Molecular Biophysics

Entropy, Boltzmann and Gibbs

Physical Biology of the Cell, chapters 5 and 6

Free energy

Helmholtz free energy

For a process that takes place at constant T

$$F = U - TS$$

Gibbs free energy

For a process that takes place at constant T and P

$$G = U - TS + PV$$

During a process the changes are:

$$\Delta F = \Delta U - T\Delta S \qquad \Delta G = \Delta U - T\Delta S + P\Delta V$$

But $\Delta V \approx 0$, so $\Delta F \approx \Delta G$ and therefore it doesn't matter whether we use F or G.

The natural direction of processes

As a system approaches equilibrium:

$$\Delta G \leq 0$$

So $G \approx U - TS$ is minimised at equilibrium.

This implies *decreasing* U or *increasing* S or both.

N.B. Entropic term becomes more significant at high temperature.

Maximising S involves finding the macrostate with the largest number of corresponding microstates

Possible models of macromolecules
(1) DNA

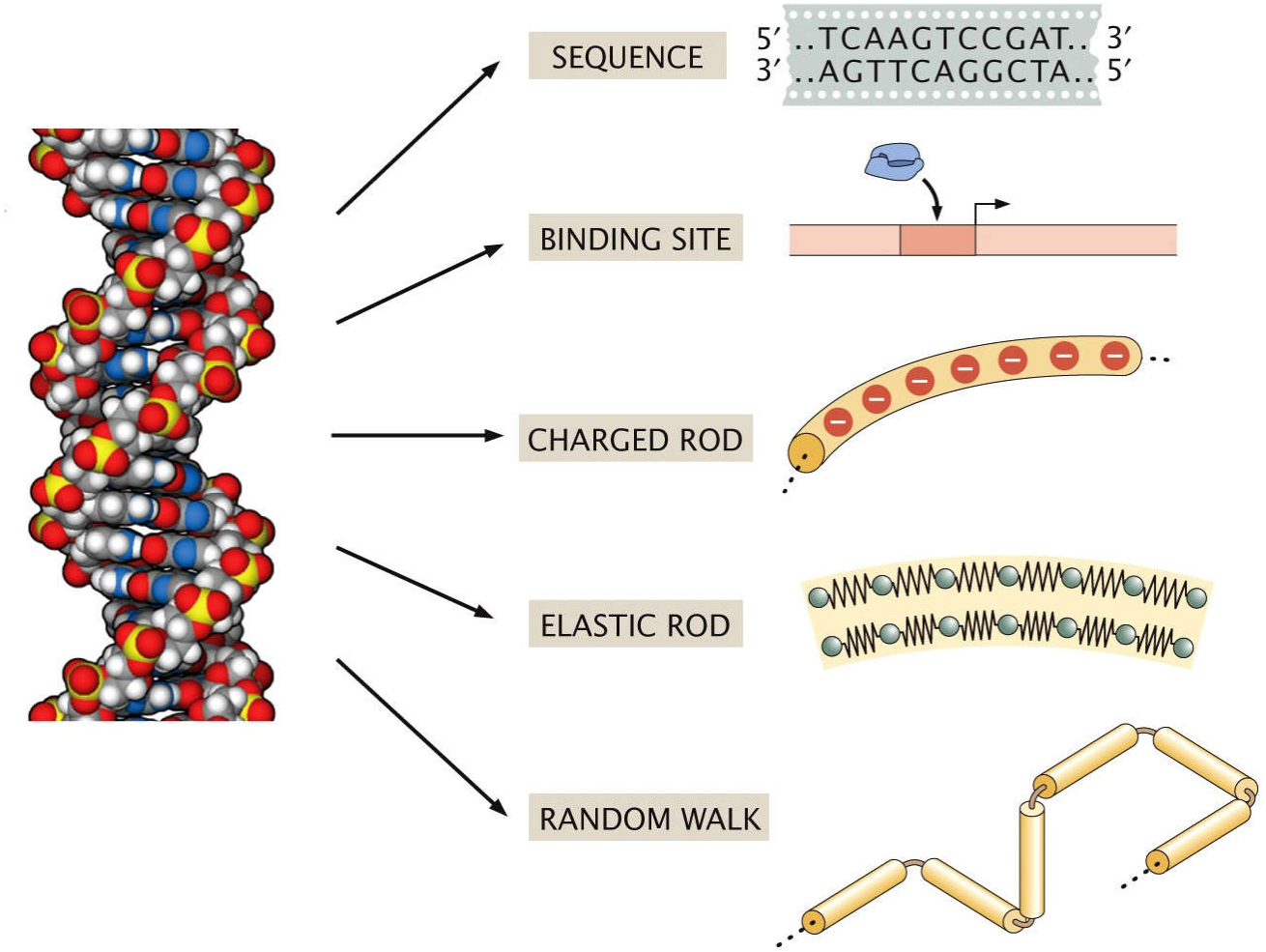
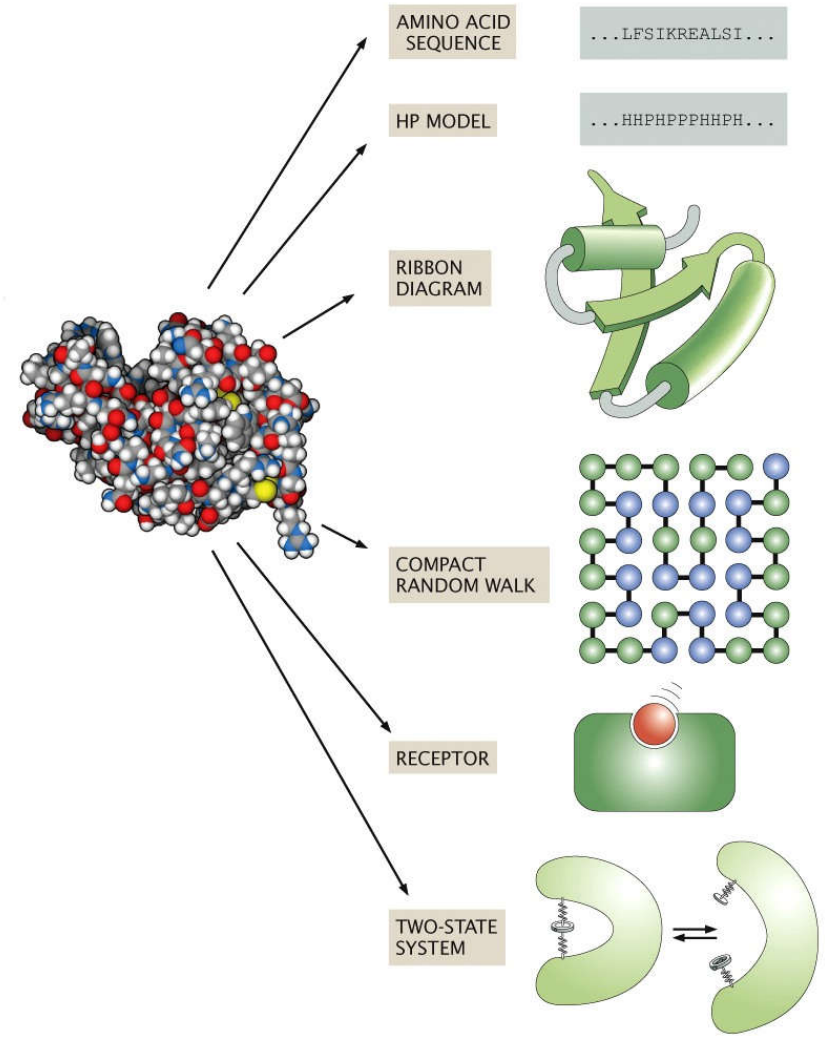


Figure 1.5 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Possible models of macromolecules
(2) Proteins



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Possible contributions to U in biological systems

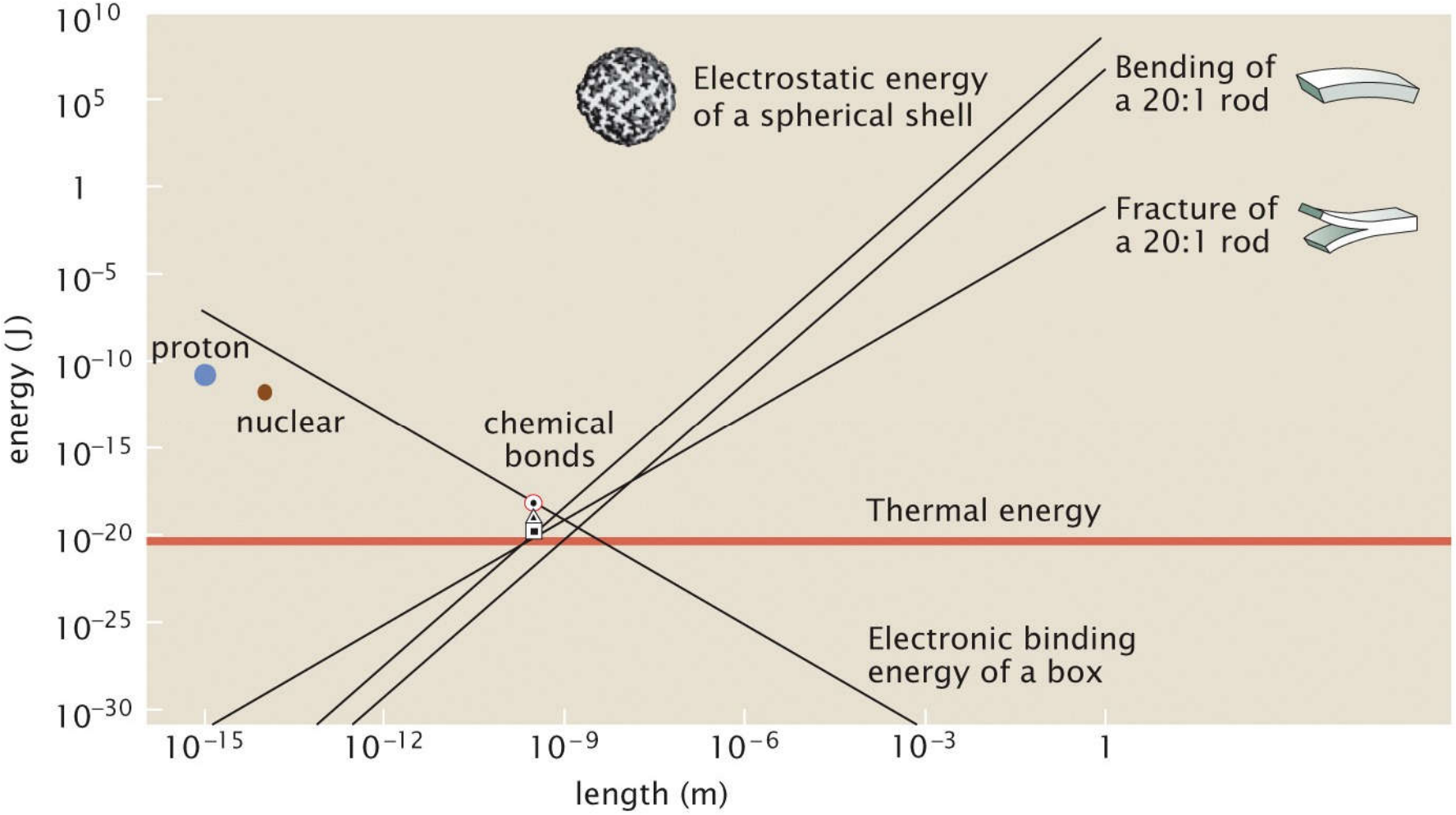
As an illustrative example, consider a polymer...

(i) ***...as a uniform rod***
U depends on the degree of stretching and bending

(ii) ***...as a collection of atoms***
U depends on
- covalent bonds – e.g. stretching
- electrostatic interactions
- van der Waals interactions
- hydrogen bonds

(iii) ***...binding to another molecule (ligand)***
U depends on the same as above plus the energy of interaction

Energy as a function of length scale



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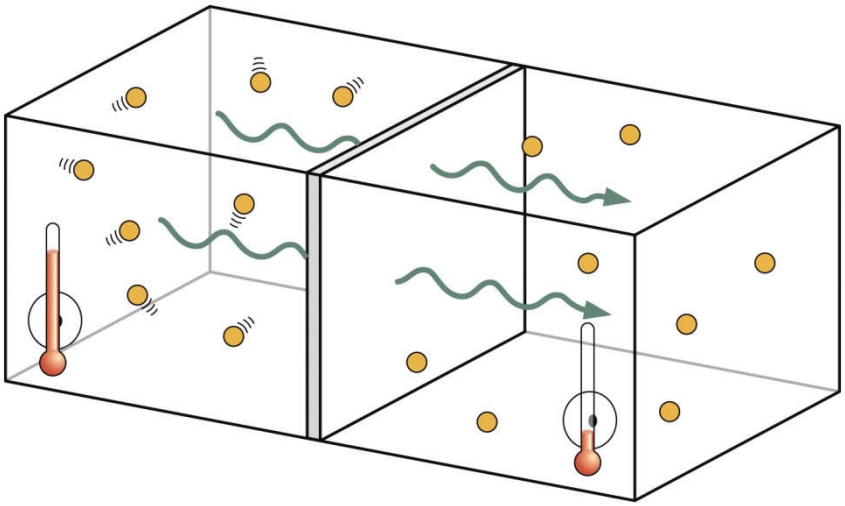
Schematic representation of an isolated system with sub-compartments separated by a barrier



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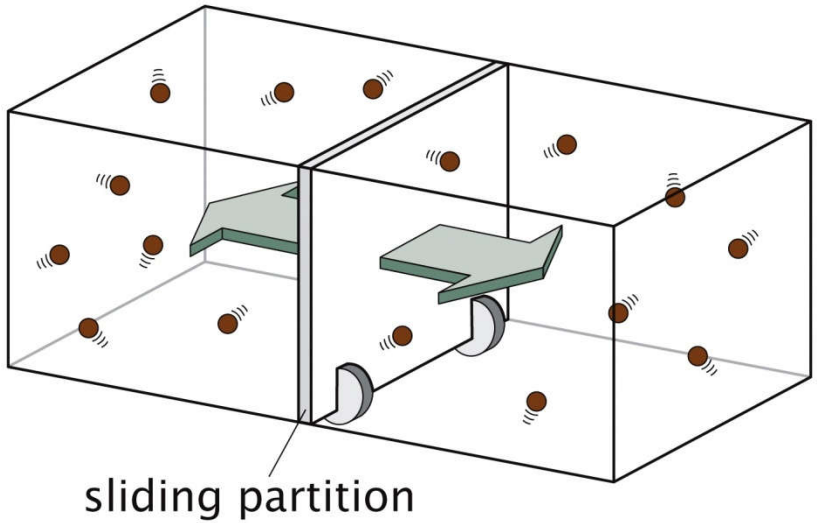


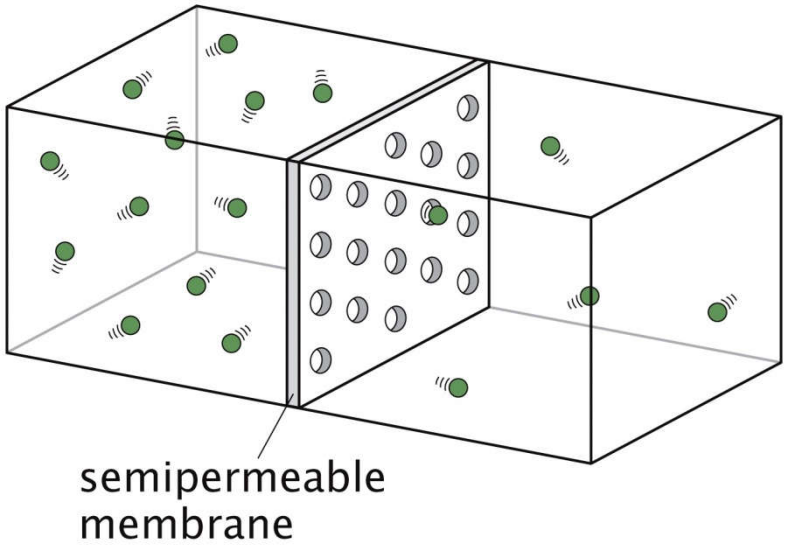
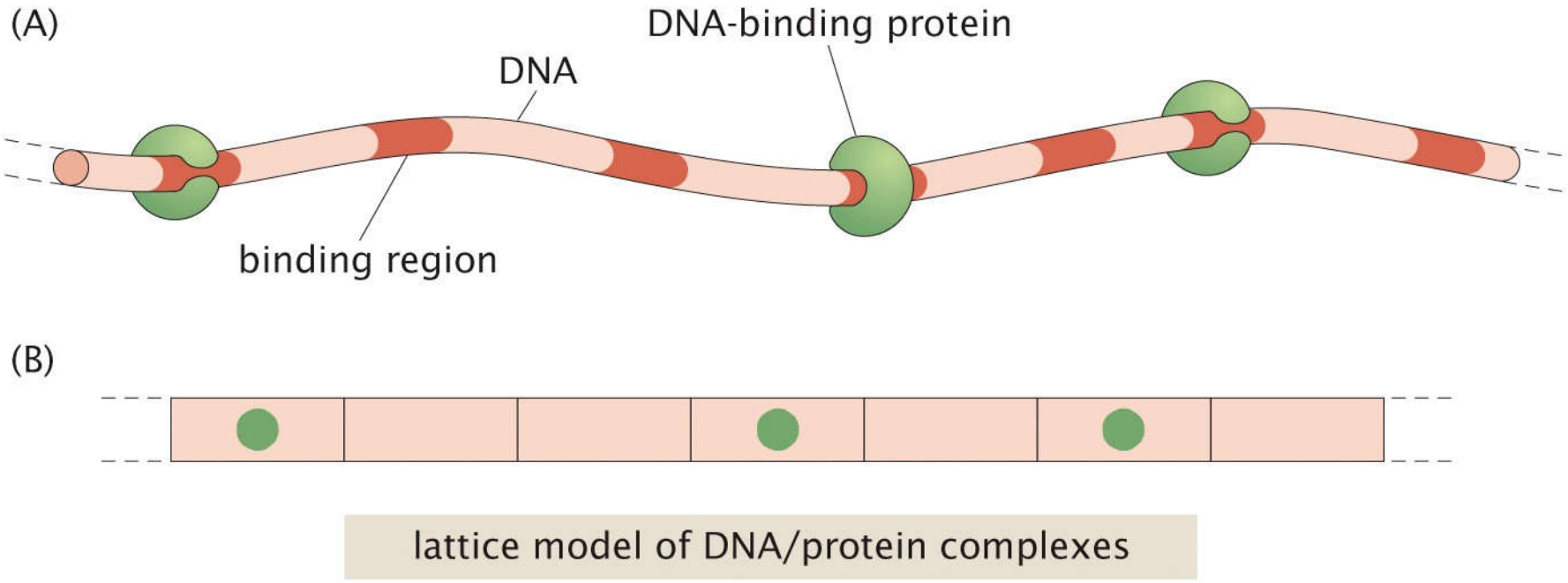


Figure 5.29c Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Possible arrangements of proteins on a DNA molecule



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Assume: N binding sites on DNA

N_P of them are occupied by a protein

Binding energy is the same at all sites

Entropy as a function of protein concentration

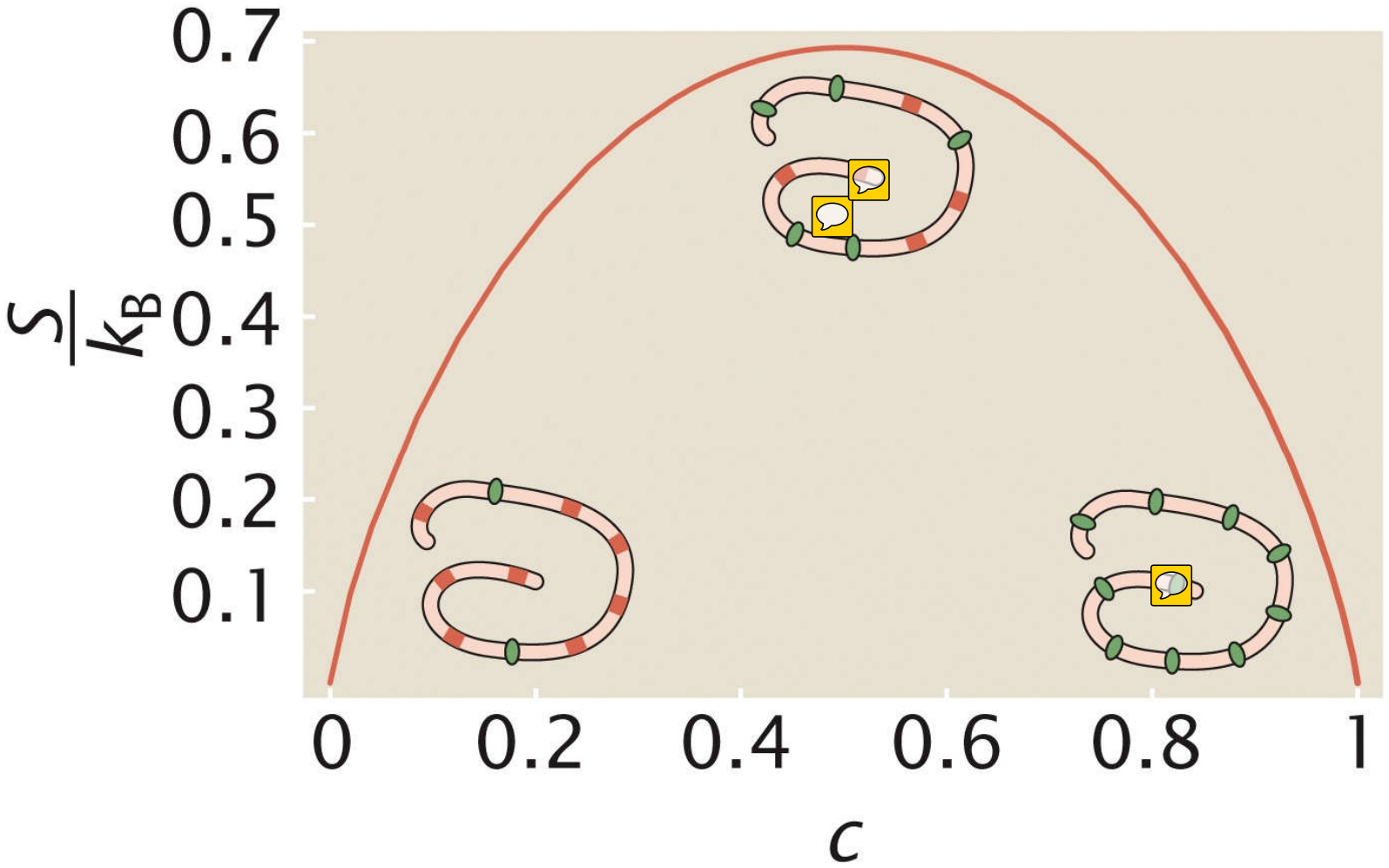


Figure 5.26 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Isolated and closed systems

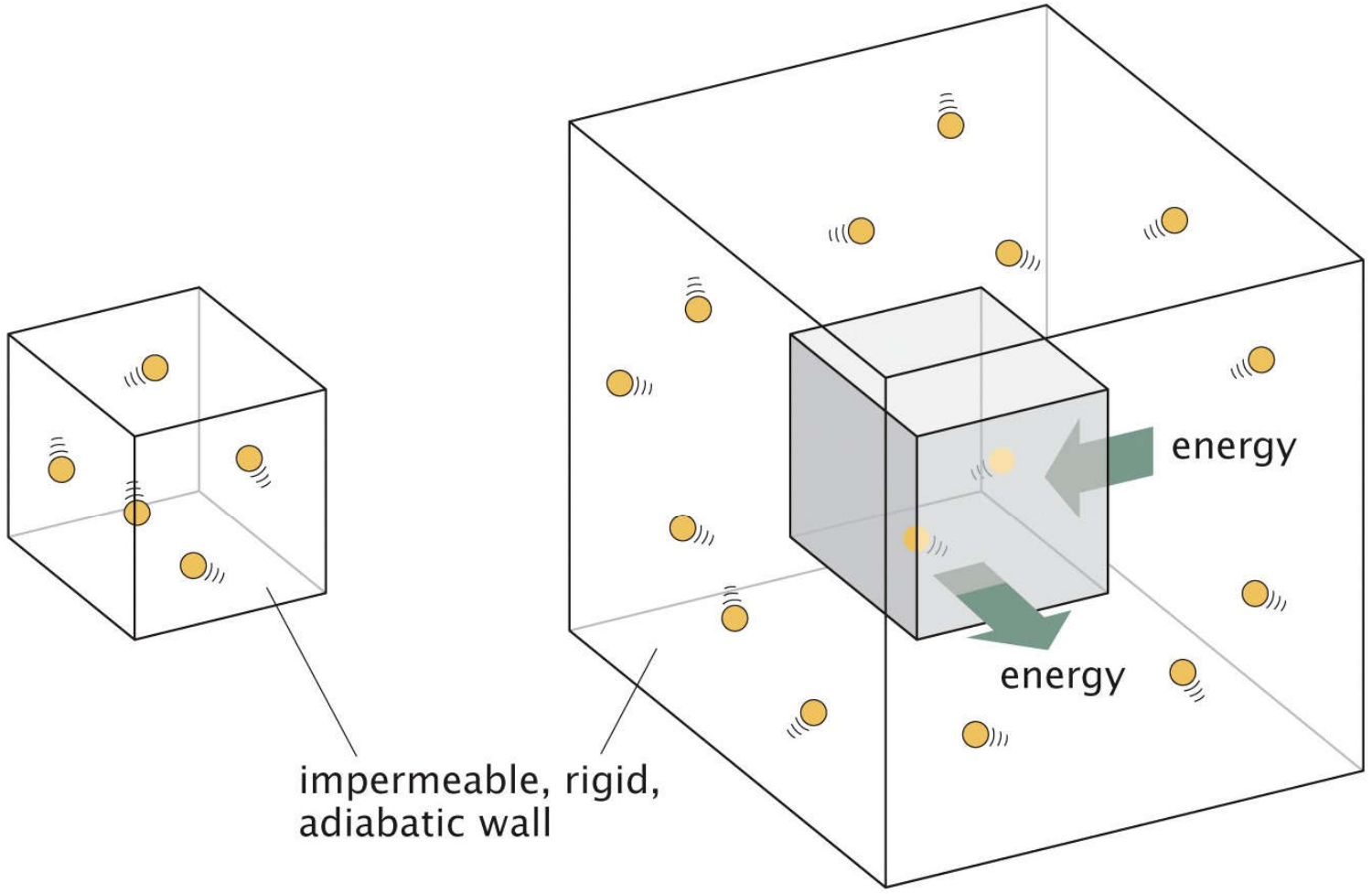


Figure 5.30 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Microstates: Simple lattice model of ligand-receptor binding

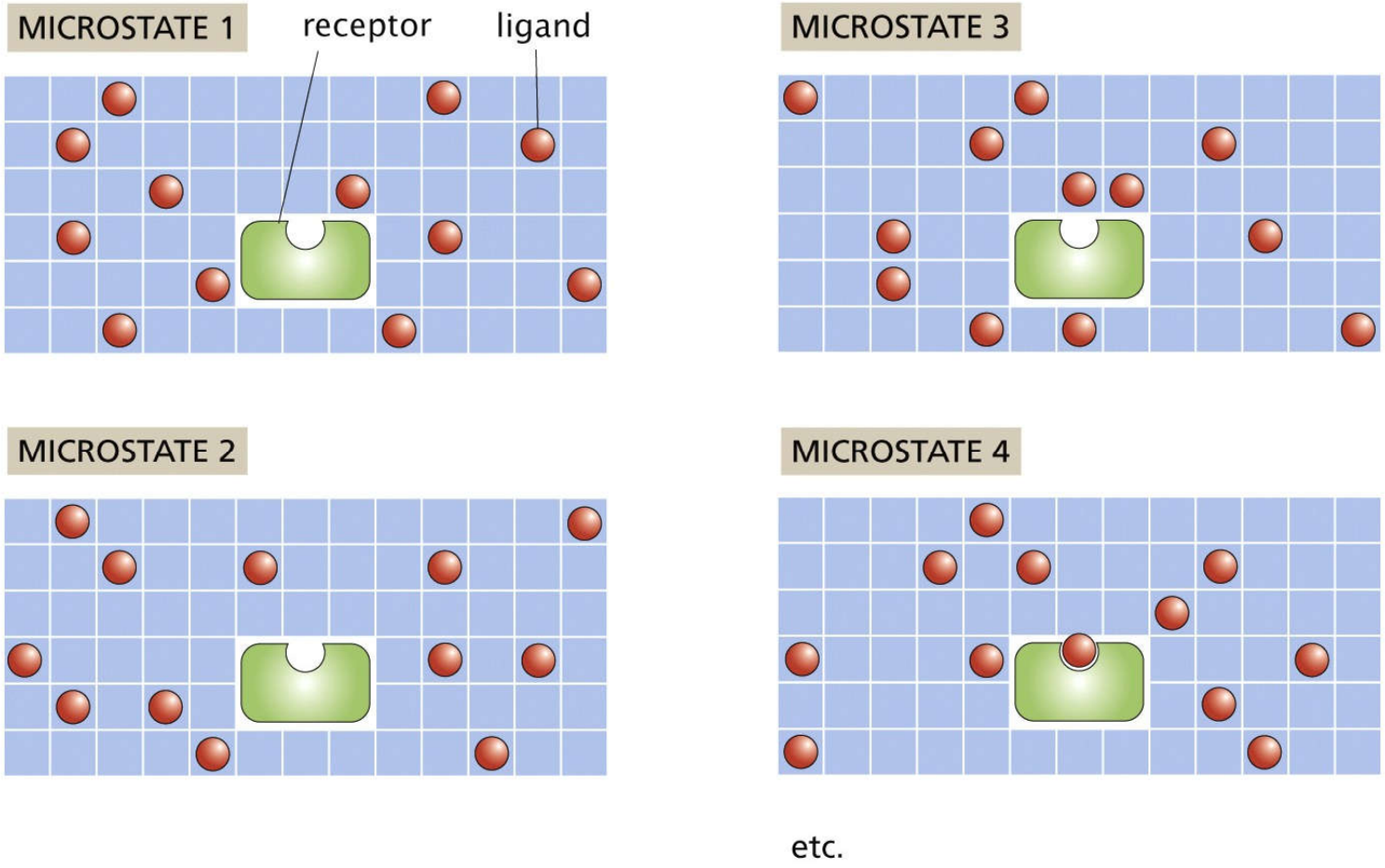


Figure 6.1 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

States and weights diagram for receptor-ligand binding

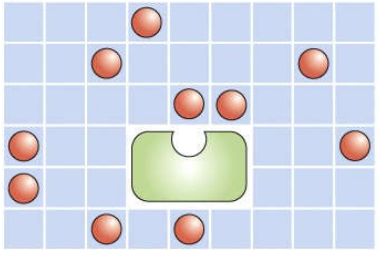
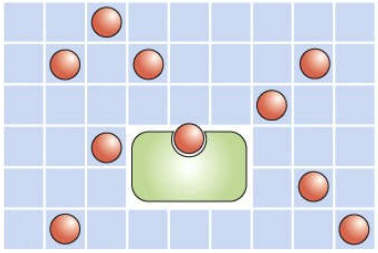
STATE	ENERGY	MULTIPLICITY	WEIGHT
(A) 	$L\varepsilon_{sol}$	$\frac{\Omega!}{L!(\Omega-L)!} \approx \frac{\Omega^L}{L!}$	$\frac{\Omega^L}{L!} e^{-\beta L\varepsilon_{sol}}$
(B) 	$(L-1)\varepsilon_{sol} + \varepsilon_b$	$\frac{\Omega!}{(L-1)!(\Omega-L+1)!} \approx \frac{\Omega^{L-1}}{(L-1)!}$	$\frac{\Omega^{L-1}}{(L-1)!} e^{-\beta[(L-1)\varepsilon_{sol} + \varepsilon_b]}$

Figure 6.4 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Assume: L ligands on Ω lattice sites
1 receptor with 1 binding site
ε_b = binding energy
ε_{sol} = energy of ligand in solution

Probability of receptor occupancy

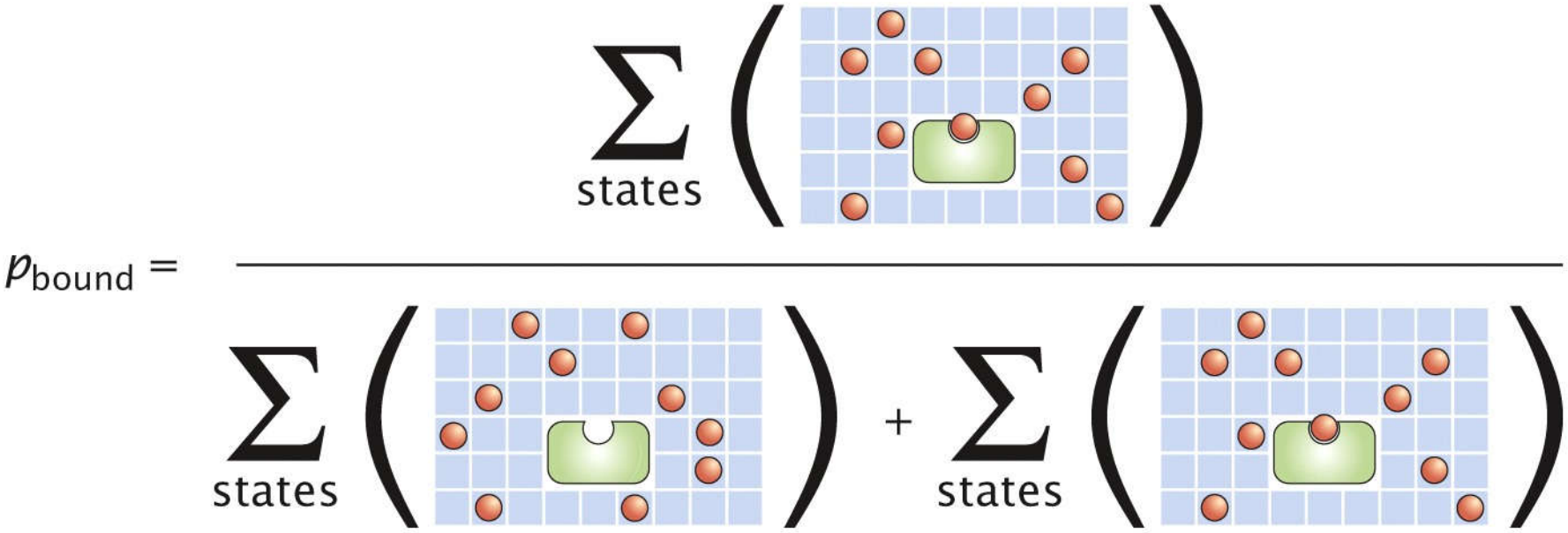


Figure 6.5 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Average occupancy as a function of ligand concentration and binding energy

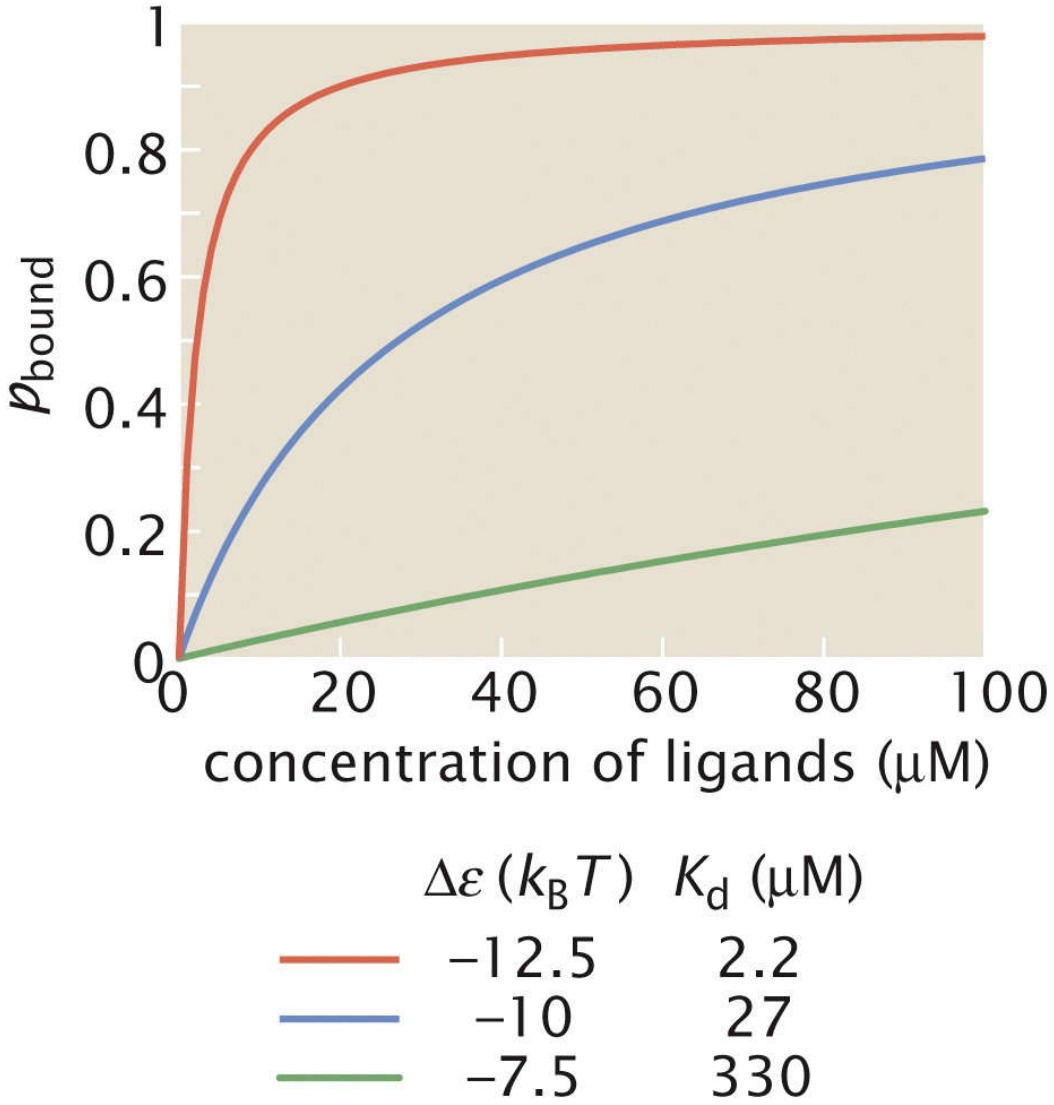


Figure 6.6 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Hydrogen bonding network in water

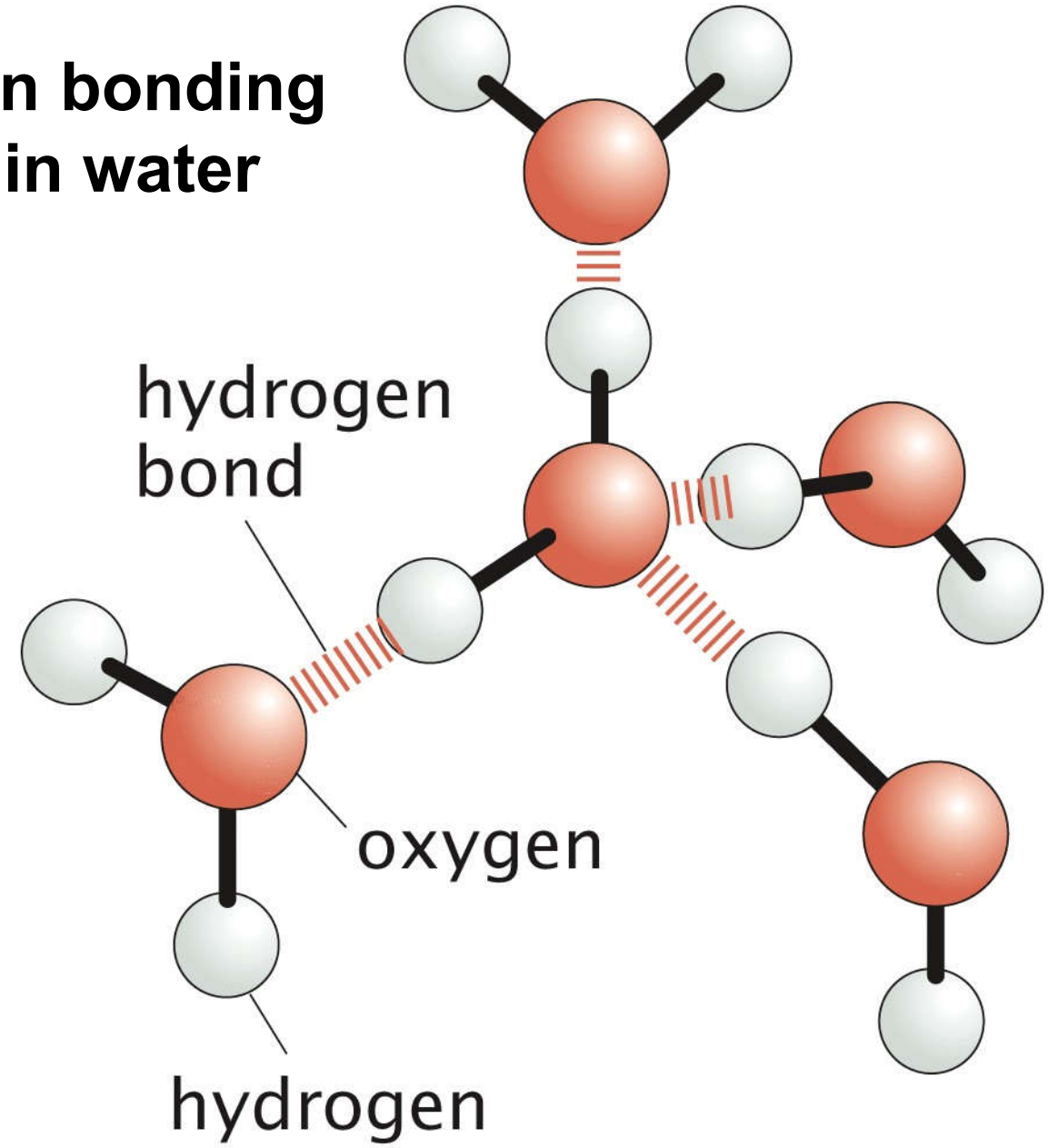


Figure 5.27 Physical Biology of the Cell, 2ed. (© Garland Science 2013)

Orientation of water molecules in a tetrahedral network

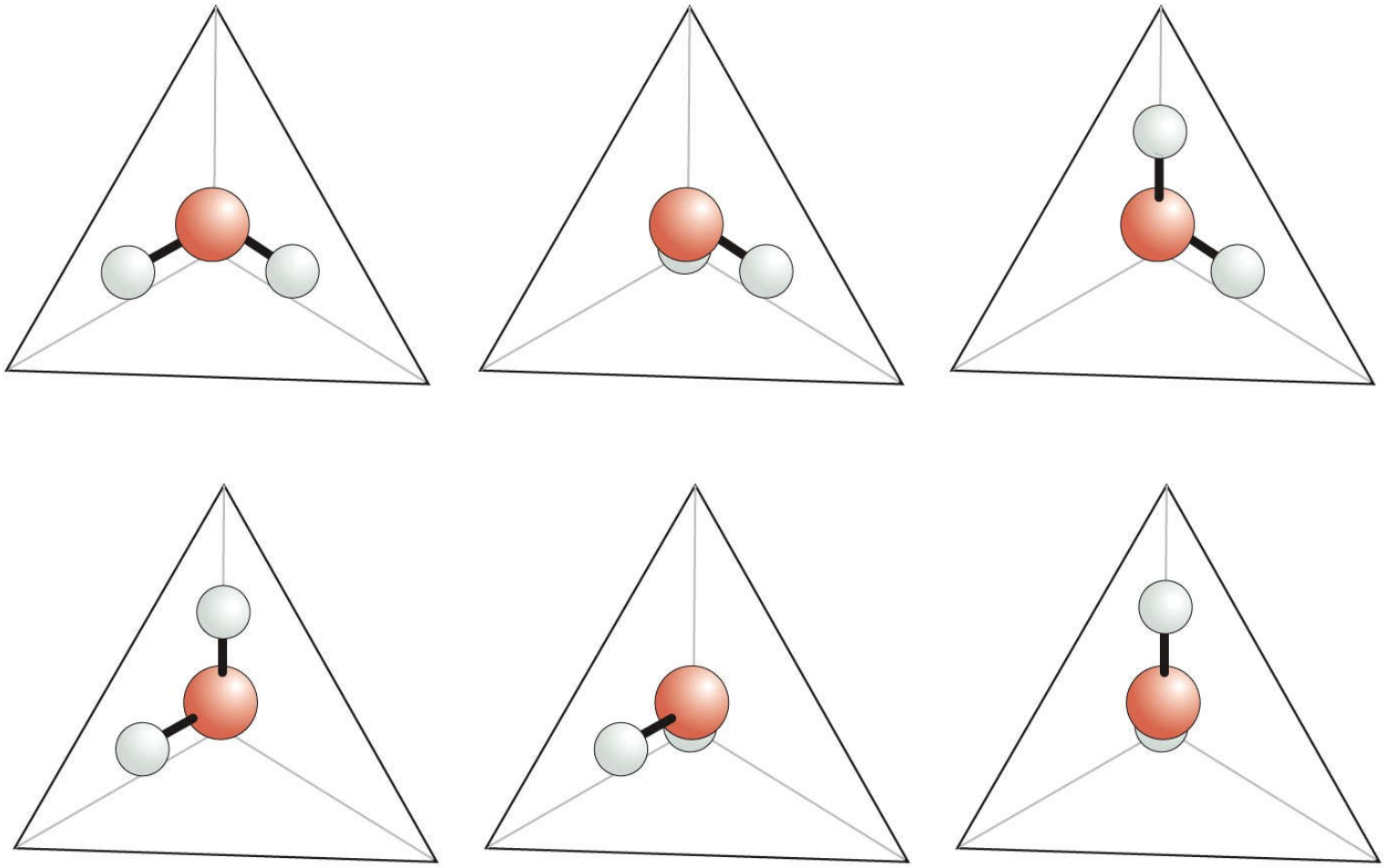


Figure 5.28 Physical Biology of the Cell, 2ed. (© Garland Science 2013)