

2.1 (Icons.) *Dramatis personæ*. Approximate relative sizes of some of the actors in our story. T2 phage is a virus that infects bacteria, for example, *Escherichia coli*. Much of this book will be occupied with phenomena relevant at length scales from the protozoan down to the DNA helix. [Adapted from Kornberg, 1989.]



2.2 (Drawing, based on light microscopy.) Relative sizes. (a) Five *Escherichia coli* bacteria cells (enlarged in Fig. 2.3). (b) Two cells of baker's yeast. (c) Human red blood cell. (d) Human white blood cell (lymphocyte). (e) Human sperm cell. (f) Human epidermal (skin) cell. (g) Human striated muscle cell (myofibril). (h) Human neuron (nerve cell). [From Goodsell, 1993.]



2.3 (Drawing, based on electron microscopy.) Relative sizes. (a) Several molecules and macromolecules (enlarged in Fig. 2.4). (b) A bacterial cell (see Figures 2.1 and 2.2a). Visible structures include flagella (trailing to the right), the nucleoid (white region in center), and the thick, rigid cell wall. The flagella propel the bacterium by a mechanism discussed in Chapter 5; they are, in turn, driven by motors discussed in Chapter 11. (c) Human immunodeficiency virus. (d) A bacterial virus, or phage. [From Goodsell, 1993.]



2.4 (Drawing, based on structural data.) Relative sizes of the objects shown in panel (a) of Fig. 2.3. (a) Single carbon atom. (b) Glucose, a simple sugar molecule. (c) ATP, a nucleotide. (d) Chlorophyll molecule. (e) Transfer RNA, or tRNA. (f) An antibody, a protein used by the immune system. (g) The ribosome, a complex of protein and RNA. (h) The virus responsible for polio. (i) Myosin, a molecular machine discussed in Chapter 10. (j) DNA, a nucleic acid. Chapter 9 will discuss the mechanical properties of long molecules like this one. (k) F-actin, a cytoskeletal element. (l) Ten enzymes (protein machines) involved in glycolysis, which is a series of coupled chemical reactions that produce ATP, the energy currency molecule, from glucose. Chapter 11 will discuss ATP production. (m) Pyruvate dehydrogenase, a large enzyme complex also discussed in Chapter 11. [From Goodsell, 1993.]



2.11 (Molecular structure.) J. Watson and F. Crick demonstrate the complementarity of DNA basepairs. The dotted lines denote hydrogen bonds (see Chapter 7). The shapes and chemical structure of the bases allow hydrogen bonds to form optimally only between adenine (A) and thymine (T) and between guanine (G) and cytosine (C); in these pairings, atoms that are able to form hydrogen bonds can be brought close together without distorting the bases' geometries. [Cartoon by Larry Gonick, from Gonick & Wheelis, 1991.]



2.15 (Structure rendered from atomic coordinates.) Stereo image of the DNA double helix. To view this image, begin with your nose a few centimeters from the page (if you're nearsighted, remove your glasses). Imagine staring through the page at a distant object. If necessary, rotate the page a few degrees, so that the two dots near the centers of each panel are aligned horizontally. Wait until the dots fuse. Concentrate on holding the dots fused as you slowly move the page away from your nose. When the page is far enough away for your eyes to focus on it, the three-dimensional image will jump off the page at you. The structure is about 2 nm wide. The portion shown consists of twelve basepairs in a vertical stack. Each basepair is roughly a flat, horizontal plate about 0.34 nm thick. The stack twists through slightly more than one full revolution from top to bottom. [From Dickerson et al., 1982.]



2.16 (Structure rendered from atomic coordinates.) A single strand of RNA uses base-pairing and other interactions to form a unique three-dimensional structure. The molecule shown is a transfer RNA from yeast; it binds the amino acid phenylalanine, transports it to the ribosome, then releases it (see Fig. 2.24). The flat, stacked nucleotides are shown as stick structures mostly on the interior; the sugar-phosphate backbone atoms are instead shown as spheres, to reveal the double helical nature of parts of the folded molecule. Longer strands of RNA can have several pairs of complementary stretches, leading to more complex folded structures than the one shown here. Section 6.7 will discuss how the folding and unfolding of RNA can be controlled by external forces.



2.17 (Molecular structure from crystallography data.) A segment of the alpha helix structure. Nine successive residues are shown. Each residue's side group has been replaced by a single ball, labeled R_1, \ldots, R_9 . Each residue has a hydrogen atom bound to one of the nitrogens on the chain. Each of these hydrogens loses its electron to an oxygen located four units farther down the chain, to form a hydrogen bond (*thin lines*). The hydrogen bonds help to stabilize the ordered, helical structure against thermal disruption. Chapter 9 will discuss the formation and loss of ordered structures like this one under changes in environmental conditions. The structure shown is "right-handed" in the following sense: Choose either direction along the helix axis, for example, upward in the figure. Point your right thumb along this direction. Then as you proceed in the direction of your thumb, the peptide backbone rotates around the axis in the same direction as your fingers point (opposite to the direction you'd have gotten using your left hand).



Color Figure 6 (Composite of structures rendered from atomic coordinates.) A DNA-binding protein. The color scheme is the same as Color Figure 5. Repressor proteins like this one bind directly to the DNA double helix, physically blocking the polymerase that makes messenger RNA. They recognize a specific sequence of DNA, generally blocking a region of 10–20 basepairs. The binding does not involve the formation of chemical bonds; instead it uses the weaker interactions discussed in Chapter 7. Repressors form a molecular switch, turning off the synthesis of a given protein until it is needed. [Digital image kindly supplied by D. Goodsell; see Goodsell, 1993.]



2.23 (Drawing, based on structural data.) Transcription of DNA to messenger RNA by RNA polymerase, a walking motor. The polymerase reads the DNA as it walks along the DNA strand, synthesizing a mRNA transcript as it moves. [From Goodsell, 1993.]



2.24 (Drawing, based on structural data.) The information in messenger RNA is translated into a sequence of amino acids making up a new protein by the combined action of over 50 molecular machines. In particular, amino acyl-tRNA synthetases supply transfer RNAs loaded with amino acids to the ribosomes, which construct the new protein as they read the messenger RNA. Not shown are some smaller auxiliary proteins, the initiation, elongation, and transcription factors, that help the ribosomes do their job. [From Goodsell, 1993.]



9.1 (Schematic.) Deformations of a thin elastic rod. (a) Definition of the bend vector, $\boldsymbol{\beta} = d\hat{\mathbf{t}}/ds$, illustrated for a circular segment of a thin rod. The parameter s is the contour length (also called arc length) along the rod. The tangent vector $\hat{\mathbf{t}}(s)$ at one point of the rod has been moved to a nearby point a distance ds away (dashed arrow), then compared with the tangent vector there, or $\hat{\mathbf{t}}(s + ds)$. The difference of these vectors, $d\hat{\mathbf{t}}$, points radially inward and has magnitude equal to $d\theta$, or ds/R. (b) Definition of stretch. For a uniformly stretched rod, $u = \Delta L/L_{tot}$. (c) Definition of twist density. For a uniformly twisted rod, $\omega = \Delta \phi_{tot}/L_{tot}$.



9.2 (Wet scanning electron micrograph.) Actin bundles in a stained CHO cell. Each bundle has a bend persistence length that is much larger than that of a single actin filament. The bundles are straight, not thermally bent, because their bend persistence length is longer than the cell's diameter. [Digital image kindly supplied by A. Nechushtan and E. Moses.]



9.3 (Engineering sketch.) Rubber-band heat engine. The light bulb sequentially heats the rubber bands on one side of the disk, making them contract. The other side is shielded by the sheet metal screen; here the rubber bands cool. The resulting asymmetrical contraction unbalances the wheel, which turns. The turning wheel brings the warm rubber bands into the shaded region, where they cool; at the same time, cool rubber bands emerge into the warm region, making the wheel turn continuously. [From Stong, 1956.]



9.4 (Experimental data with fit.) Force f versus relative extension z/L_{tot} for a DNA molecule made of 10 416 basepairs, in high-salt solution. The regimes labeled A, B, C, D, and E are described in the text. The extension z was measured by video imaging of the positions of beads attached to each end; the force was measured by using the change of light momentum exiting a dual-beam optical tweezers apparatus (see Section 6.7). L_{tot} is the DNA's total contour length in its relaxed state. The quantity z/L_{tot} becomes larger than 1 when the molecule begins to stretch, at around 20 pN. The solid curve shows a theoretical model obtained by a combination of the approaches in Sections 9.4.1' and 9.5.1[[Source: see for example Cizeau & Viovy, 1997; Storm & Nelson, 2003]]. [Experimental data kindly supplied by S. B. Smith; theoretical model and fit kindly supplied by C. Storm.]



9.5 (Experimental data with fits.) Log-log plot of relative extension $z/L_{\rm tot}$ at low applied stretching force f for lambda phage DNA in 10 mM phosphate buffer. The points show experimental data corresponding to the regimes A-B in Fig. 9.4. The curves show various theoretical models discussed in the text. For comparison, the value of $L_{\rm seg}$ has been adjusted in each model so that all the curves agree at low force. Top curve: One-dimensional freely jointed chain (Equation 9.10), with $L_{\rm seg}^{(1d)} = 35 \,\mathrm{nm}$. Long-dash curve: One-dimensional cooperative chain (see Your Turn 9H (b)), with $L_{\rm seg}^{(1d)}$ held fixed at 35 nm and γ very large. Short-dash curve: Three-dimensional FJC (Your Turn 9O), with $L_{\rm seg} = 104 \,\mathrm{nm}$. Black curve through data points: Three-dimensional elastic rod model (Section 9.4.1' on page 379), with $A = 51 \,\mathrm{nm}$. [Data kindly supplied by V. Croquette; see also Bouchiat et al., 1999.]



9.6 (Experimental data with fit.) Linear plot of the stretching of DNA in regime C of Fig. 9.4. A DNA molecule with 38 800 basepairs was stretched with optical tweezers, in a buffer solution with pH 8.0. For each value of the force, the ratio of the observed relative extension and the prediction of the inextensible elastic rod model is plotted. The fact that this ratio is a linear function of applied force implies that the molecule has a simple elastic stretching response to the applied force. The solid line is a straight line through the point (0 pN, 1), with fitted slope $1/(Bk_{\rm B}T_{\rm r}) = 1/(1400 \text{ pN})$. [Data kindly supplied by M. D. Wang; see Wang et al., 1997.]