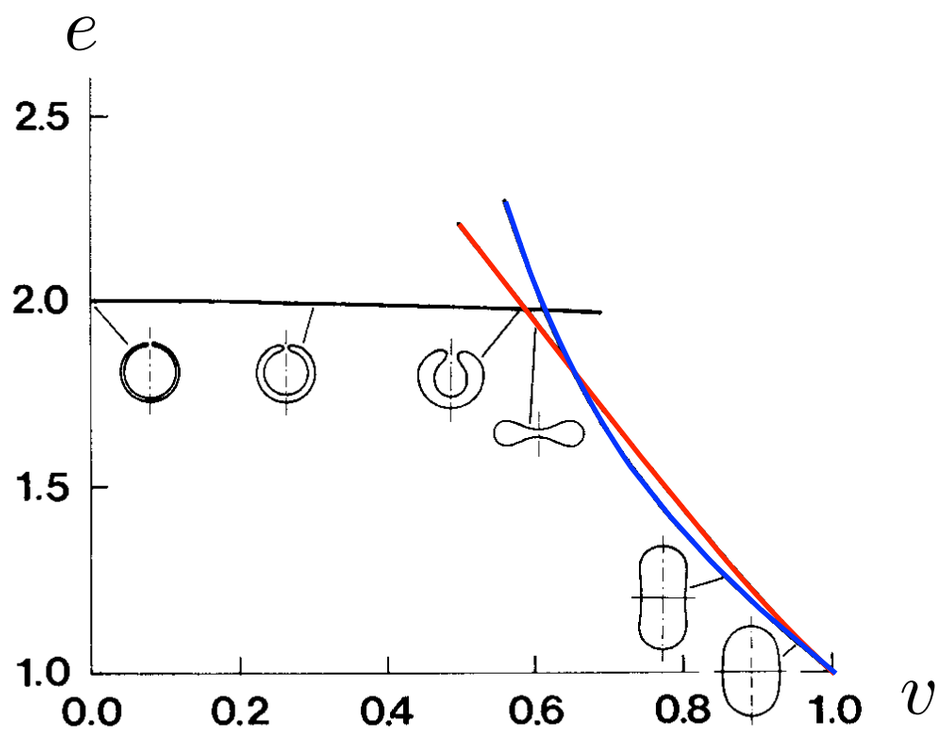
stomatocytes **oblates** **prolates**







U. Seifert *et al.*, PRA 44, 1182 (1991)

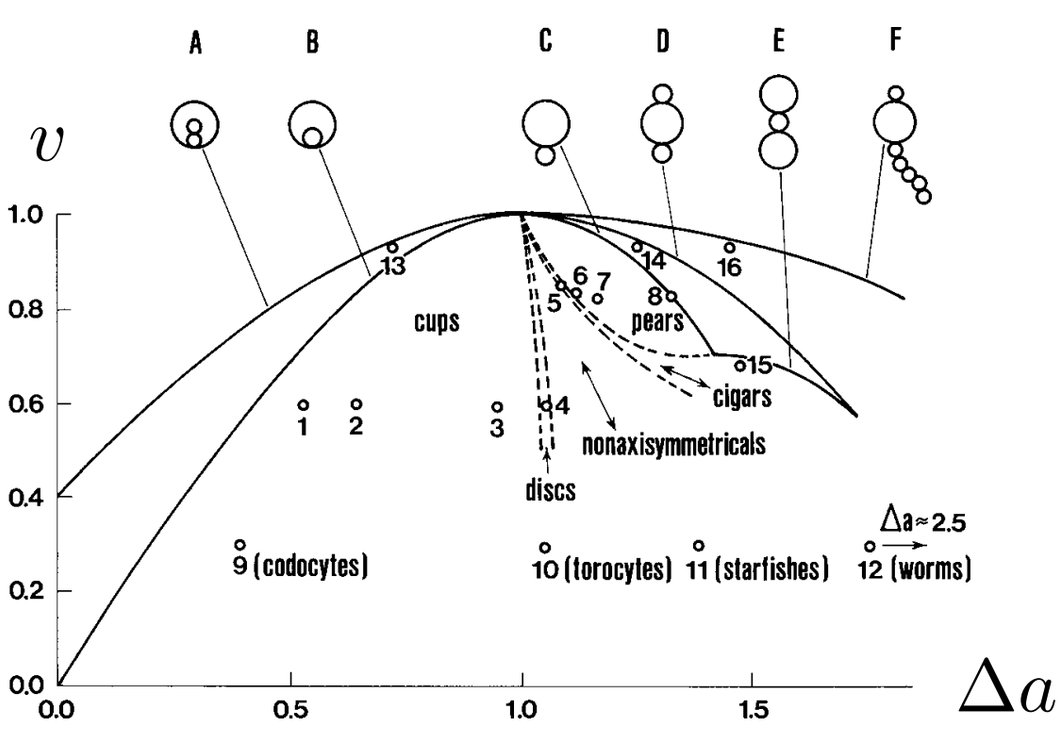


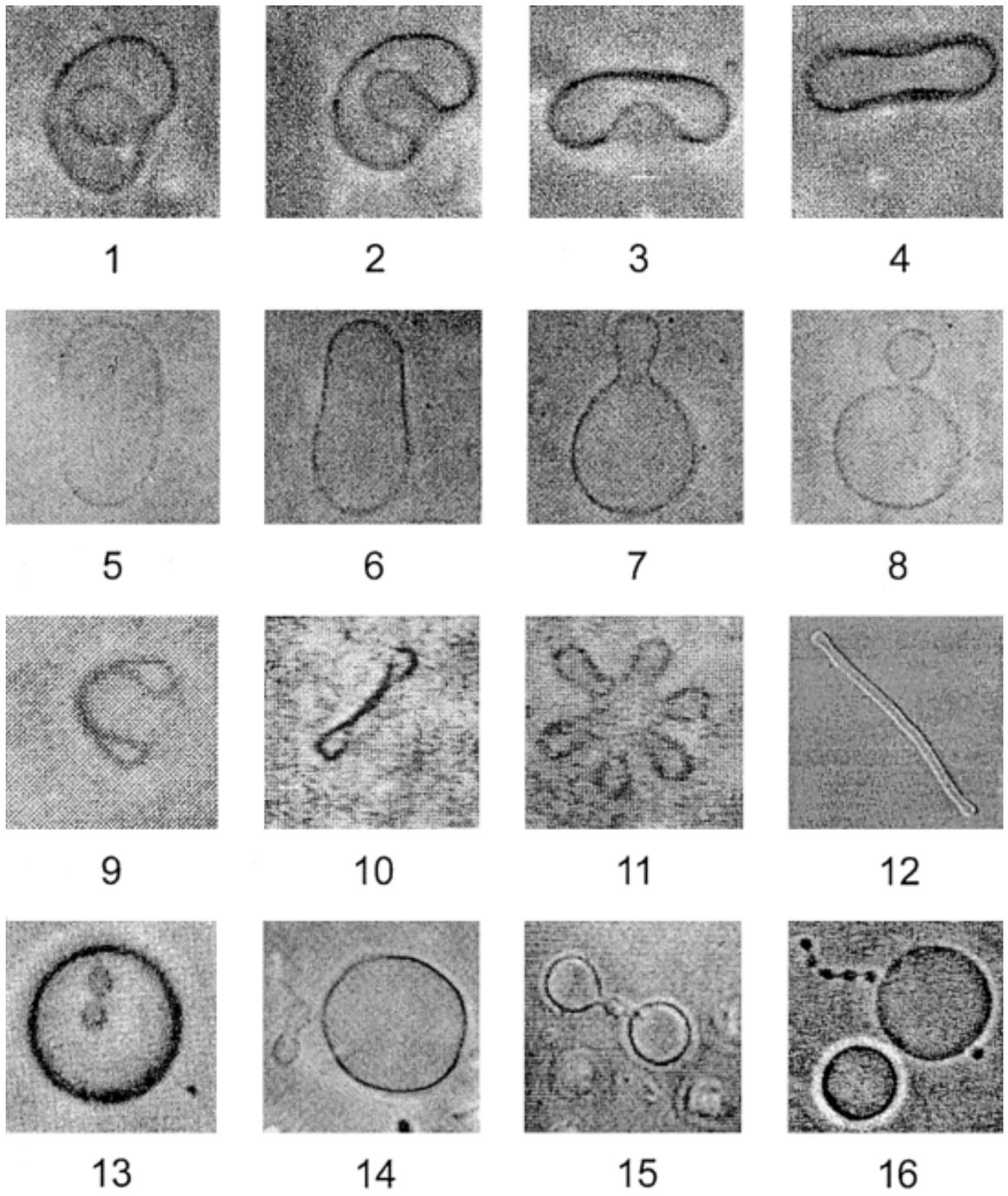
S. Svetina and B. Zeks,
Anat. Rec. 268, 215 (2002)

Bilayer couple model of vesicles

$$e = \int \frac{da}{4} \left(\frac{1}{r_1} + \frac{1}{r_2} - c_0 \right)^2 + \frac{k_r}{\kappa} \left(\Delta a - \Delta a_0 \right)^2$$

Phase diagram of vesicle shapes that minimize the free energy for $c_0 = 0,\ k_r/\kappa \to \infty$ **.**

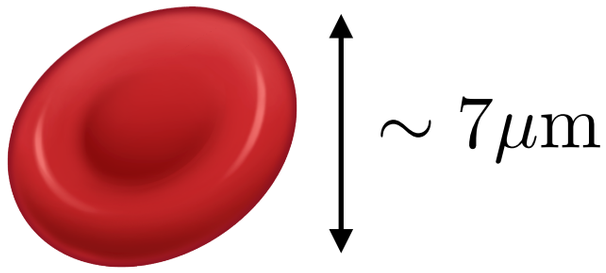




S. Svetina and B. Zeks,
Anat. Rec. 268, 215 (2002)

Shape of red blood cells

In the usual environment red blood cells have discocyte shape. Modifying cell environment can induce different shapes.

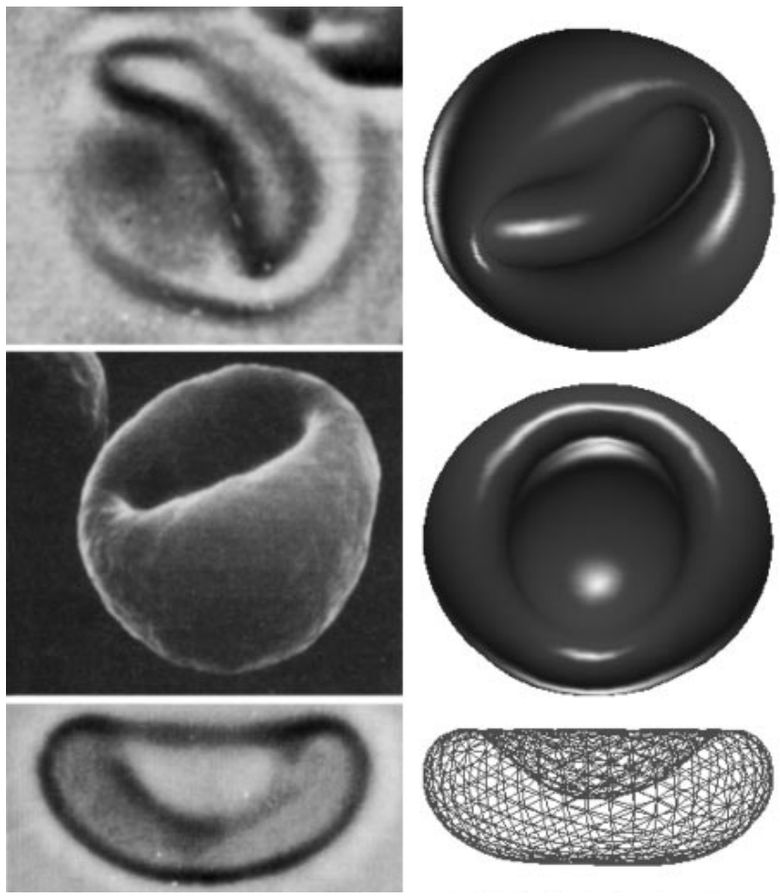


cationic amphipaths, low salt, low pH, cholesterol depletion

anionic amphipaths, high salt, high pH, cholesterol enrichment

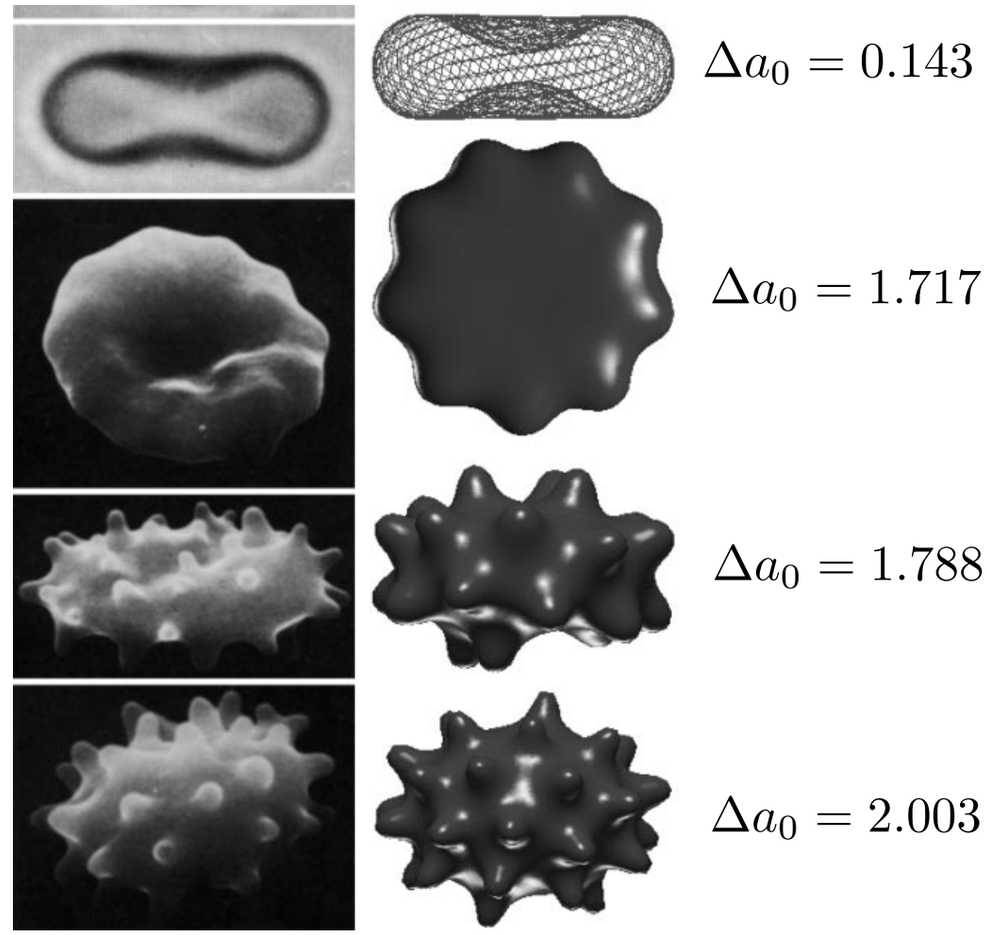
experiments **simulations** $v = 0.950$

stomatocytes



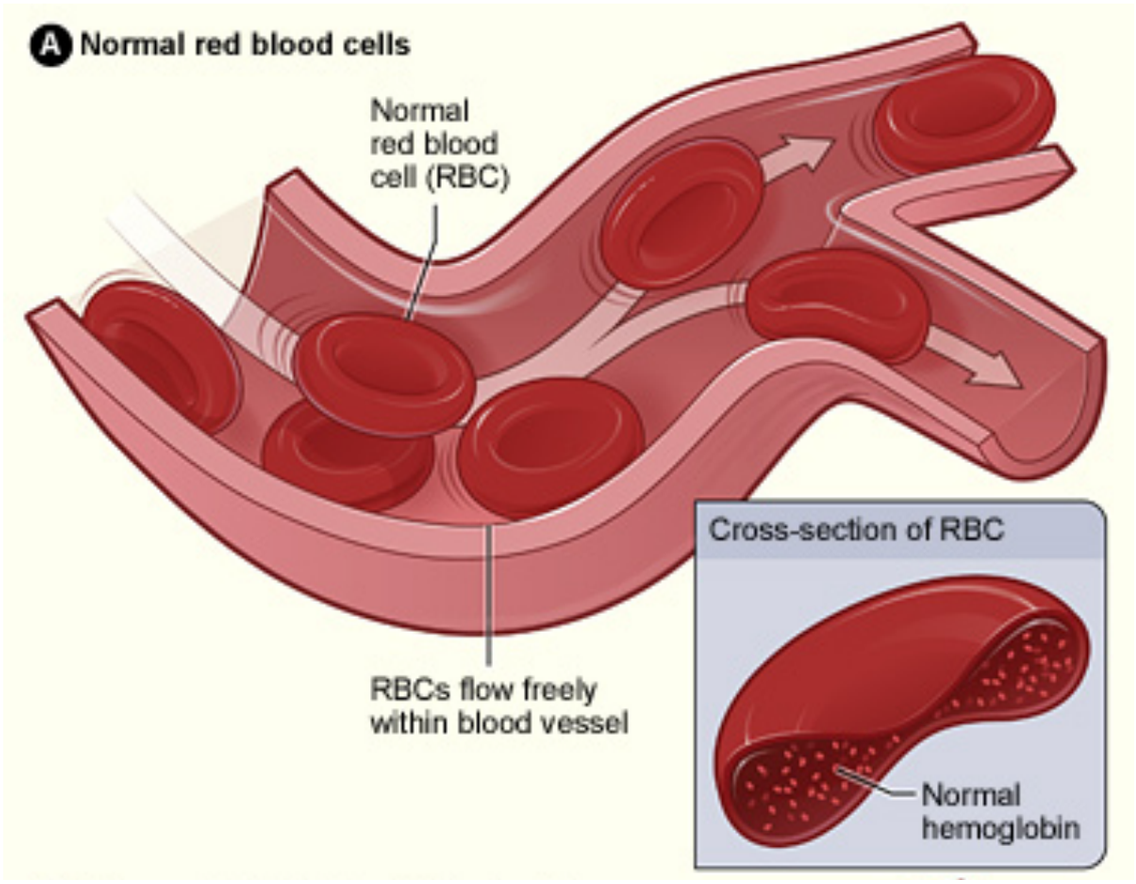
experiments **simulations** $v = 0.950$

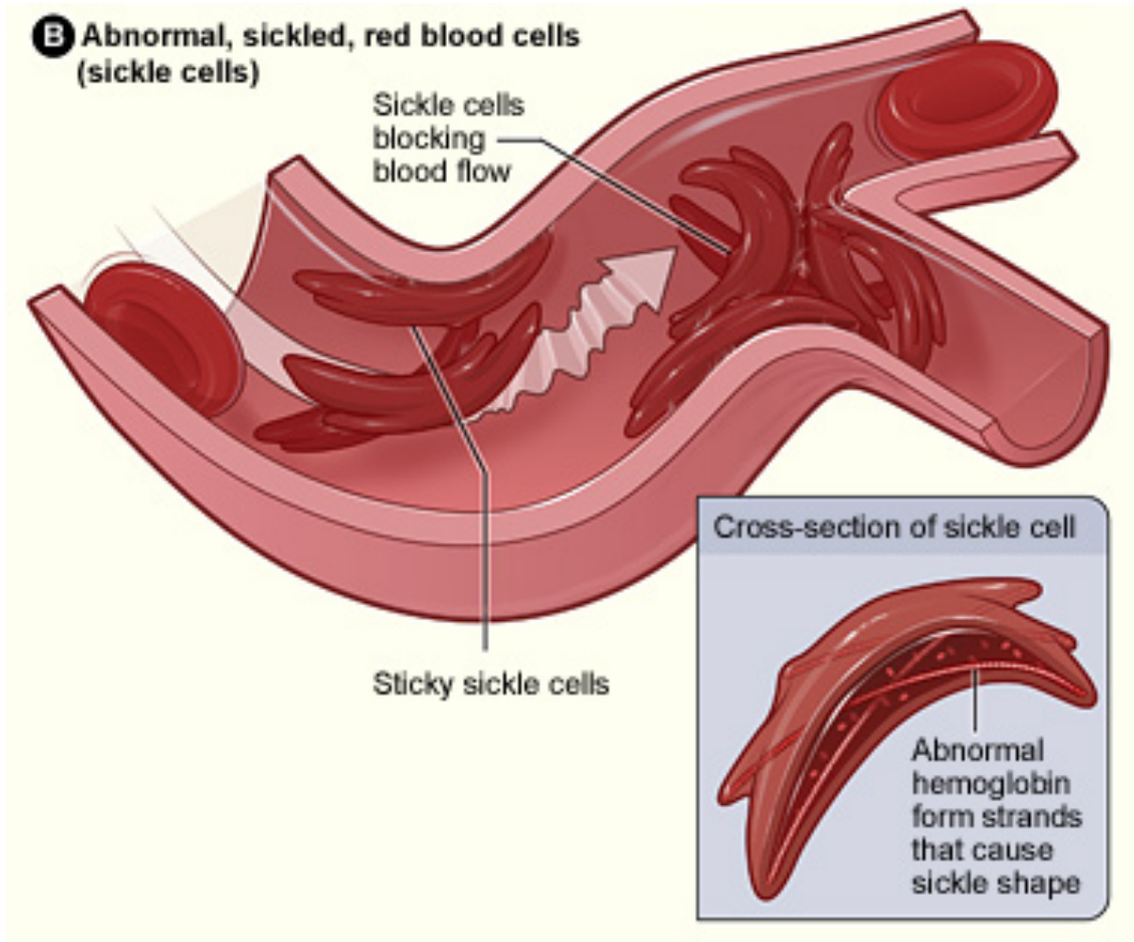
echinocytes



G. Lim *et al.*, PNAS 99, 16766 (2002)

Sickle-cell disease (anaemia)





In low oxygen environment hemoglobin proteins inside sickle cells polymerize and form long strands.

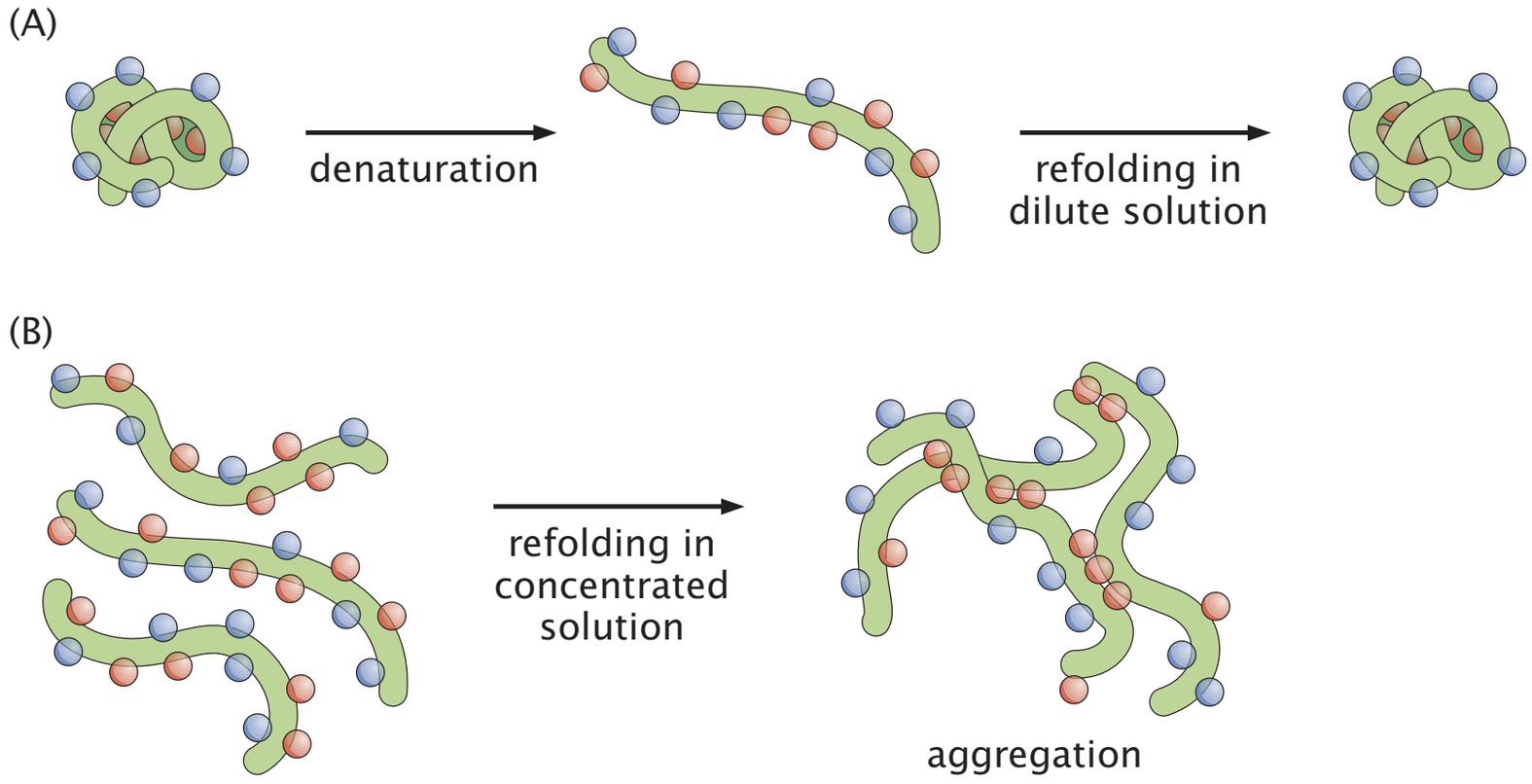
Sickle cells are much stiffer and cannot deform in order to pass through small capillaries.

Wikipedia

Protein aggregation and diseases

(A) In dilute solution misfolded proteins refold back into their native state.

R. Phillips et al., Physical Biology of the Cell



hydrophilic amino acids

hydrophobic amino acids

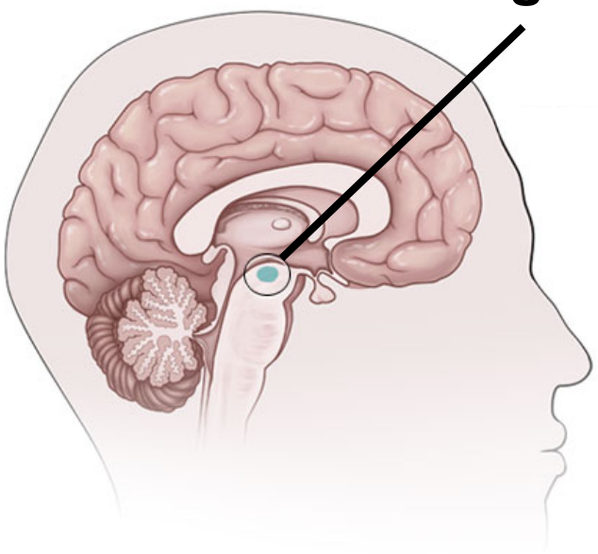
(B) In concentrated solution misfolded proteins tend to form aggregates.

Cells have special proteins called chaperons, which assist proteins folding into their native state and thus prevent aggregation.

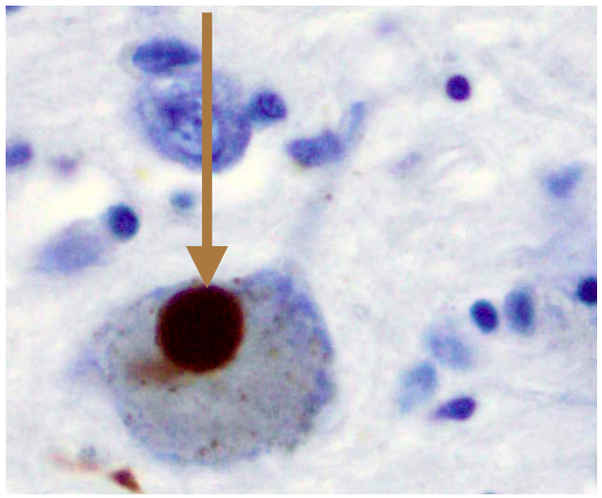
Protein aggregation is a cause of many diseases (Alzheimer's, Parkinson's, …)

Protein aggregates are associated with diseases

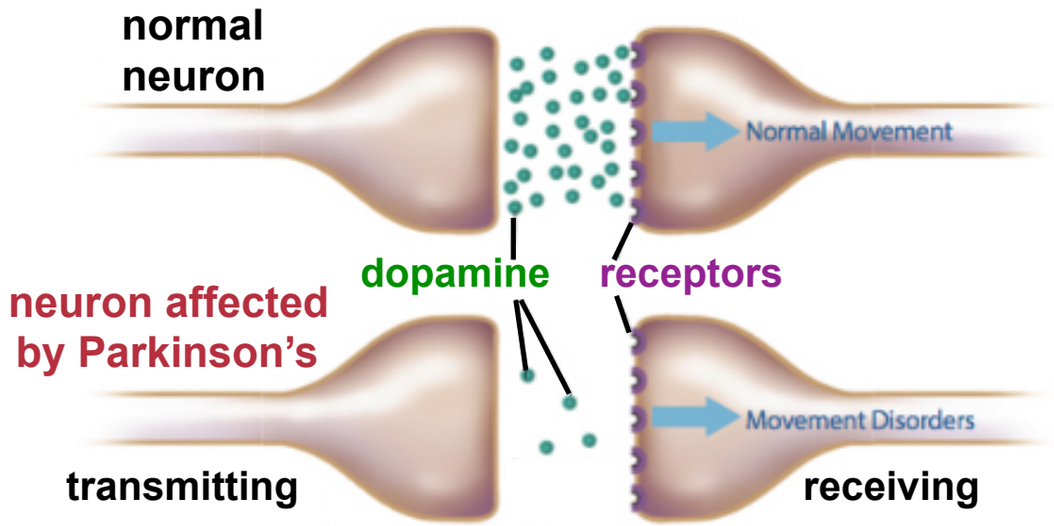
Parkinson's disease



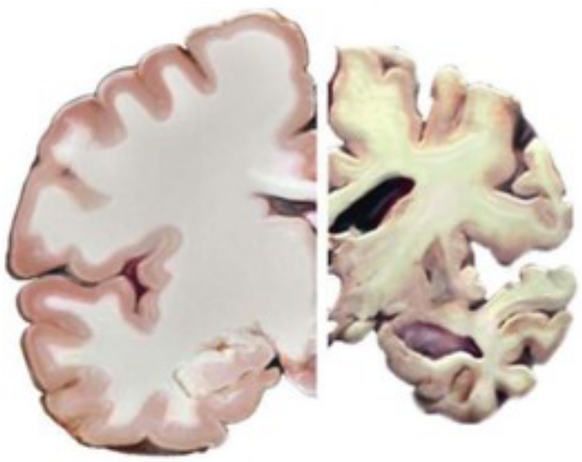
α-synuclein aggregates in dopamine producing nerve cells

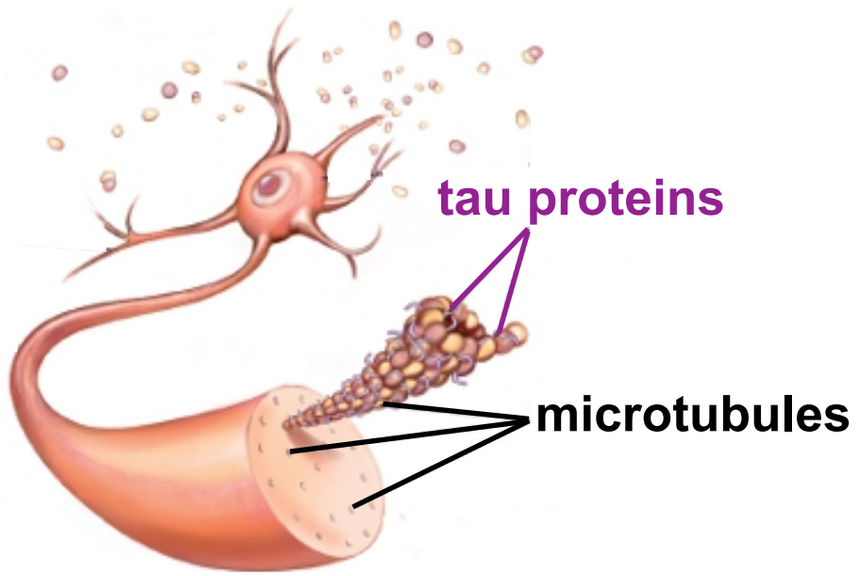


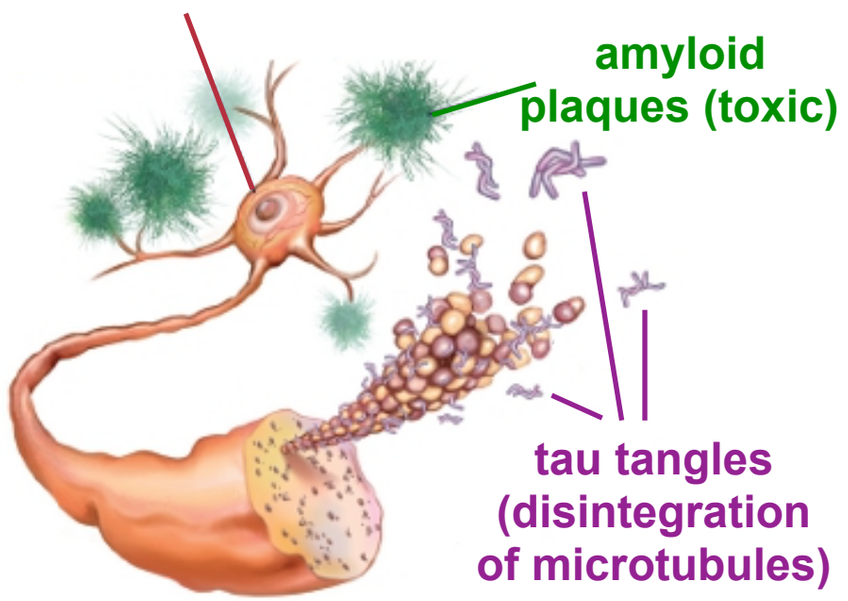
Loss of dopamine neurotransmitters results in movement disorders



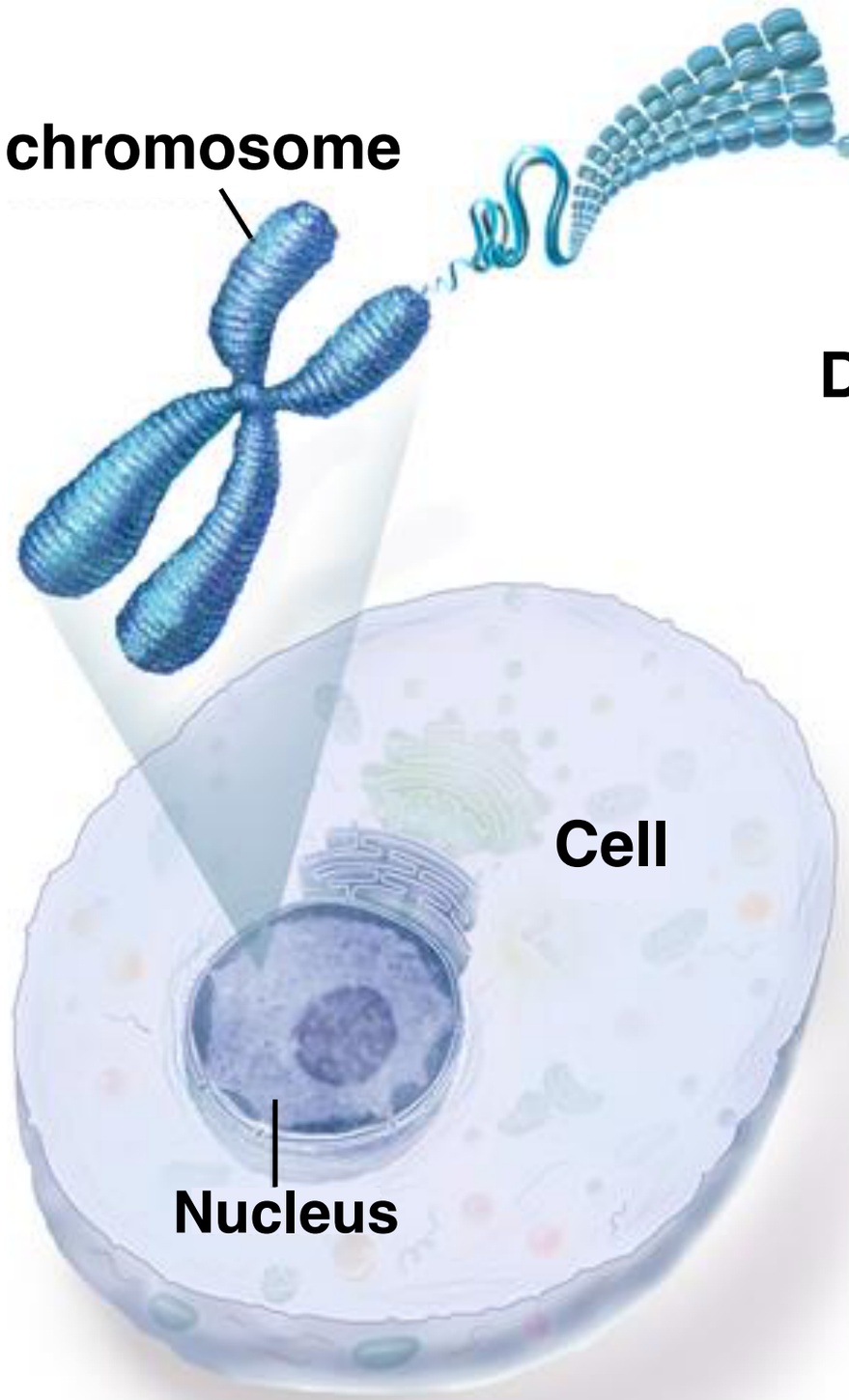
Alzheimer's disease

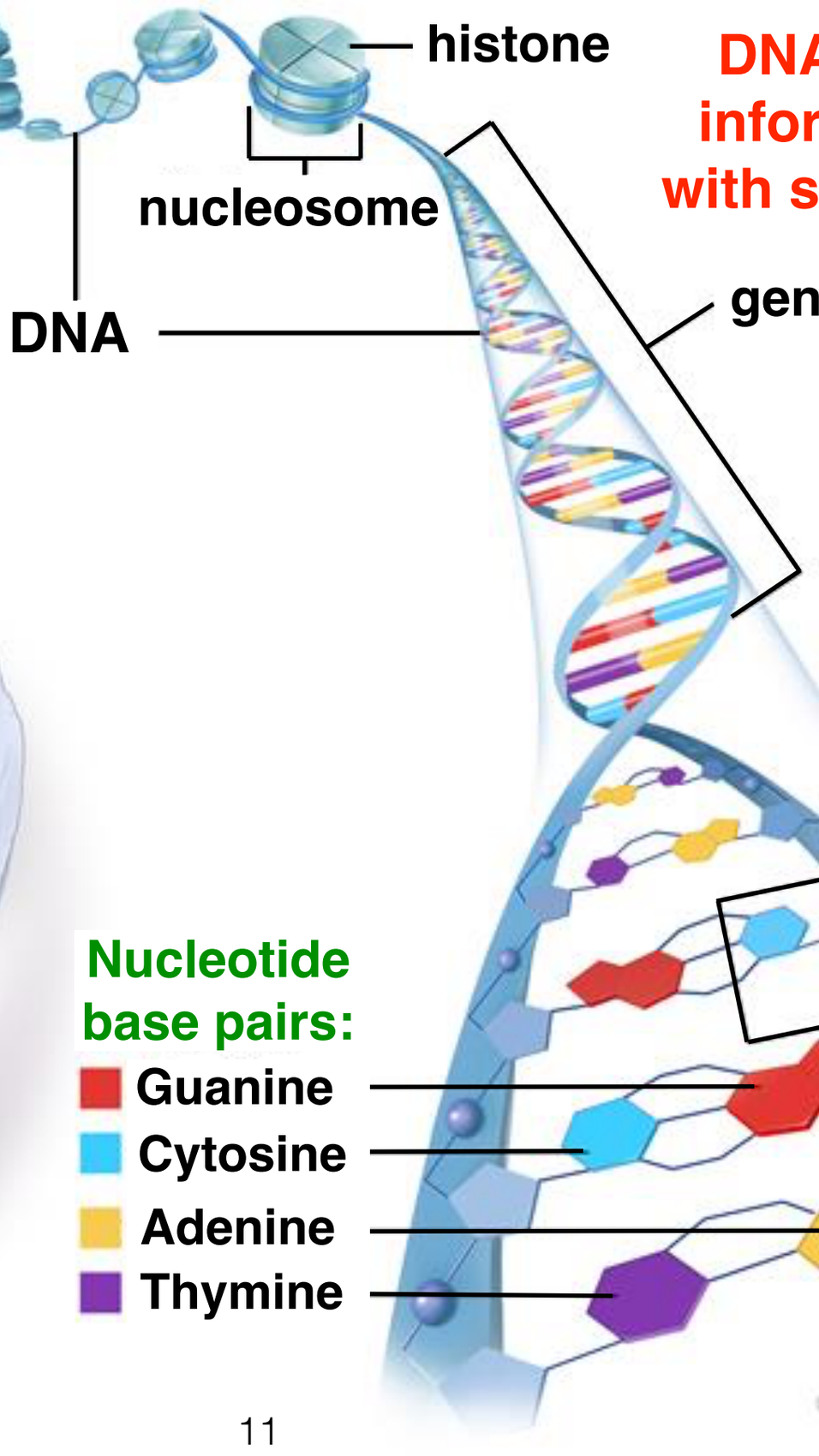






DNA structure





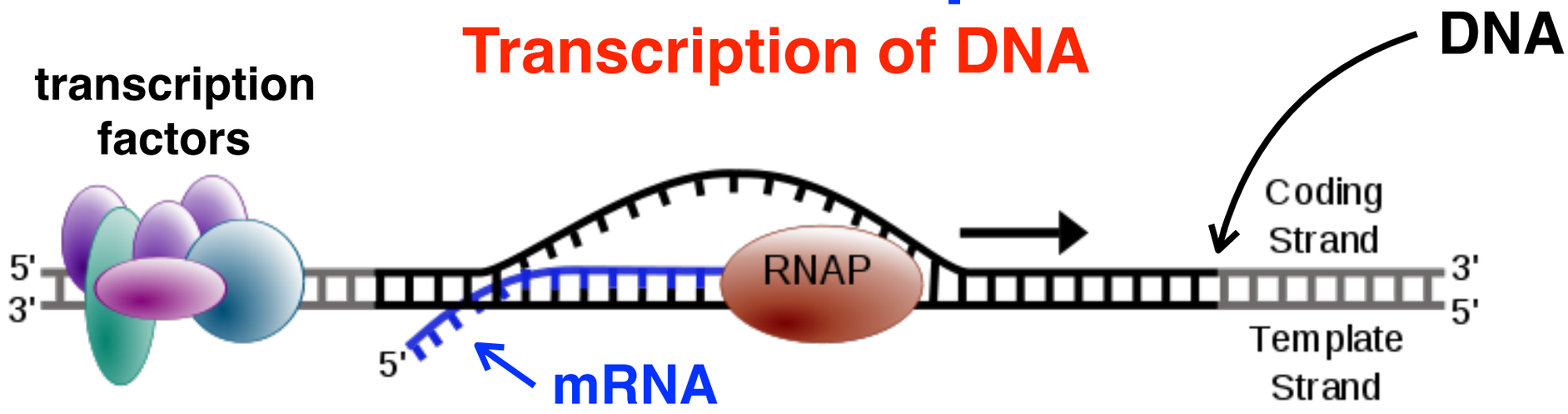
DNA stores genetic information encoded with sequence of bases

Nucleotide base pairs:

- Guanine
- Cytosine
- Adenine
- Thymine

Production of new proteins

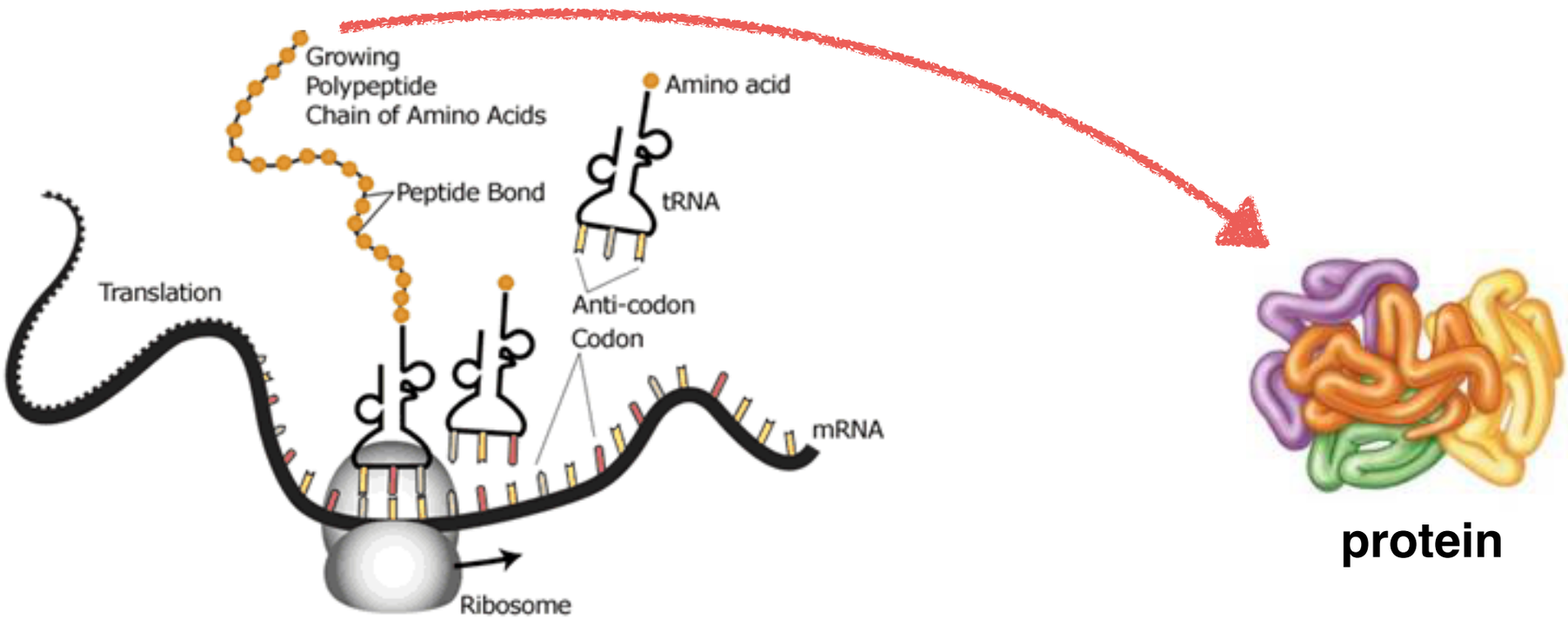
Transcription of DNA



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.

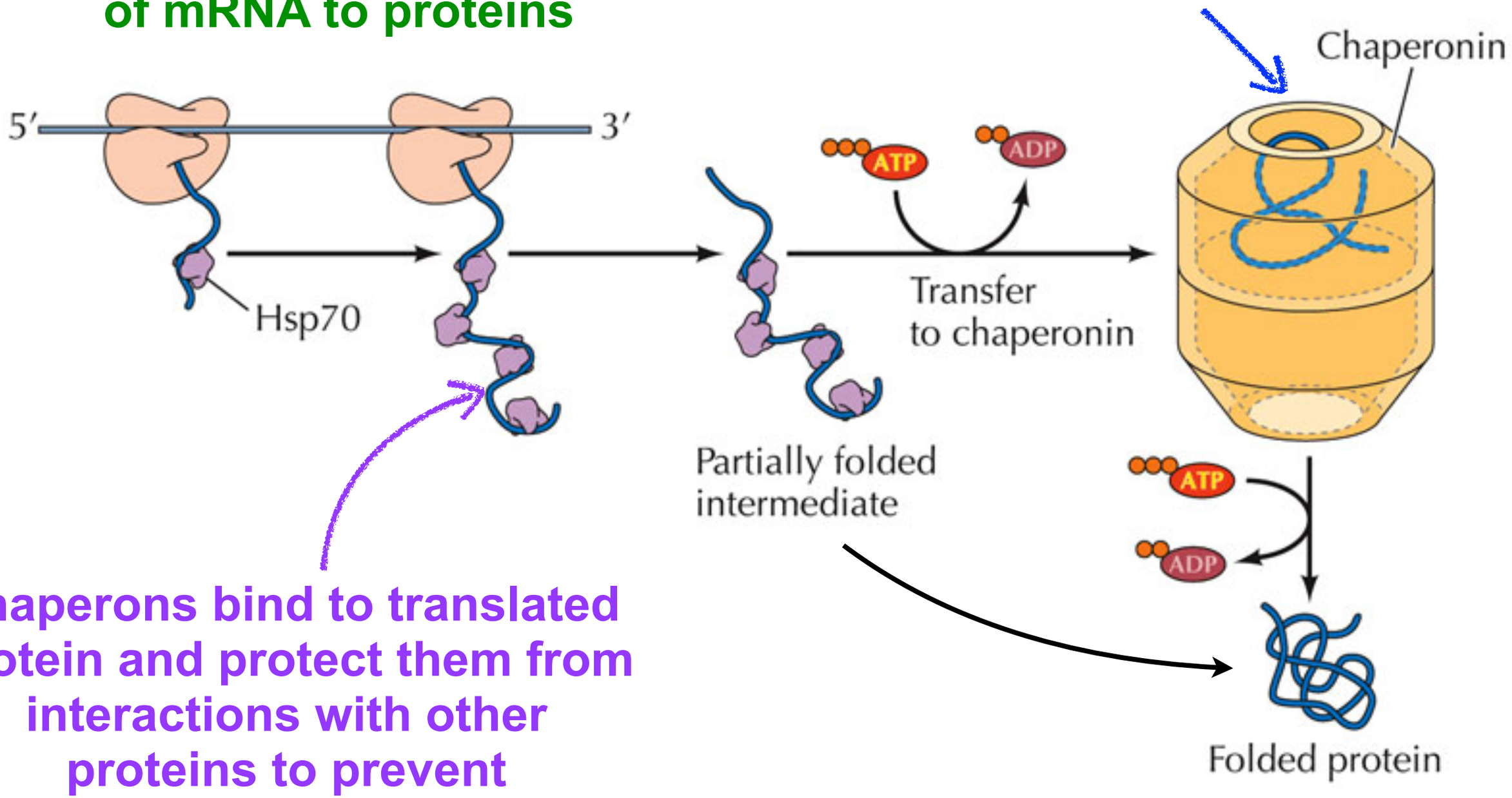
Translation of mRNA



Chaperons assist with protein folding and prevent protein aggregation

ribosome translation of mRNA to proteins

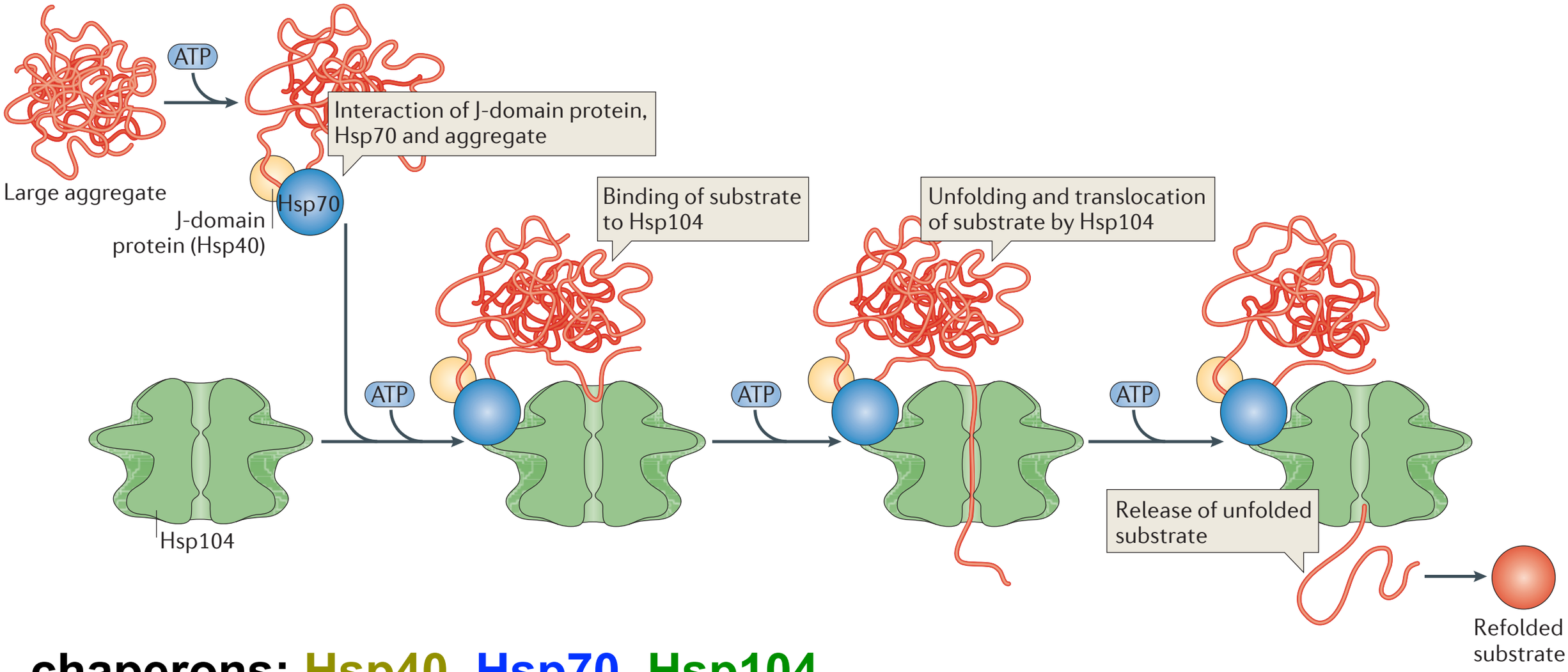
isolated proteins in chaperonin chambers fold into their compact native state



chaperons bind to translated protein and protect them from interactions with other proteins to prevent aggregation of proteins

B. Alberts et al., Molecular Biology of the Cell

Chaperons assist with disassembly of protein aggregates



chaperons: Hsp40, Hsp70, Hsp104

Under normal cell conditions, protein aggregates are small and short lived!

S. M. Doyle *et al.*, Nat. Rev. Mol. Cell Biol. **14**, 617 (2013)