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Chapter 2

2.1. If no bias then 50:50, but if one or both isomers are autocatalytic then simple rate equation indicates that steady state solution converges to one of the isomer populations, relevant to D/L sugars since all natural sugars are in D form. Evolutionary pressure to select one of the isomer over the other depends upon what the isomer binds to in the cell e.g. is that structure isomer-dependent or not.

2.2 (a) ca. 6.3×10^{-18} kg or ~6.3×10^{-15} g (assume mostly water in cell to get total mass). (b) Assuming roughly equal numbers of all four bases indicates mean Mw of 0.265 kDa per base. Using result from (a) implies ~14.3×10^{6} bases, or ~7,200 kbp, then 0.34 separate per bp implies contour length of ~2.4 mm.

2.3 If you tally up all one-base changes there are 134 which do not change the amino acid coded for, implying no effect on evolutionary fitness, or 134/576=23% of one-base mutations have no effect, or 0.23×55%= 13% of the DNA sequence has changed without affecting the amino acid sequence, and 42% has changed with consequent changes in the amino acid sequence. This roughly accounts for the observation. There are other more complex factors also e.g. there may also be posttranslational modification of mRNA.

2.4 Assume total mass of protein in cell is ~20% as stated in chapter text, and assume E. coli has a mass roughly equivalent to a sphere of diameter 1 micron as per answer to Question 2.2, and assume mean amino acid Mw is ~137 Da as given also, indicates total number of amino acids per cell of ~3.2×10^{6} residues. Assume 3 nucleotides per amino acid residues implies ~9.5×10^{6} residues. If range of transcription speed of RNAP is 20-90 nucleotides per second then this would take ~5-20 $x10^{5}$ seconds or a mean of ~20×10^{3} min. This suggests there are ~1,000 active RNAP molecules in the cell at any one time since all of this protein would need to be replicated in one 20 min cell doubling time, and this output of mRNA can be amply accommodated for translation into peptides/protein by the ~20,000 ribosomes present per cell.

2.5 Force is –grad(potential energy). Force is vector so we need to consider up magnitudes and directions of total force, but potential energy can be summed as a scaler and then a final calculation at end to calculate total force vector, and so is computationally more efficient to do this way.

2.6 Van der Waals interactions are due to dispersion-steric forces, modeled by –grad of Lennard-Jones potential, or $12A/r^{13}-6B/r^{7}$. When this is zero $r=r_m=(2A/B)^{1/6}$ and $U=V_m=A/(2A/B)^{12/6}-B/(2A/B)^{6/6}=B^2/4A-B^2/2A=-B^2/4A$, so $B=2A/r_m^{6}=-B^2/2V_m r_m^{6}$ or $B=-2V_m r_m^{6}$ and $A=Br_m^{6}/2=-V_m r_m^{12}$, so $U=-V_m((r_m/r)^{12}-2(r_m/r)^{6})$

2.7 (a) Energy required to break a single H-bond is ~$5k_BT$, so mismatch energy difference equivalent to breaking either 2(AT or TA) or 3 (CG or GC) H-bonds, so if equal proportion of A, T, C, G then mean number of H-bonds to break is 2.5, mean energy of ~$12.5k_BT$. Probability of this transition given by Boltzmann factor $\exp(-12.5k_BT/k_BT)$ or 10^{-5} – 10^{-6}, which is roughly as observed. (b) Total 'diploid' genome (i.e. chromosomes from each parent) is $2 \times 3 \times 10^{9}$, or ~6×10^{9} bp. Thus probability or error equivalent to $1/(6 \times 10^{9})$ or ~2×10^{-10}. This is much smaller than (a), due to error checking mechanisms in living cell correcting for many mismatches (typically using alternative strand in DNA double helix as a template).

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2.8 Typical transmembrane voltage V is ca. -200mV, so free energy change in moving charge q through V is simply Vq, or 3.2 x 10^{-20} J, or ~8 k_BT at room temperature. The activation barrier for spontaneously translocating across intact lipid bilayer membrane is ca. an order of magnitude higher if substitute in values to electrical self energy of $q/8\pi r\varepsilon_0\varepsilon_r$, – to prove this consider energy to charge up a spherical capacitor of capacitance $C = CV^2/2 = 1qV$ where V is indicate electrostatic potential energy. For spherical shall, using Gauss's law, $V=Q/4\pi r\varepsilon_0\varepsilon_r$., result follows.

If sodium ions allowed to translocate freely across pores into water 'reservoir' of much larger volume than cell, then all sodium ions will be lost from cell, equivalent to VC where V is volume of cell and c is initial concentration of sodium ions, which assuming cell is perfect sphere gives V=5.2 x 10^{-16} m^3 = 5.2 x 10-^{13} L, c=150mM, so number of ions is ~4.6 x 10^{10} ions.

2.9 (a) Energy per mole released from 38 ATP is 38 x 18k_BT x Avogadro's number which is 38 x 18 x 1.38 x 10^{-23} x 300 x 6.02 x 10^{23} =1705 kJ mol^{-1}. Thus efficiency is ~1705/2870 or ~59%. (b) Length scale of bacterial cell ~1 micron, so volume ~10^{-18} m^3 or 10^{-15} L. Number of glucose molecules ~5 x 10^{-3} x 10^{-15} x 6.02 x 10^{23} = 3 x 10^6 molecules, equivalent to ~2 billion k_BT of energy, much greater than required transition energy for molecular processes in cell, so cell breaks this down into smaller manageable chunks of single ATP chemical potential energy.

2.10 (a) Same as answer to Question 2.8 or ~8 k_BT. (b) Sum of two half reactions (see Equations 2.1 and 2.2), gives electrochemical voltage E total for reaction = -0.315 -(-0.166)=-0.149V, free energy change per mole given by -nEq, n =2 as 2 H+ transferred, giving 4.8 x 10^{-20} J = 4.8 x 10^{-20} /(1.38 x 10^{-23} x 300) or ~12 k_BT. Three molecules of NAD+ per TCA cycle, so ~36 k_BT total available, or ~4 H+ pumped per TCA cycle, assuming majority of chemical potential energy available from NAD+ coupled to proton pumping (i.e. negligible loss as heat). (c) Use Equation 2.4 and assume $\Delta G=0$ if no loss of heat, and ΔG_0 is under 'standard' conditions for everything apart from pH=7.5, gives $[NADH]/[NAD+]=([Malate]/[Oxaloacetate][H+])\exp(-\Delta G_0/k_BT)$. From chapter we are told the concentrations of oxaloacetate and malate are kept relatively low in the cell at 50 nM and 0.2 mM, The concentration of protons is given by difference in concentration between pH7.5 and standard conditions of pH7 =10(7-7.5)= 0.32 M. Substituting in these values gives [NADH]/[NAD+] ~0.08 – i.e. > an order of magnitude excess of NAD+, the low concentration of oxaloacetate drives forwards the whole TCA cycle.

2.11 Quite possibly

2.12 Bacteria (mainly in gut).

2.15 Variation as proportion of mean in height is much greater than the variation due just to bp spontaneous mutation of probability ~1 in 10^9, so the 'phenotype' variation is due to more than just spontaneous genetic mutation (many factors).

2.16 After n dilutions, if I out of T (=9) cultures are infected then number N of virus molecules in original 1mL volume of undiluted culture is $(T/I)10^n$ from simple probability considerations if just one virus is required to infect a culture and assuming that I<T (i.e. not 'saturated' with excess viruses) and I>0 (i.e. there is at least one virus particle present). So taking average from 10^{th} and 11^{th} dilutions suggests $N=((6/9)10^{10}+(2/9)10^{11})/2=1.4 \times 10^{10}$ viruses, in 1mL. Thus is 1L there are 1.4 x 10^{13} viruses, which is a molarity of 1.4 x $10^{13}/(6.02 \times 10^{23})=2.3 \times 10^{-11}$ M

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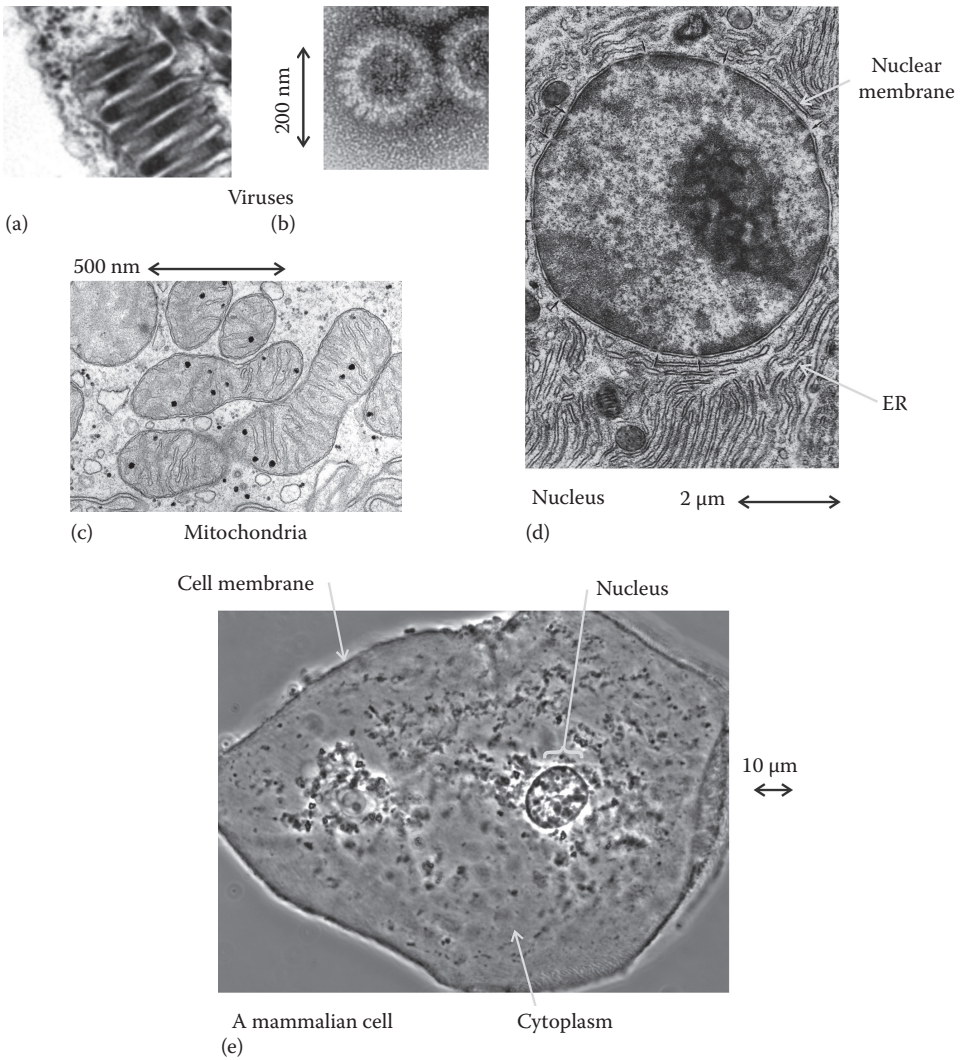


Figure 2.1 The architecture of biological structures. A range of typical cellular structures, in addition to viruses. (a) Rodlike Maize mosaic viruses, (b) obtained using negative-staining followed by transmission electron microscopy, TEM (see Chapter 5); (c) mitochondria from guinea pig pancreas cells, (d) TEM of nucleus with endoplasmic reticulum (ER), (e) phase contrast image of a human cheek cell. (a: Adapted from Cell Image Library, University of California at San Diego, CIL:12417 c: Courtesy of G.E. Palade, CIL:37198; d: Courtesy of D. Fawcett, CIL:11045; e: Adapted from CIL:12594.)

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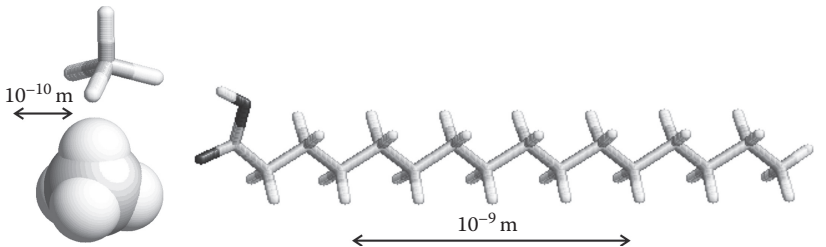


Figure 2.2 Carbon chemistry. (a) Rod and space-filling tetrahedral models for carbon atom bound to four hydrogen atoms in methane. (b) Chain of carbon atoms, here as palmitic acid, an essential fatty acid.

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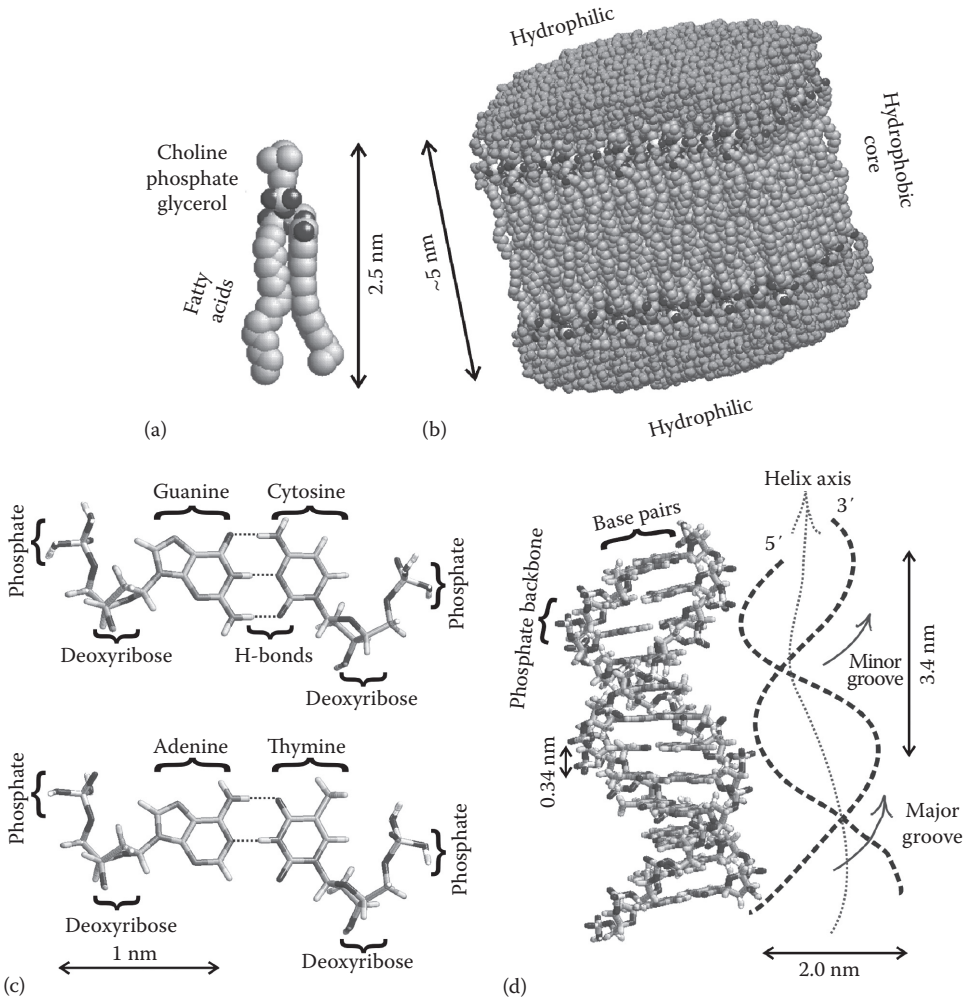


Figure 2.3 **(See color insert.)** Fats and nucleic acids. (a) Single phospholipid molecule. (b) Bilayer of phospholipids in water. (c) Hydrogen-bonded nucleotide base pairs. (d) B-DNA double-helical structure.

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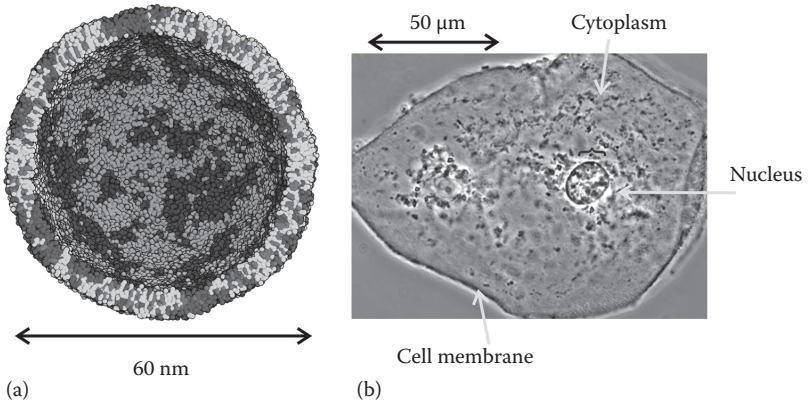


Figure 2.4 Structures formed from lipid bilayers. (a) Liposome, light and dark showing different phases of phospholipids from molecular dynamics simulation (see Chapter 8). (b) The cell membrane and nuclear membranes, from a human cheek cell taken using phase contrast microscopy (Chapter 3). (a: Courtesy of M. Sansom; b: Courtesy of G. Wright, CIL:12594.)

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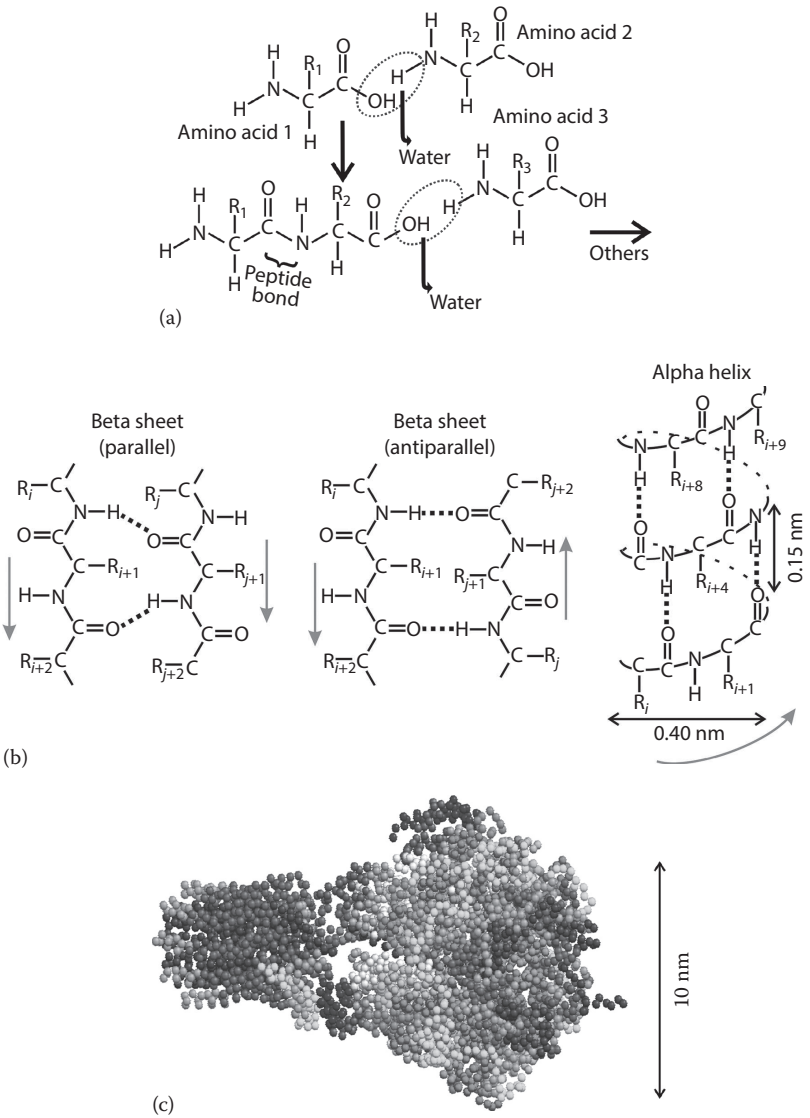


Figure 2.5 Peptide and proteins. (a) Formation of peptide bond between amino acids to form primary structure. (b) Secondary structure formation via hydrogen bonding to form beta sheets and alpha helices. (c) Example of a complex 3D tertiary structure, here of an enzyme that makes ATP.

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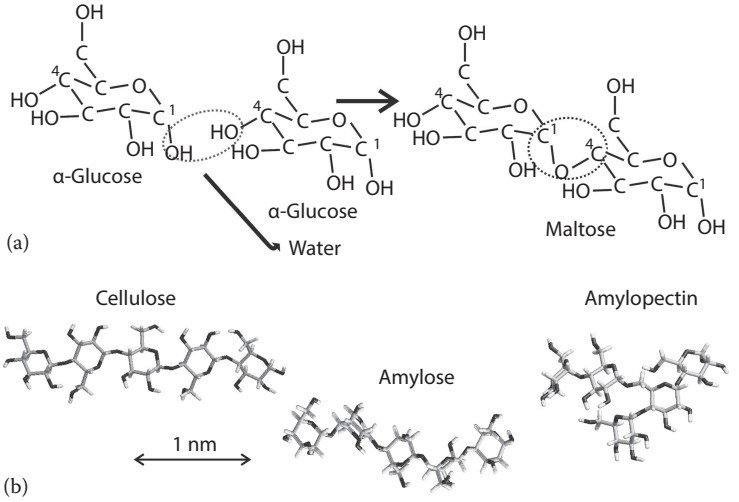


Figure 2.6 Sugars. (a) Formation of larger sugars from monomer units of monosaccharide molecules via loss of water molecule to form a disaccharide molecule. (b) Examples of polysaccharide molecules.

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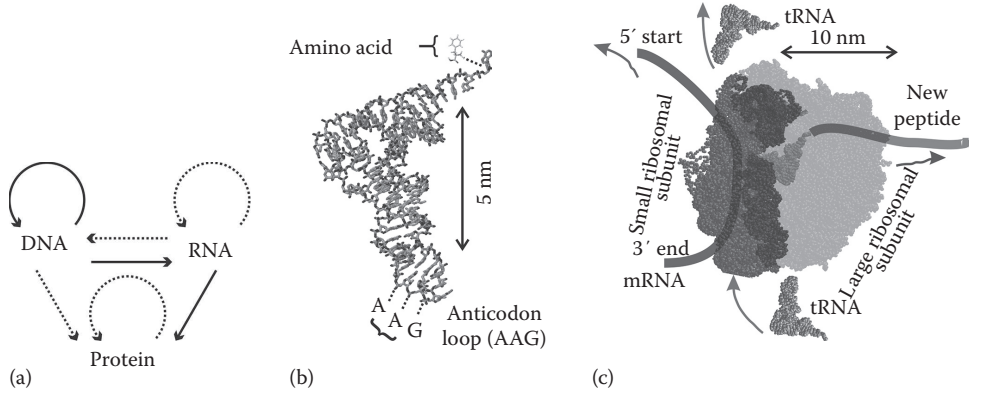


Figure 2.7 Central dogma of molecular biology. (a) Schematic of the flow of information between nucleic acids and proteins. (b) Structure of tRNA. (c) Interaction of tRNA with ribosome during peptide manufacture.

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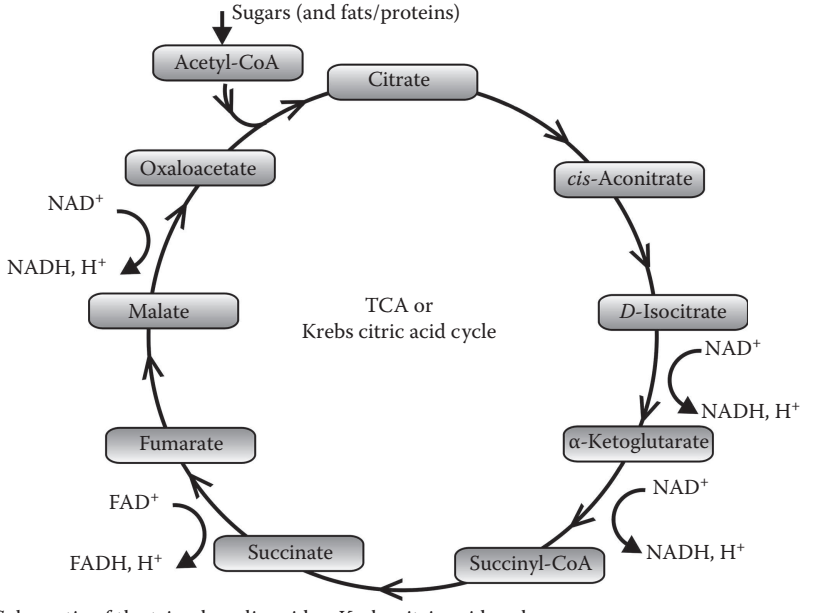


Figure 2.8 Schematic of the tricarboxylic acid or Krebs citric acid cycle.

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