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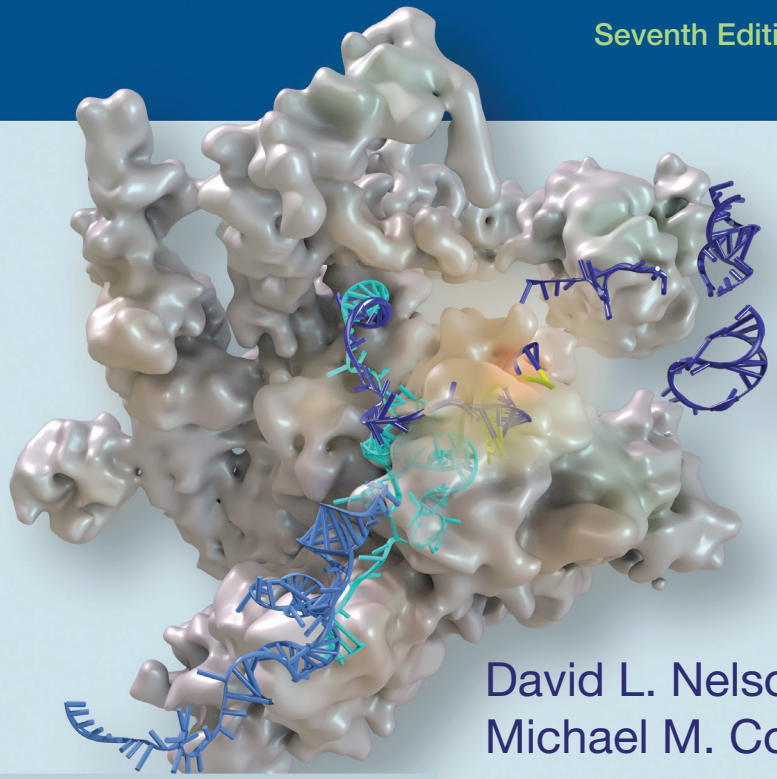


David L. Nelson
Michael M. Cox

INSIDE: **SAMPLE CHAPTER 5**
PROTEIN FUNCTION

w.h.freeman
Macmillan Learning

ABOUT THE AUTHORS

Source: Robin Davies, UW–Madison Biochemistry MediaLab

David L. Nelson, born in Fairmont, Minnesota, received his BS in Chemistry and Biology from St. Olaf College in 1964 and earned his PhD in Biochemistry at Stanford Medical School under Arthur Kornberg. He was a postdoctoral fellow at the Harvard Medical School with Eugene P. Kennedy, who was one of Albert Lehninger's first graduate students. Nelson joined the faculty of the University of Wisconsin–Madison in 1971 and became a full professor of biochemistry in 1982. He was for eight years the Director of the Center for Biology Education at the University of Wisconsin–Madison. He became Professor Emeritus in 2013.

Nelson's research focused on the signal transductions that regulate ciliary motion and exocytosis in the protozoan *Paramecium*. He has a distinguished record as a lecturer and research supervisor. For 43 years he taught (with Mike Cox) an intensive survey of biochemistry for advanced biochemistry undergraduates in the life sciences. He has also taught a survey of biochemistry for nursing students, and graduate courses on membrane structure and function and on molecular neurobiology. He has received awards for his outstanding teaching, including the Dreyfus Teacher–Scholar Award, the Atwood Distinguished Professorship, and the Unterkofler Excellence in Teaching Award from the University of Wisconsin System. In 1991–1992 he was a visiting professor of chemistry and biology at Spelman College. His second love is history, and in his dotage he teaches the history of biochemistry and collects antique scientific instruments for use in the Madison Science Museum, of which he is the founding president.

Michael M. Cox was born in Wilmington, Delaware. In his first biochemistry course, the first edition of Lehninger's *Biochemistry* was a major influence in refocusing his fascination with biology and inspiring him to pursue a career in biochemistry. After graduating from the University of Delaware in 1974, Cox went to Brandeis University to do his doctoral work with William P. Jencks, and then to Stanford in 1979 for postdoctoral study with I. Robert Lehman. He moved to the University of Wisconsin–Madison in 1983 and became a full professor of biochemistry in 1992.

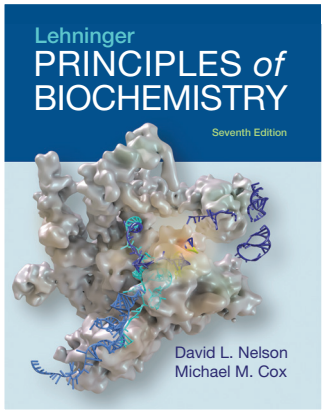
Cox's doctoral research was on general acid and base catalysis as a model for enzyme-catalyzed reactions. At Stanford, he began work on the enzymes involved in genetic recombination. The work focused particularly on the RecA protein, designing purification and assay methods that are still in use, and illuminating the process of DNA branch migration. Exploration of the enzymes of genetic recombination has remained a central theme of his research.

Mike Cox has coordinated a large and active research team at Wisconsin, investigating the enzymology, topology, and energetics of the recombinational DNA repair of double strand breaks in DNA. The work has focused on the bacterial RecA protein, a wide range of proteins that play auxiliary roles in recombinational DNA repair, the molecular basis of extreme resistance to ionizing radiation, directed evolution of new phenotypes in bacteria, and the applications of all of this work to biotechnology. For more than three decades he has taught a survey of biochemistry to undergraduates and has lectured in graduate courses on DNA structure and topology, protein-DNA interactions, and the biochemistry of recombination. More recent projects have been the organization of a new course on professional responsibility for first-year graduate students and the establishment of a systematic program to draw talented biochemistry undergraduates into the laboratory at an early stage of their collegiate career. He has received awards for both his teaching and his research, including the Dreyfus Teacher–Scholar Award, the 1989 Eli Lilly Award in Biological Chemistry, and the 2009 Regents Teaching Excellence Award from the University of Wisconsin. He is also highly active in national efforts to provide new guidelines for undergraduate biochemistry education. His hobbies include turning 18 acres of Wisconsin farmland into an arboretum, wine collecting, and assisting in the design of laboratory buildings.

LEHNINGER

PRINCIPLES OF BIOCHEMISTRY

SEVENTH EDITION



LEHNINGER PRINCIPLES OF BIOCHEMISTRY
Seventh Edition

David L. Nelson, University of Wisconsin–Madison
Michael M. Cox, University of Wisconsin–Madison

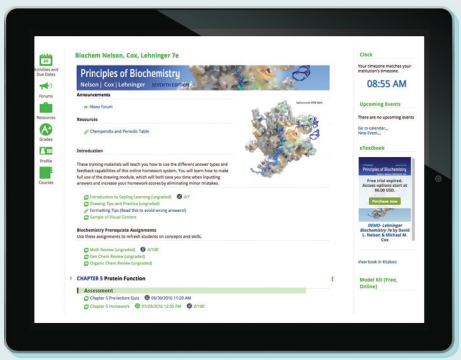
December 2016 (©2017)
Cloth // 1328 pages // 978-1-4641-2611-6

Lehninger Principles of Biochemistry is the #1 bestseller for the introductory biochemistry course because it brings clarity and coherence to an often unwieldy discipline, offering a thoroughly updated survey of biochemistry's enduring principles, definitive discoveries, and ground-breaking new advances with each edition.

This new Seventh Edition maintains the qualities that have distinguished the text since Albert Lehninger's original edition—clear writing, careful explanations of difficult concepts, helpful problem-solving support, and insightful communication of contemporary biochemistry's core ideas, new techniques, and pivotal discoveries. Again, David Nelson and Michael Cox introduce students to an extraordinary amount of exciting new findings without an overwhelming amount of extra discussion or detail.

And with this edition, W.H. Freeman and Sapling Learning have teamed up to provide the book's richest, most completely integrated text/media learning experience yet, through an extraordinary new online resource: SaplingPlus.

To request your review copy of Nelson/Cox, *Lehninger Principles of Biochemistry*, Seventh Edition, and to explore SaplingPlus, visit macmillanlearning.com/Lehninger7e.



LEHNINGER HALLMARKS

Students taking biochemistry for the first time often have difficulty with two key aspects of the course: approaching quantitative problems and applying what they learned in organic chemistry. Central to this book's popularity are the effective ways it helps students overcome these difficulties:

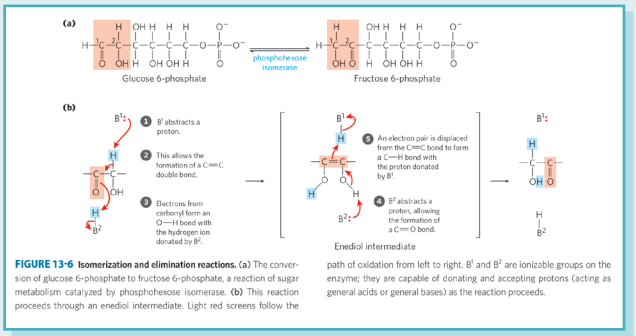


FIGURE 13-6 **Isomerization and elimination reactions.** **(a)** The conversion of glucose 6-phosphate to fructose 6-phosphate, a reaction of sugar metabolism catalyzed by phosphohexose isomerase. **(b)** This reaction proceeds through an enediol intermediate. Light red screens follow the path of oxidation from left to right. B^1 and B^2 are ionizable groups on the enzyme; they are capable of donating and accepting protons (acting as general acids or general bases) as the reaction proceeds.

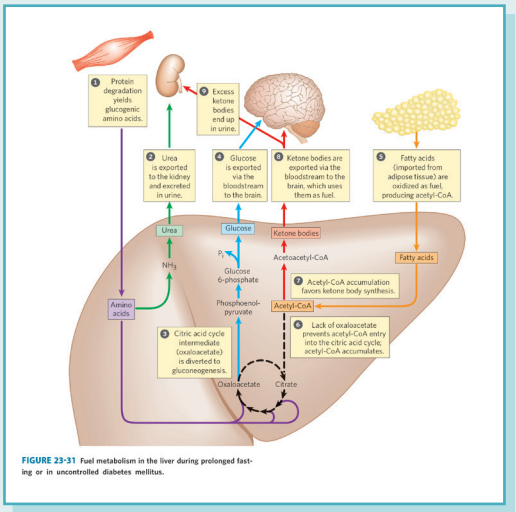


FIGURE 23-31 **Fuel metabolism in the liver during prolonged fasting or in uncontrolled diabetes mellitus.**

FOCUS ON CHEMICAL LOGIC

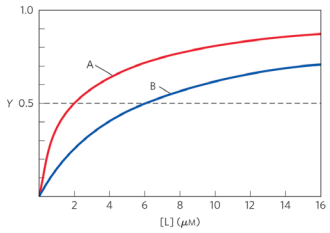
- Section 13.2, Chemical Logic and Common Biochemical Reactions, discusses the common biochemical reaction types that underlie all metabolic reactions, helping students to connect organic chemistry with biochemistry.
- Chemical logic figures for each of the central metabolic pathways highlight the conservation of mechanism and illustrate patterns that make learning pathways easier.
- Mechanism figures help students understand the reaction process step by step, using a consistent set of conventions for each mechanism.

CLEAR ART

- Smarter renditions of classic figures are easier to interpret.
- Molecular structures created specifically for this book use consistent shapes and color schemes.
- Figures with numbered, annotated steps help explain complex processes.
- Summary figures help students keep the big picture in mind while learning the specifics.

WORKED EXAMPLE 5-1 **Receptor-Ligand Dissociation Constants**

Two proteins, A and B, bind to the same ligand, L, with the binding curves shown below.



What is the dissociation constant, K_d, for each protein? Which protein (A or B) has a greater affinity for ligand L?

Solution: We can determine the dissociation constants by inspecting the graph. Since Y represents the fraction of binding sites occupied by ligand, the concentration of ligand at which half the binding sites are occupied—that is, the point where the binding curve crosses the line where $Y = 0.5$—is the dissociation constant. For A, $K_d = 2\ \mu M$; for B, $K_d = 6\ \mu M$. Because A is half-saturated at a lower [L], it has a higher affinity for the ligand.

PROBLEM-SOLVING TOOLS

- In-text Worked Examples take students through difficult equations to improve their quantitative problem-solving skills.
- More than 600 end-of-chapter problems give students further opportunity to practice what they have learned.
- Data Analysis Problems (one at the end of each chapter), contributed by Brian White of the University of Massachusetts–Boston, encourage students to synthesize what they have learned and apply their knowledge to the interpretation of data from the literature.

Data Analysis Problem

19. Protein Function During the 1980s, the structures of actin and myosin were known only at the resolution shown in Figure 5-28a, b. Although researchers knew that the S1 portion of myosin bound to actin and hydrolyzed ATP, there was a substantial debate about where in the myosin molecule the contractile force was generated. At the time, two competing models were proposed for the mechanism of force generation in myosin.

In the "hinge" model, S1 bound to actin, but the pulling force was generated by contraction of the "hinge region" in the myosin tail. The hinge region is in the heavy meromyosin portion of the myosin molecule, near where trypsin cleaves off light meromyosin (see Fig. 5-27b); this is roughly the point labeled "Two supercoiled α helices" in Figure 5-27a. In the "S1" model, the pulling force was generated in the S1 "head" itself and the tail was just for structural support.

two partial myosin molecules (Fig. 5-27b): (1) heavy meromyosin (HMM), made by briefly digesting myosin with trypsin; HMM consists of S1 and the part of the tail that includes the hinge; and (2) short heavy meromyosin (SHMM), made from a more extensive digestion of HMM with trypsin; SHMM consists of S1 and a shorter part of the tail that does not include the hinge. Brief digestion of myosin with trypsin produces HMM and light meromyosin, by cleavage of a single specific peptide bond in the myosin molecule.

(d) Why might trypsin attack this peptide bond first rather than other peptide bonds in myosin?

Spudich and colleagues prepared bead-antibody-myosin complexes with varying amounts of myosin, HMM, and SHMM and measured their speed of movement along *Nitella* actin fibers in the presence of ATP. The graph below sketches their results.

» Key Convention: The three-letter code is transparent, the abbreviations generally consisting of the first three letters of the amino acid name. The one-letter code was devised by Margaret Oakley Dayhoff, considered by many to be the founder of the field of bioinformatics. The one-letter code reflects an attempt to reduce the size of the data files (in an era of punch-card computing) used to describe amino acid sequences. It was designed to be easily memorized, and understanding its origin can help students do just that. For six amino acids (CHIMSV), the first letter of the amino acid name is unique and thus is used as the symbol. For five others (AGLPT), the first letter of the name is not unique but is assigned to the amino acid that is most common in proteins (for example, leucine is more common than lysine). For another four, the letter used is phonetically suggestive (RFYW: aRginine, Fenylalanine, tYrosine, tWiptophan). The rest were harder to assign. Four (DNEQ) were assigned letters found within or suggested by their names (asparDic, asparagiNe, glutamEke, Q-tamine). That left lysine. Only a few letters were left, and K was chosen because it was the closest to L. **«**

Margaret Oakley Dayhoff, 1925–1983

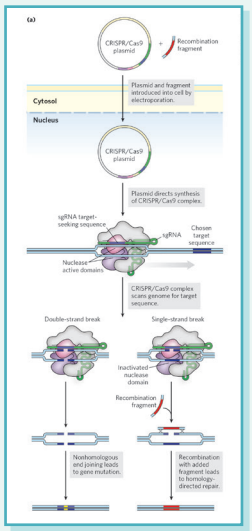
KEY CONVENTIONS

For review and easy reference throughout, *Lehninger Principles of Biochemistry* highlights important assumptions and ideas that students are expected to assimilate without being told (for example, peptide sequences are written from amino- to carboxyl-terminal end, left to right; nucleotide sequences are written from 5' to 3' end, left to right).

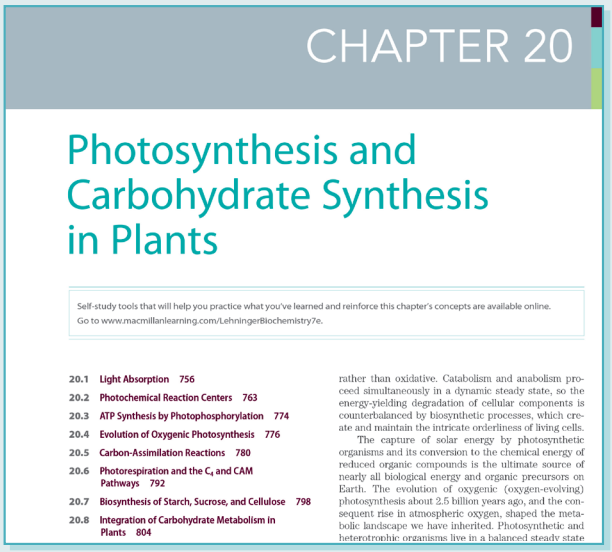
IN THE NEW EDITION

NEW LEADING-EDGE SCIENCE TOPICS, INCLUDING:

- Synthetic cells and disease genomics (Chapter 1)
- Intrinsically disordered protein segments (Chapter 4)
- Pre-steady state enzyme kinetics (Chapter 6)
- Gene annotation (Chapter 9)
- Gene editing via CRISPR (Chapter 9)
- Membrane trafficking and dynamics (Chapter 11)
- Importance of intrinsically disordered proteins in signaling (Chapter 12)
- Specialized pro-resolving mediators (Chapter 21)
- New roles for NADH (Chapter 13)
- Peptide hormones: incretins and blood glucose, irisin and exercise (Chapter 23)
- Chromosomal territories (Chapter 24)
- New details of eukaryotic DNA replication (Chapter 25)
- Cap snatching; spliceosome structure (Chapter 26)
- Ribosome rescue; RNA editing update (Chapter 27)
- New roles for non-coding RNAs (Chapters 26 and 28)
- The RNA recognition motif (Chapter 28)



Gene editing via CRISPR from Ch. 9, DNA-Based Information Technologies



CHAPTER 20

Photosynthesis and Carbohydrate Synthesis in Plants

Self-study tools that will help you practice what you've learned and reinforce this chapter's concepts are available online. Go to www.macmillanlearning.com/LehningerBiochemistry7e.

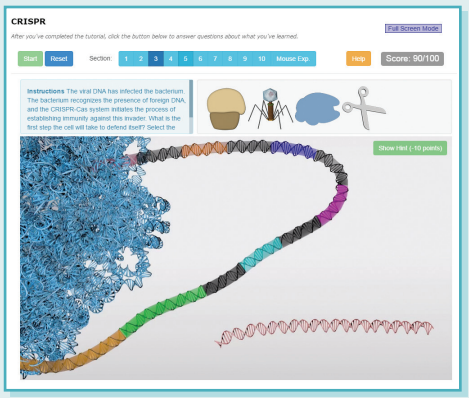
rather than oxidative. Catabolism and anabolism proceed simultaneously in a dynamic steady state, so the energy-yielding degradation of cellular components is counterbalanced by biosynthetic processes, which create and maintain the intricate orderliness of living cells.

The capture of solar energy by photosynthetic organisms and its conversion to the chemical energy of reduced organic compounds is the ultimate source of nearly all biological energy and organic precursors on Earth. The evolution of oxygenic (oxygen-evolving) photosynthesis about 2.5 billion years ago, and the consequent rise in atmospheric oxygen, shaped the metabolic landscape we have inherited. Photosynthetic and heterotrophic organisms live in a balanced steady state

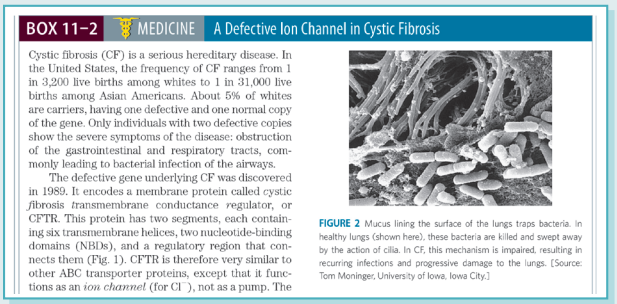
NEW Chapter 20, Photosynthesis and Carbohydrate Synthesis in Plants. All coverage of plant metabolism is now consolidated into a single chapter, separate from oxidative phosphorylation, Chapter 19. Chapter 20 includes light-driven ATP synthesis, carbon fixation, photorespiration, the glyoxylate cycle, cellulose synthesis, and regulatory mechanisms that ensure integration of all of these activities throughout the plant.

NEW TOOLS AND TECHNOLOGY, INCLUDING:

- Next-generation DNA sequencing now includes ion-torrent and single molecule real time (SMRT) sequencing platforms, and the discussion has moved to follow classical Sanger sequencing (Chapter 8).
- Gene editing via CRISPR is one of many updates to the discussion of genomics (Chapter 9).
- LIPID MAPS database and system of classifying lipids is included in the discussion of lipidomics (Chapter 10).
- Cryo-electron microscopy is described in a new box (Chapter 19).
- Ribosome profiling to determine which genes are being translated at any given moment, and many related technologies, are included to illustrate the versatility and power of deep DNA sequencing (Chapter 27).
- Online data resources such as NCBI, PDB, SCOP2, KEGG, and BLAST, mentioned throughout the text, are listed in the back endpapers for easy reference.



Gene editing via CRISPR, from a simulation in SaplingPlus.



BOX 11–2 MEDICINE A Defective Ion Channel in Cystic Fibrosis

Cystic fibrosis (CF) is a serious hereditary disease. In the United States, the frequency of CF ranges from 1 in 3,200 live births among whites to 1 in 31,000 live births among Asian Americans. About 5% of whites are carriers, having one defective and one normal copy of the gene. Only individuals with two defective copies show the severe symptoms of the disease: obstruction of the gastrointestinal and respiratory tracts, commonly leading to bacterial infection of the airways.

The defective gene underlying CF was discovered in 1989. It encodes a membrane protein called cystic *f*ibrosis *t*ransmembrane conductance *r*egulator, or CFTR. This protein has two segments, each containing six transmembrane helices, two nucleotide-binding domains (NBDs), and a regulatory region that connects them (Fig. 1). CFTR is therefore very similar to other ABC transporter proteins, except that it functions as an *ion channel* (for Cl^-), not as a pump. The

FIGURE 2 Mucus lining the surface of the lungs traps bacteria. In healthy lungs (shown here), these bacteria are killed and swept away by the action of cilia. In CF, this mechanism is impaired, resulting in recurring infections and progressive damage to the lungs. [Source: Tom Moninger, University of Iowa, Iowa City.]

Medical Insights and Applications. New topics for this feature include Guillain-Barré syndrome and gangliosides, cystic fibrosis, and xenobiotics as endocrine disruptors.

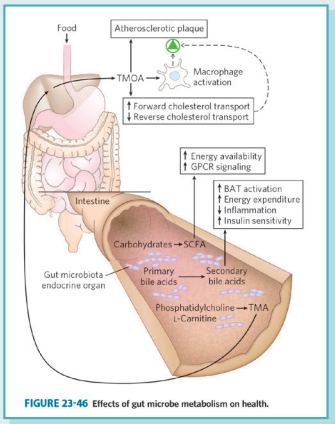


FIGURE 23-46 Effects of gut microbe metabolism on health.

Special Theme: Metabolic Integration, Obesity and Diabetes. New topics for this running theme include the use of gliflozins in the treatment of type 2 diabetes (Chapter 11) and the effects of gut microbe metabolism on health (Chapter 23).

MEDIA & SUPPLEMENTS

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Proven effective at raising students' comprehension and problem-solving skills and recently updated with hundreds of additional questions, Sapling Learning's innovative online homework for biochemistry offers:

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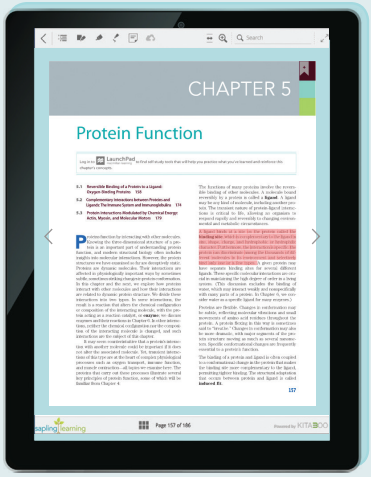
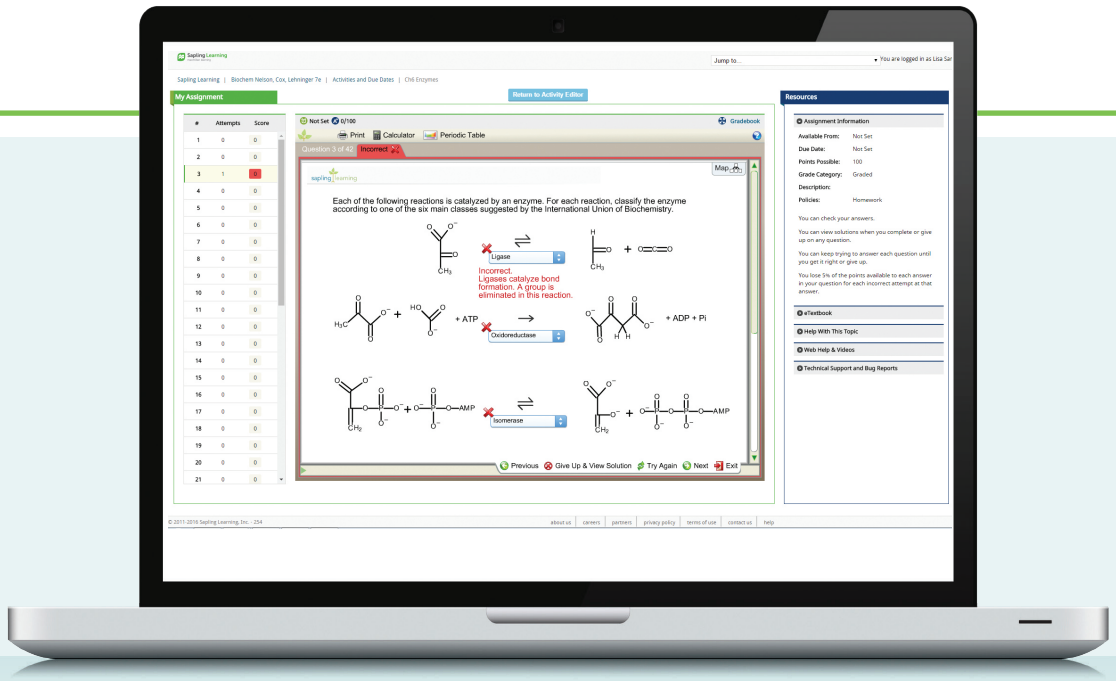
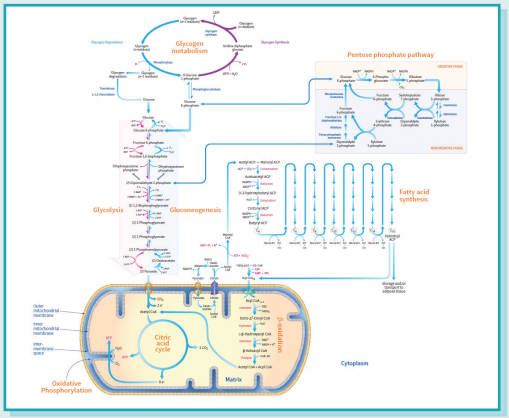


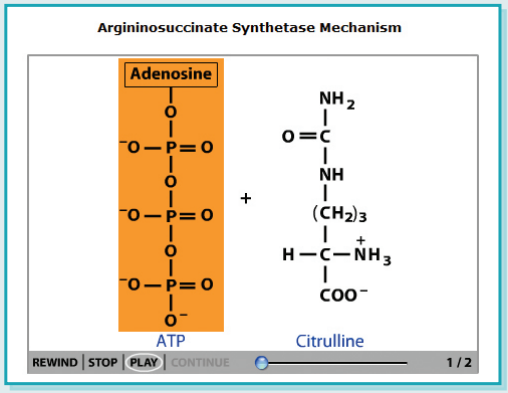
A fully interactive e-Book. The e-Book contains the full contents of the text and links to all student media integrated at point of use.

NEW Case Studies, Justin Hines, Lafayette College. Each case study introduces students to a biochemical mystery and allows them to determine what investigations will solve it. Accompanying assessments ensure that students have fully completed and understood the case study.





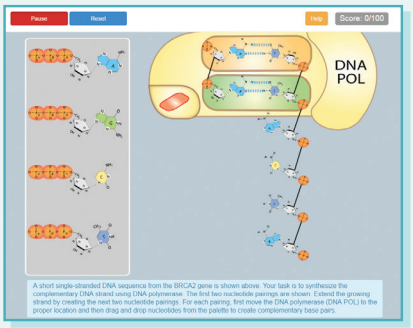
NEW Interactive Metabolic Map. With this interactive tool, students can navigate and zoom between overview and detailed views of the most commonly taught metabolic pathways—glycolysis, the citric acid cycle, and ß-oxidation. Tutorials with periodic concept check questions take students through the pathways step by step.



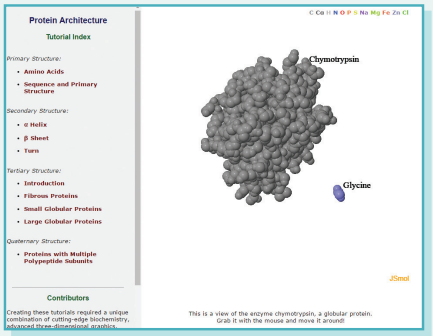
UPDATED Animated Mechanism Figures. Many mechanisms from the text are available as animations accompanied by assessment with targeted feedback.

More about SaplingPlus

MORE MEDIA & SUPPLEMENTS



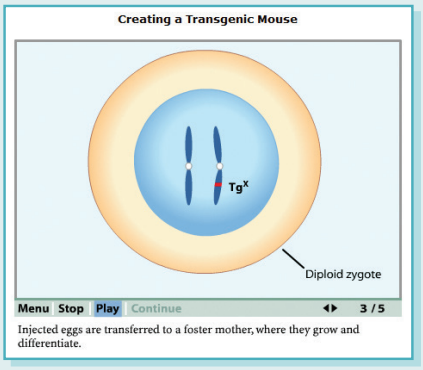
NEW Simulations. Based on figures in the text, these biochemical simulations let students interact with biochemical structures and processes.



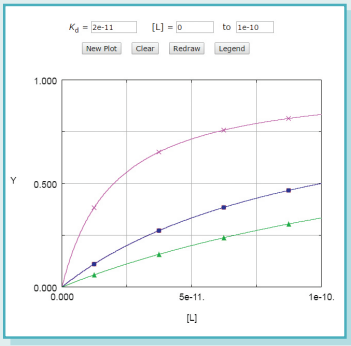
UPDATED Molecular Structure Tutorials — now in JSmol. These tutorials now include assessment with targeted feedback to ensure that students get a deeper understanding of molecular structures.

nature

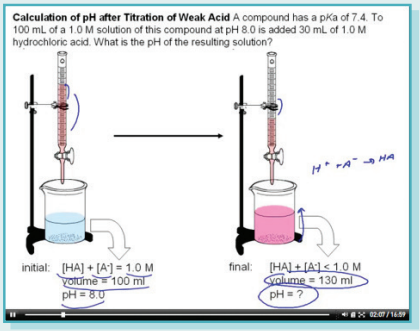
Six articles from *Nature* are available accompanied by tailored, automatically gradable assessment to engage students in reading primary literature and to encourage critical thinking. Also included are open-ended questions that are suitable for use in flipped classrooms and active learning discussions either in class or online.



Animated Biochemical Techniques. Nine animations illustrate the principles behind some of the most commonly used laboratory methods.



Living Graphs and Equations. These interactive tools, with manipulable variables, help students understand concepts and work through problems.



Problem-Solving Videos, Scott Ensign of Utah State University. With diagrams, graphs, and narration, these videos walk students through problems on topics that typically prove difficult, helping them understand the right approach to the solution.

TABLE OF CONTENTS

TABLE OF CONTENTS

CHAPTER 5

Protein Function

Self-study tools that will help you practice what you've learned and reinforce this chapter's concepts are available online. Go to www.macmillanlearning.com/LehningerBiochemistry7e.

Proteins function by interacting with other molecules. Knowing the three-dimensional structure of a protein is an important part of understanding protein function, and modern structural biology often includes insights into molecular interactions. However, the protein structures we have examined so far are deceptively static. Proteins are dynamic molecules. Their interactions are affected in physiologically important ways by sometimes subtle, sometimes striking changes in protein conformation. In this chapter and the next, we explore how proteins interact with other molecules and how their interactions are related to dynamic protein structure. We divide these interactions into two types. In some interactions, the result is a reaction that alters the chemical configuration or composition of the interacting molecule, with the protein acting as a reaction catalyst, or **enzyme**; we discuss enzymes and their reactions in Chapter 6. In other interactions, neither the chemical configuration nor the composition of the interacting molecule is changed, and such interactions are the subject of this chapter.

It may seem counterintuitive that a protein's interaction with another molecule could be important if it does not alter the associated molecule. Yet, transient interactions of this type are at the heart of complex physiological processes such as oxygen transport, immune function, and muscle contraction—all topics we examine here. The proteins that carry out these processes illustrate several key principles of protein function, some of which will be familiar from Chapter 4:

The functions of many proteins involve the reversible binding of other molecules. A molecule bound reversibly by a protein is called a **ligand**. A ligand may be any kind of molecule, including another protein. The transient nature of protein-ligand interactions is critical to life, allowing an organism to respond rapidly and reversibly to changing environmental and metabolic circumstances.

A ligand binds at a site on the protein called the **binding site**, which is complementary to the ligand in size, shape, charge, and hydrophobic or hydrophilic character. Furthermore, the interaction is specific: the protein can discriminate among the thousands of different molecules in its environment and selectively bind only one or a few types. A given protein may have separate binding sites for several different ligands. These specific molecular interactions are crucial in maintaining the high degree of order in a living system. (This discussion excludes the binding of water, which may interact weakly and nonspecifically with many parts of a protein. In Chapter 6, we consider water as a specific ligand for many enzymes.)

Proteins are flexible. Changes in conformation may be subtle, reflecting molecular vibrations and small movements of amino acid residues throughout the protein. A protein flexing in this way is sometimes said to "breathe." Changes in conformation may also be more dramatic, with major segments of the protein structure moving as much as several nanometers. Specific conformational changes are frequently essential to a protein's function.

The binding of a protein and ligand is often coupled to a conformational change in the protein that makes the binding site more complementary to the ligand, permitting tighter binding. The structural adaptation that occurs between protein and ligand is called **induced fit**.

In a multisubunit protein, a conformational change in one subunit often affects the conformation of other subunits.

Interactions between ligands and proteins may be regulated, usually through specific interactions with one or more additional ligands. These other ligands may cause conformational changes in the protein that affect the binding of the first ligand.

The enzymes represent a special case of protein function. They bind and chemically transform other molecules. The molecules acted upon by enzymes are called reaction **substrates** rather than ligands, and the ligand-binding site is called the **catalytic site** or **active site**. As you will see, the themes in our discussion of noncatalytic functions of proteins in this chapter—binding, specificity, and conformational change—are continued in Chapter 6, with the added element of proteins participating in chemical transformations.

5.1 Reversible Binding of a Protein to a Ligand: Oxygen-Binding Proteins

Myoglobin and **hemoglobin** may be the most-studied and best-understood proteins. They were the first proteins for which three-dimensional structures were determined, and these two molecules illustrate almost every aspect of that critical biochemical process: the reversible binding of a ligand to a protein. This classic model of protein function tells us a great deal about how proteins work.

Oxygen Can Bind to a Heme Prosthetic Group

Oxygen is poorly soluble in aqueous solutions (see Table 2-3) and cannot be carried to tissues in sufficient quantity if it is simply dissolved in blood serum. Also, diffusion of oxygen through tissues is ineffective over distances greater than a few millimeters. The evolution of larger, multicellular animals depended on the evolution of proteins that could transport and store oxygen. However, none of the amino acid side chains in proteins are suited for the reversible binding of oxygen molecules. This role is filled by certain transition metals, among them iron and copper, that have a strong tendency to bind oxygen. Multicellular organisms exploit the properties of metals, most commonly iron, for oxygen transport. However, free iron promotes the formation of highly reactive oxygen species such as hydroxyl radicals that can damage DNA and other macromolecules. Iron used in cells is therefore bound in forms that sequester it and/or make it less reactive. In multicellular organisms—especially those in which iron, in its oxygen-carrying capacity, must be transported over large distances—iron is often incorporated into a protein-bound prosthetic group called **heme** (or haem). (Recall from Chapter 3 that a prosthetic group is a compound permanently associated with a protein that contributes to the protein's function.)

Heme consists of a complex organic ring structure, **protoporphyrin**, to which is bound a single iron atom in its ferrous (Fe^{2+}) state **(Fig. 5-1)**. The iron atom has six coordination bonds, four to nitrogen atoms that are part of the flat **porphyrin ring** system and two perpendicular to the porphyrin. The coordinated nitrogen atoms (which have an electron-donating character) help prevent conversion of the heme iron to the ferric (Fe^{3+}) state. Iron in the Fe^{2+} state binds oxygen reversibly; in the Fe^{3+} state it does not bind oxygen. Heme is found in many oxygen-transporting proteins, as well as in some proteins, such as the cytochromes, that participate in oxidation-reduction (electron-transfer) reactions (Chapter 19).

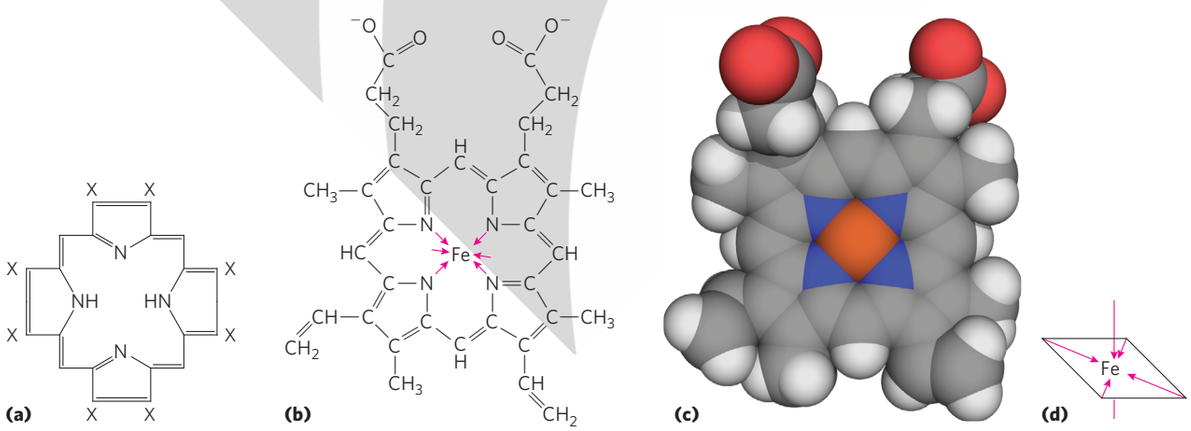


FIGURE 5-1 Heme. The heme group is present in myoglobin, hemoglobin, and many other proteins, designated **heme proteins**. Heme consists of a complex organic ring structure, protoporphyrin IX, with a bound iron atom in its ferrous (Fe^{2+}) state. **(a)** Porphyrins, of which protoporphyrin IX is just one example, consist of four pyrrole rings linked by methene bridges, with substitutions at one or more of the positions denoted X. **(b, c)** Two representations of heme. The iron atom of heme has six coordination bonds: four in the plane of, and bonded to, the flat porphyrin ring system, and **(d)** two perpendicular to it. [Source: (c) Heme extracted from PDB ID 1CCR, H. Ochi et al., *J. Mol. Biol.* 166:407, 1983.]

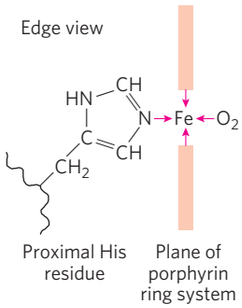


FIGURE 5-2 The heme group viewed from the side. This view shows the two coordination bonds to Fe^{2+} that are perpendicular to the porphyrin ring system. One is occupied by a His residue called the proximal His, His^{93} in myoglobin, also designated His F8 (the 8th residue in α helix F; see Fig. 5-3); the other is the binding site for oxygen. The remaining four coordination bonds are in the plane of, and bonded to, the flat porphyrin ring system.

Free heme molecules (heme not bound to protein) leave Fe^{2+} with two "open" coordination bonds. Simultaneous reaction of one O_2 molecule with two free heme molecules (or two free Fe^{2+}) can result in irreversible conversion of Fe^{2+} to Fe^{3+}. In heme-containing proteins, this reaction is prevented by sequestering each heme deep within the protein structure. Thus, access to the two open coordination bonds is restricted. In globins, one of these two coordination bonds is occupied by a side-chain nitrogen of a highly conserved His residue referred to as the **proximal His**. The other is the binding site for molecular oxygen (O_2) **(Fig. 5-2)**. When oxygen binds, the electronic properties of heme iron change; this accounts for the change in color from the dark purple of oxygen-depleted venous blood to the bright red of oxygen-rich arterial blood. Some small molecules, such as carbon monoxide (CO) and nitric oxide (NO), coordinate to heme iron with greater affinity than does O_2. When a molecule of CO is bound to heme, O_2 is excluded, which is why CO is highly toxic to aerobic organisms (a topic explored later, in Box 5-1). By surrounding and sequestering heme, oxygen-binding proteins regulate the access of small molecules to the heme iron.

Globins Are a Family of Oxygen-Binding Proteins

The **globins** are a widespread family of proteins, all having similar primary and tertiary structures. Globins are commonly found in eukaryotes of all classes and even in some bacteria. Most function in oxygen transport or storage, although some play a role in the sensing of oxygen, nitric oxide, or carbon monoxide. The simple nematode worm *Caenorhabditis elegans* has genes encoding 33 different globins. In humans and other mammals, there are at least four kinds of globins. The monomeric myoglobin facilitates oxygen diffusion in muscle tissue. Myoglobin is particularly abundant in the muscles of diving marine mammals such as seals and whales, where it also has an oxygen-storage function for prolonged excursions undersea. The tetrameric hemoglobin is responsible for oxygen transport in the bloodstream. The monomeric neuroglobin is expressed largely in neurons and helps to protect the brain from hypoxia (low oxygen) or ischemia (restricted blood supply). Cytoglobin, another monomeric globin, is found at high concentrations in the walls of blood vessels, where it functions to regulate levels of nitric oxide (discussed in Chapters 12 and 23).

Myoglobin Has a Single Binding Site for Oxygen

Myoglobin (M_r 16,700; abbreviated Mb) is a single polypeptide of 153 amino acid residues with one molecule of heme. As is typical for a globin polypeptide, myoglobin is made up of eight α-helical segments connected by bends **(Fig. 5-3)**. About 78% of the amino acid residues in the protein are found in these α helices.

Any detailed discussion of protein function inevitably involves protein structure. In the case of myoglobin, we first introduce some structural conventions peculiar to globins. As seen in Figure 5-3, the helical segments are named A through H. An individual amino acid residue is designated either by its position in the amino acid sequence or by its location in the sequence of a particular α-helical segment. For example, the His residue coordinated to the heme in myoglobin—the proximal His—is His^{93} (the 93rd residue from the amino-terminal end of the myoglobin polypeptide sequence) and is also called His F8 (the 8th residue in α helix F). The bends in the structure are designated AB, CD, EF, FG, and so forth, reflecting the α-helical segments they connect.

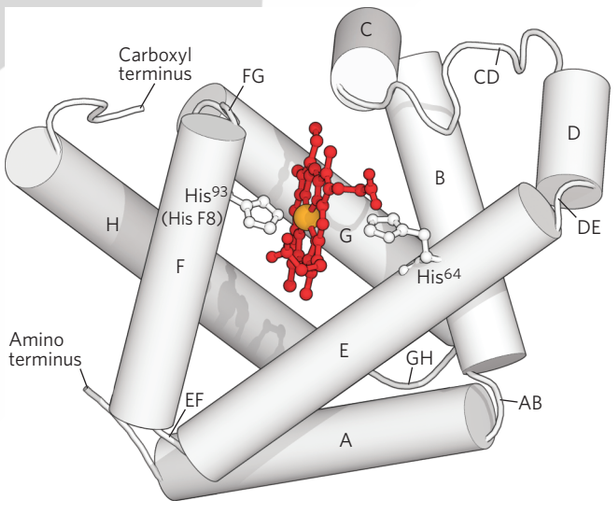


FIGURE 5-3 Myoglobin. The eight α-helical segments (shown here as cylinders) are labeled A through H. Nonhelical residues in the bends that connect them are labeled AB, CD, EF, and so forth, indicating the segments they interconnect. A few bends, including BC and DE, are abrupt and do not contain any residues; these are not normally labeled. The heme is bound in a pocket made up largely of the E and F helices, although amino acid residues from other segments of the protein also participate. [Source: PDB ID 1MBO, S. E. Phillips, *J. Mol. Biol.* 142:531, 1980.]

Protein-Ligand Interactions Can Be Described Quantitatively

The function of myoglobin depends on the protein's ability not only to bind oxygen but also to release it when and where it is needed. Function in biochemistry often revolves around a reversible protein-ligand interaction of this type. A quantitative description of this interaction is a central part of many biochemical investigations.

In general, the reversible binding of a protein (P) to a ligand (L) can be described by a simple **equilibrium expression**:

$$\mathrm{P} + \mathrm{L} \rightleftharpoons \mathrm{PL} \qquad (5\text{-}1)$$

The reaction is characterized by an equilibrium constant, K_a, such that

$$K_a = \frac{[\mathrm{PL}]}{[\mathrm{P}]\,[\mathrm{L}]} = \frac{k_a}{k_d} \qquad (5\text{-}2)$$

where k_a and k_d are rate constants (more on these below). The term $\boldsymbol{K_a}$ is an **association constant** (not to be confused with the K_a that denotes an acid dissociation constant; p. 62) that describes the equilibrium between the complex and the unbound components of the complex. The association constant provides a measure of the affinity of the ligand L for the protein. K_a has units of M^{-1}; a higher value of K_a corresponds to a higher affinity of the ligand for the protein.

The equilibrium term K_a is also equivalent to the ratio of the rates of the forward (association) and reverse (dissociation) reactions that form the PL complex. The association rate is described by the rate constant k_a, and dissociation by the rate constant k_d. As discussed further in the next chapter, rate constants are proportionality constants, describing the fraction of a pool of reactant that reacts in a given amount of time. When the reaction involves one molecule, such as the dissociation reaction $\mathrm{PL} \longrightarrow \mathrm{P} + \mathrm{L}$, the reaction is *first order* and the rate constant (k_d) has units of reciprocal time (s^{-1}). When the reaction involves two molecules, such as the association reaction $\mathrm{P} + \mathrm{L} \longrightarrow \mathrm{PL}$, it is called *second order*, and its rate constant (k_a) has units of $\mathrm{M}^{-1}\,\mathrm{s}^{-1}$.

›› Key Convention: Equilibrium constants are denoted with a capital K and rate constants with a lowercase k. **‹‹**

A rearrangement of the first part of Equation 5-2 shows that the ratio of bound to free protein is directly proportional to the concentration of free ligand:

$$K_a[\mathrm{L}] = \frac{[\mathrm{PL}]}{[\mathrm{P}]} \qquad (5\text{-}3)$$

When the concentration of the ligand is much greater than the concentration of ligand-binding sites, the binding of the ligand by the protein does not appreciably change the concentration of free (unbound) ligand—that is, [L] remains constant. This condition is broadly applicable to most ligands that bind to proteins in cells and simplifies our description of the binding equilibrium.

We can now consider the binding equilibrium from the standpoint of the fraction, Y, of ligand-binding sites on the protein that are occupied by ligand:

$$Y = \frac{\text{binding sites occupied}}{\text{total binding sites}} = \frac{[\mathrm{PL}]}{[\mathrm{PL}] + [\mathrm{P}]} \qquad (5\text{-}4)$$

Substituting $K_a[\mathrm{L}][\mathrm{P}]$ for [PL] (see Eqn 5-3) and rearranging terms gives

$$Y = \frac{K_a[\mathrm{L}]\,[\mathrm{P}]}{K_a[\mathrm{L}]\,[\mathrm{P}] + [\mathrm{P}]} = \frac{K_a[\mathrm{L}]}{K_a[\mathrm{L}] + 1} = \frac{[\mathrm{L}]}{[\mathrm{L}] + \dfrac{1}{K_a}} \qquad (5\text{-}5)$$

The value of K_a can be determined from a plot of Y versus the concentration of free ligand, [L] **(Fig. 5-4a)**. Any equation of the form $x = y/(y + z)$ describes a hyperbola, and Y is thus found to be a hyperbolic function of [L]. The fraction of ligand-binding sites occupied approaches saturation asymptotically as [L] increases. The [L] at which half of the available ligand-binding sites are occupied (that is, $Y = 0.5$) corresponds to $1/K_a$.

It is more common (and intuitively simpler), however, to consider the **dissociation constant, $\boldsymbol{K_d}$**, which is the reciprocal of K_a ($K_d = 1/K_a$) and has units of molar

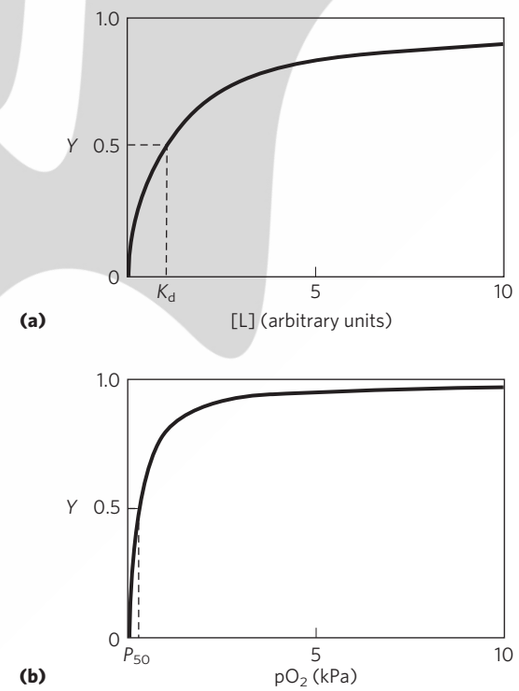
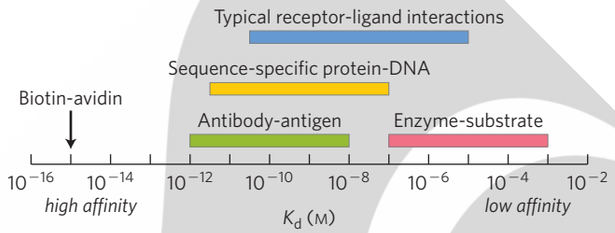


FIGURE 5-4 Graphical representations of ligand binding. The fraction of ligand-binding sites occupied, Y, is plotted against the concentration of free ligand. Both curves are rectangular hyperbolas. **(a)** A hypothetical binding curve for a ligand L. The [L] at which half of the available ligand-binding sites are occupied is equivalent to $1/K_a$, or K_d. The curve has a horizontal asymptote at $Y = 1$ and a vertical asymptote (not shown) at $[\mathrm{L}] = -1/K_a$. **(b)** A curve describing the binding of oxygen to myoglobin. The partial pressure of O_2 in the air above the solution is expressed in kilopascals (kPa). Oxygen binds tightly to myoglobin, with a P_{50} of only 0.26 kPa.

TABLE 5-1 Protein Dissociation Constants: Some Examples and Range

Protein	Ligand	K_d (M)[a]
Avidin (egg white)	Biotin	1×10^{-15}
Insulin receptor (human)	Insulin	1×10^{-10}
Anti-HIV immunoglobulin (human)[b]	gp41 (HIV-1 surface protein)	4×10^{-10}
Nickel-binding protein (*E. coli*)	Ni^{2+}	1×10^{-7}
Calmodulin (rat)[c]	Ca^{2+}	3×10^{-6}
		2×10^{-5}



Color bars indicate the range of dissociation constants typical of various classes of interactions in biological systems. A few interactions, such as that between the protein avidin and the enzyme cofactor biotin, fall outside the normal ranges. The avidin-biotin interaction is so tight it may be considered irreversible. Sequence-specific protein-DNA interactions reflect proteins that bind to a particular sequence of nucleotides in DNA, as opposed to general binding to any DNA site.

[a] A reported dissociation constant is valid only for the particular solution conditions under which it was measured. K_d values for a protein-ligand interaction can be altered, sometimes by several orders of magnitude, by changes in the solution's salt concentration, pH, or other variables.

[b] This immunoglobulin was isolated as part of an effort to develop a vaccine against HIV. Immunoglobulins (described later in the chapter) are highly variable, and the K_d reported here should not be considered characteristic of all immunoglobulins.

[c] Calmodulin has four binding sites for calcium. The values shown reflect the highest- and lowest-affinity binding sites observed in one set of measurements.

concentration (M). K_d is the equilibrium constant for the release of ligand. The relevant expressions change to

$$K_d = \frac{[P][L]}{[PL]} = \frac{k_d}{k_a} \qquad (5\text{-}6)$$

$$[PL] = \frac{[P][L]}{K_d} \qquad (5\text{-}7)$$

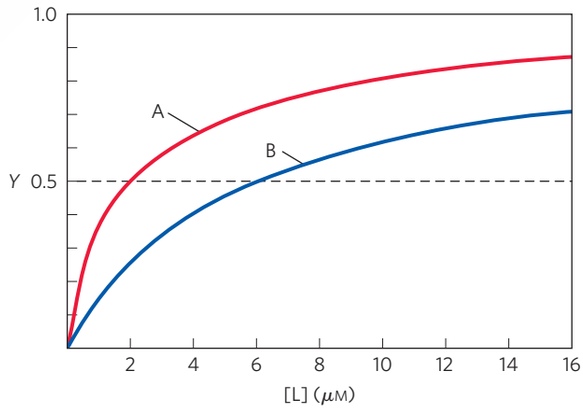
$$Y = \frac{[L]}{[L] + K_d} \qquad (5\text{-}8)$$

When [L] equals K_d, half of the ligand-binding sites are occupied. As [L] falls below K_d, progressively less of the protein has ligand bound to it. For 90% of the available ligand-binding sites to be occupied, [L] must be nine times greater than K_d.

In practice, K_d is used much more often than K_a to express the affinity of a protein for a ligand. Note that a lower value of K_d corresponds to a higher affinity of ligand for the protein. The mathematics can be reduced to simple statements: K_d is equivalent to the molar concentration of ligand at which half of the available ligand-binding sites are occupied. At this point, the protein is said to have reached half-saturation with respect to ligand binding. The more tightly a protein binds a ligand, the lower the concentration of ligand required for half the binding sites to be occupied, and thus the lower the value of K_d. Some representative dissociation constants are given in Table 5-1; the scale shows typical ranges for dissociation constants found in biological systems.

WORKED EXAMPLE 5-1 Receptor-Ligand Dissociation Constants

Two proteins, A and B, bind to the same ligand, L, with the binding curves shown below.



What is the dissociation constant, K_d, for each protein? Which protein (A or B) has a greater affinity for ligand L?

Solution: We can determine the dissociation constants by inspecting the graph. Since Y represents the fraction of binding sites occupied by ligand, the concentration of ligand at which half the binding sites are occupied—that is, the point where the binding curve crosses the line where $Y = 0.5$—is the dissociation constant. For A, $K_d = 2\ \mu M$; for B, $K_d = 6\ \mu M$. Because A is half-saturated at a lower [L], it has a higher affinity for the ligand.

The binding of oxygen to myoglobin follows the patterns discussed above. However, because oxygen is a gas, we must make some minor adjustments to the equations so that laboratory experiments can be carried out more conveniently. We first substitute the concentration of dissolved oxygen for [L] in Equation 5-8 to give

$$Y = \frac{[O_2]}{[O_2] + K_d} \qquad (5\text{-}9)$$

As for any ligand, K_d equals the $[O_2]$ at which half of the available ligand-binding sites are occupied, or $[O_2]_{0.5}$. Equation 5-9 thus becomes

$$Y = \frac{[O_2]}{[O_2] + [O_2]_{0.5}} \qquad (5\text{-}10)$$

In experiments using oxygen as a ligand, it is the partial pressure of oxygen (pO_2) in the gas phase above the solution that is varied, because this is easier to measure than the concentration of oxygen dissolved in the solution. The concentration of a volatile substance in solution is always proportional to the local partial pressure of the gas. So, if we define the partial pressure of oxygen at $[O_2]_{0.5}$ as P_{50}, substitution in Equation 5-10 gives

$$Y = \frac{pO_2}{pO_2 + P_{50}} \qquad (5\text{-}11)$$

A binding curve for myoglobin that relates Y to pO_2 is shown in Figure 5-4b.

Protein Structure Affects How Ligands Bind

The binding of a ligand to a protein is rarely as simple as the above equations would suggest. The interaction is greatly affected by protein structure and is often accompanied by conformational changes. For example, the specificity with which heme binds its various ligands is altered when the heme is a component of myoglobin. For free heme molecules, carbon monoxide binds more than 20,000 times better than does O_2 (that is, the K_d or P_{50} for CO binding to free heme is more than 20,000 times lower than that for O_2), but it binds only about 40 times better than O_2 when the heme is bound in myoglobin. For free heme, the tighter binding by CO reflects differences in the way the orbital structures of CO and O_2 interact with Fe^{2+}. Those same orbital structures lead to different binding geometries for CO and O_2 when they are bound

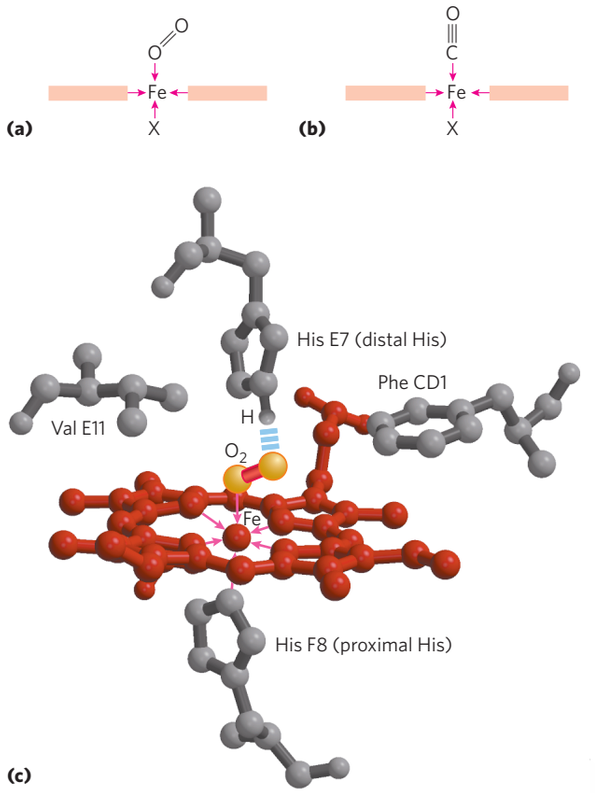


FIGURE 5-5 Steric effects caused by ligand binding to the heme of myoglobin. (a) Oxygen binds to heme with the O_2 axis at an angle, a binding conformation readily accommodated by myoglobin. **(b)** Carbon monoxide binds to free heme with the CO axis perpendicular to the plane of the porphyrin ring. **(c)** Another view of the heme of myoglobin, showing the arrangement of key amino acid residues around the heme. The bound O_2 is hydrogen-bonded to the distal His, His E7 (His^{64}), facilitating the binding of O_2 compared with its binding to free heme. [Source: (c) Derived from PDB ID 1MBO, S. E. Phillips, *J. Mol. Biol.* 142:531, 1980.]

to heme **(Fig. 5-5a, b)**. The change in relative affinity of CO and O_2 for heme when the heme is bound to a globin is mediated by the globin structure.

When heme is bound to myoglobin, its affinity for O_2 is selectively increased by the presence of the **distal His** (His^{64}, or His E7 in myoglobin). The Fe-O_2 complex is much more polar than the Fe-CO complex. There is a partial negative charge distributed across the oxygen atoms in the bound O_2 due to partial oxidation of the interacting iron atom. A hydrogen bond between the imidazole side chain of His E7 and the bound O_2 stabilizes this polar complex electrostatically (Fig. 5-5c). The affinity of myoglobin for O_2 is thus selectively increased by a factor of about 500; there is no such effect for Fe-CO binding in myoglobin. Consequently, the 20,000-fold stronger binding affinity of free heme for CO compared with O_2 declines to approximately 40-fold for heme embedded in myoglobin. This favorable electrostatic effect on O_2 binding is even more dramatic in some invertebrate hemoglobins, where two groups in the binding pocket can form strong hydrogen

bonds with O_2, causing the heme group to bind O_2 with greater affinity than CO. This selective enhancement of O_2 affinity in globins is physiologically important and helps prevent poisoning by the CO generated from heme catabolism (see Chapter 22) or other sources.

The binding of O_2 to the heme in myoglobin also depends on molecular motions, or "breathing," in the protein structure. The heme molecule is deeply buried in the folded polypeptide, with limited direct paths for oxygen to move from the surrounding solution to the ligand-binding site. If the protein were rigid, O_2 could not readily enter or leave the heme pocket. However, rapid molecular flexing of the amino acid side chains produces transient cavities in the protein structure, and O_2 makes its way in and out by moving through these cavities. Computer simulations of rapid structural fluctuations in myoglobin suggest there are many such pathways. The distal His acts as a gate to control access to one major pocket near the heme iron. Rotation of that His residue to open and close the pocket occurs on a nanosecond (10^{-9} s) time scale. Even subtle conformational changes can be critical for protein activity.

The distal His functions somewhat differently in some other globins. In neuroglobin, cytoglobin, and some globins found in plants and invertebrates, the distal His is directly coordinated with the heme iron at the location where ligands must bind. In these globins, the O_2 or other ligand must displace the distal His in the process of binding, with a hydrogen bond again forming between the distal His and O_2 after the binding occurs.

Hemoglobin Transports Oxygen in Blood

Nearly all the oxygen carried by whole blood in animals is bound and transported by hemoglobin in erythrocytes (red blood cells). Normal human erythrocytes are small (6 to 9 μm in diameter), biconcave disks. They are formed from precursor stem cells called **hemocytoblasts**. In the maturation process, the stem cell produces daughter cells that form large amounts of hemoglobin and then lose their organelles—nucleus, mitochondria, and endoplasmic reticulum. Erythrocytes are thus incomplete, vestigial cells, unable to reproduce and, in humans, destined to survive for only about 120 days. Their main function is to carry hemoglobin, which is dissolved in the cytosol at a very high concentration (~34% by weight).

In arterial blood passing from the lungs through the heart to the peripheral tissues, hemoglobin is about 96% saturated with oxygen. In the venous blood returning to the heart, hemoglobin is only about 64% saturated. Thus, each 100 mL of blood passing through a tissue releases about one-third of the oxygen it carries, or 6.5 mL of O_2 gas at atmospheric pressure and body temperature.

Myoglobin, with its hyperbolic binding curve for oxygen (Fig. 5-4b), is relatively insensitive to small changes in the concentration of dissolved oxygen and so functions well as an oxygen-storage protein. Hemoglobin, with its multiple subunits and O_2-binding sites, is better suited to oxygen transport. As we shall see, interactions between the subunits of a multimeric protein can permit a highly sensitive response to small changes in ligand concentration. Interactions among the subunits in hemoglobin cause conformational changes that alter the affinity of the protein for oxygen. The modulation of oxygen binding allows the O_2-transport protein to respond to changes in oxygen demand by tissues.

Hemoglobin Subunits Are Structurally Similar to Myoglobin

Hemoglobin (M_r 64,500; abbreviated Hb) is roughly spherical, with a diameter of nearly 5.5 nm. It is a tetrameric protein containing four heme prosthetic groups, one associated with each polypeptide chain. Adult hemoglobin contains two types of globin, two α chains (141 residues each) and two β chains (146 residues each). Although fewer than half of the amino acid residues are identical in the polypeptide sequences of the α and β subunits, the three-dimensional structures of the two types of subunits are very similar. Furthermore, their structures are very similar to that of myoglobin **(Fig. 5-6)**, even though the amino acid sequences of the three polypeptides are identical at only 27 positions **(Fig. 5-7)**. All three polypeptides are members of the globin family of proteins. The helix-naming convention described for myoglobin is also applied to the hemoglobin polypeptides, except that the α subunit lacks the short D helix. The heme-binding pocket is made up largely of the E and F helices in each of the subunits.

The quaternary structure of hemoglobin features strong interactions between unlike subunits. The $\alpha_1\beta_1$ interface (and its $\alpha_2\beta_2$ counterpart) involves more than 30 residues, and its interaction is sufficiently strong that although mild treatment of hemoglobin with urea tends to disassemble the tetramer into $\alpha\beta$ dimers, these dimers remain intact. The $\alpha_1\beta_2$ (and $\alpha_2\beta_1$) interface involves 19 residues **(Fig. 5-8)**. The hydrophobic effect

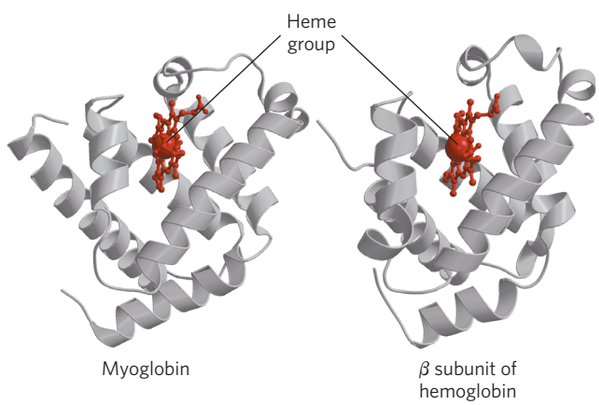


FIGURE 5-6 Comparison of the structures of myoglobin and the β subunit of hemoglobin. [Sources: (left) PDB ID 1MBO, S. E. Phillips, *J. Mol. Biol.* 142:531, 1980. (right) Derived from PDB ID 1HGA, R. Liddington et al., *J. Mol. Biol.* 228:551, 1992.]

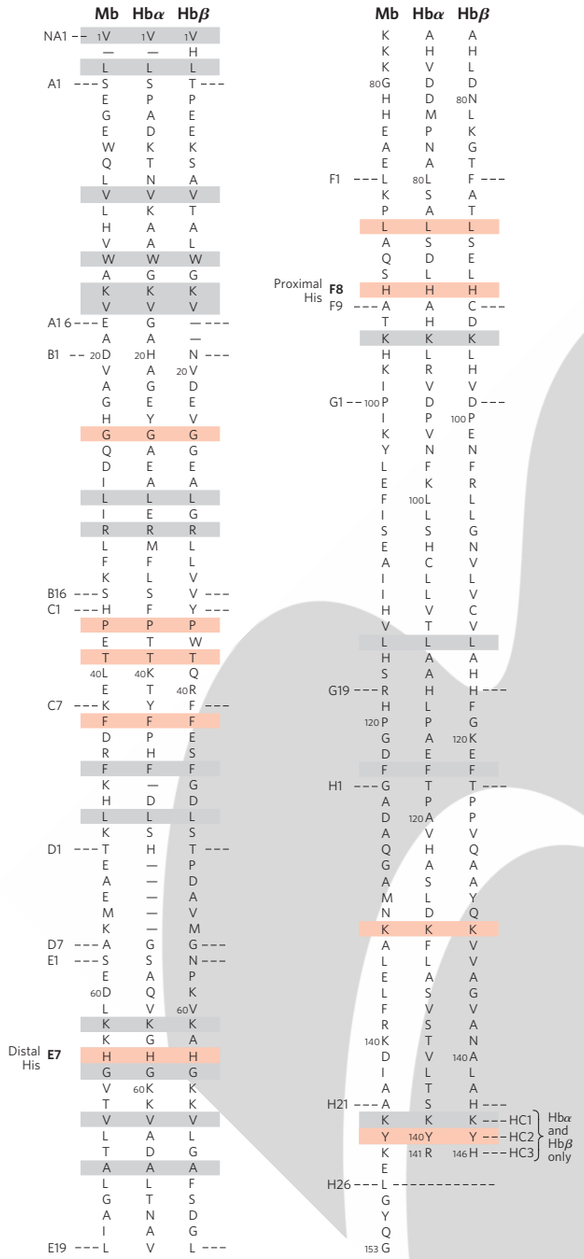


FIGURE 5-7 The amino acid sequences of whale myoglobin and the α and β chains of human hemoglobin. Dashed lines mark helix boundaries. To align the sequences optimally, short gaps must be introduced into both Hb sequences where a few amino acids are present in the other, compared sequences. With the exception of the missing D helix in the Hb α chain (Hbα), this alignment permits the use of the helix lettering convention that emphasizes the common positioning of amino acid residues that are identical in all three structures (shaded). Residues shaded in light red are conserved in all known globins. Note that the common helix-letter-and-number designation for amino acids does not necessarily correspond to a common position in the linear sequence of amino acids in the polypeptides. For example, the distal His residue is His E7 in all three structures, but corresponds to His^{64}, His^{58}, and His^{63} in the linear sequences of Mb, Hbα, and Hbβ, respectively. Nonhelical residues at the amino and carboxyl termini, beyond the first (A) and last (H) α-helical segments, are labeled NA and HC, respectively.

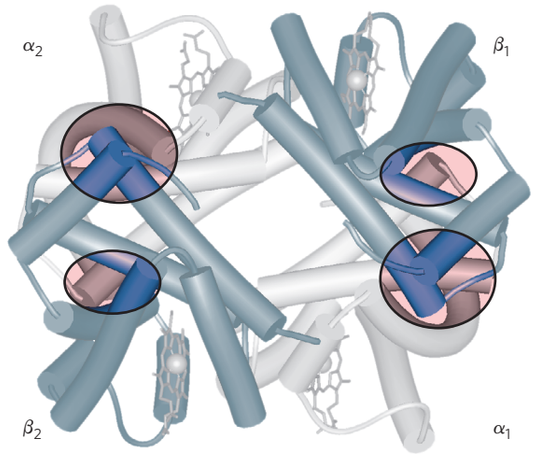


FIGURE 5-8 Dominant interactions between hemoglobin subunits. In this representation, α subunits are light and β subunits are dark. The strongest subunit interactions (highlighted) occur between unlike subunits. When oxygen binds, the $\alpha_1\beta_1$ contact changes little, but there is a large change at the $\alpha_1\beta_2$ contact, with several ion pairs broken. [Source: PDB ID 1HGA, R. Liddington et al., *J. Mol. Biol.* 228:551, 1992.]

plays the major role in stabilizing these interfaces, but there are also many hydrogen bonds and a few ion pairs (or salt bridges), whose importance is discussed below.

Hemoglobin Undergoes a Structural Change on Binding Oxygen

X-ray analysis has revealed two major conformations of hemoglobin: the **R state** and the **T state**. Although oxygen binds to hemoglobin in either state, it has a significantly higher affinity for hemoglobin in the R state. Oxygen binding stabilizes the R state. When oxygen is absent experimentally, the T state is more stable and is thus the predominant conformation of **deoxyhemoglobin**. T and R originally denoted "tense" and "relaxed," respectively, because the T state is stabilized by a greater number of ion pairs, many of which lie at the $\alpha_1\beta_2$ (and $\alpha_2\beta_1$) interface **(Fig. 5-9)**. The binding of O_2 to a hemoglobin subunit in the T state triggers a change in conformation to the R state. When the entire protein undergoes this transition, the structures of the individual subunits change little, but the $\alpha\beta$ subunit pairs slide past each other and rotate, narrowing the pocket between the β subunits **(Fig. 5-10)**. In this process, some of the ion pairs that stabilize the T state are broken and some new ones are formed.

Max Perutz proposed that the T $\rightarrow$ R transition is triggered by changes in the positions of key amino acid side chains surrounding the heme. In the T state, the porphyrin is slightly puckered, causing the heme iron to protrude somewhat on the proximal His (His F8) side. The binding of O_2 causes the heme to assume a more planar conformation, shifting the position of the proximal His and the attached F helix **(Fig. 5-11)**. These changes lead to adjustments in the ion pairs at the $\alpha_1\beta_2$ interface.

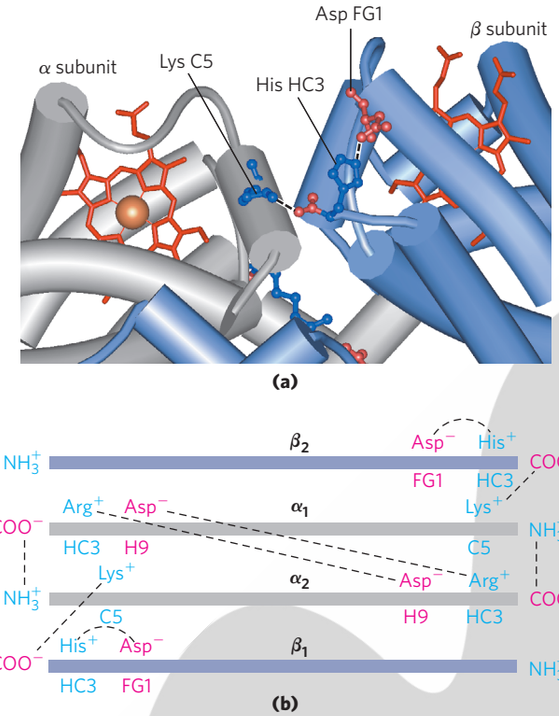


FIGURE 5-9 Some ion pairs that stabilize the T state of deoxyhemoglobin. **(a)** Close-up view of a portion of a deoxyhemoglobin molecule in the T state. Interactions between the ion pairs His HC3 and Asp FG1 of the β subunit (blue) and between Lys C5 of the α subunit (gray) and His HC3 (its α-carboxyl group) of the β subunit are shown with dashed lines. (Recall that HC3 is the carboxyl-terminal residue of the β subunit.) **(b)** Interactions between these ion pairs, and between others not shown in (a), are schematized in this representation of the extended polypeptide chains of hemoglobin. [Source: (a) PDB ID 1HGA, R. Liddington et al., *J. Mol. Biol.* 228:551, 1992.]

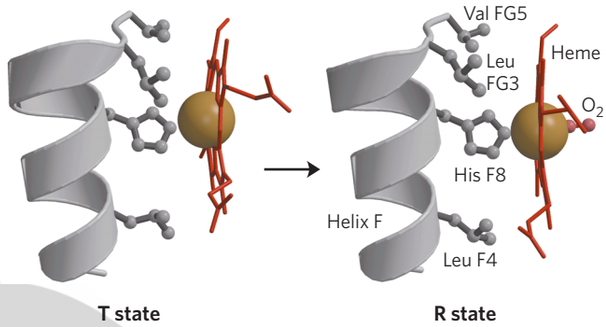


FIGURE 5-11 Changes in conformation near heme on O_2 binding to deoxyhemoglobin. The shift in the position of helix F when heme binds O_2 is thought to be one of the adjustments that triggers the T → R transition. [Sources: T state: derived from PDB ID 1HGA, R. Liddington et al., *J. Mol. Biol.* 228:551, 1992. R state: derived from PDB ID 1BBB, M. M. Silva et al., *J. Biol. Chem.* 267:17,248, 1992; R state modified to represent O_2 instead of CO.]

Hemoglobin Binds Oxygen Cooperatively

Hemoglobin must bind oxygen efficiently in the lungs, where the pO_2 is about 13.3 kPa, and release oxygen in the tissues, where the pO_2 is about 4 kPa. Myoglobin, or any protein that binds oxygen with a hyperbolic binding curve, would be ill-suited to this function, for the reason illustrated in **Figure 5-12**. A protein that bound O_2 with high affinity would bind it efficiently in the lungs but would not release much of it in the tissues. If the protein bound oxygen with a sufficiently low affinity to release it in the tissues, it would not pick up much oxygen in the lungs.

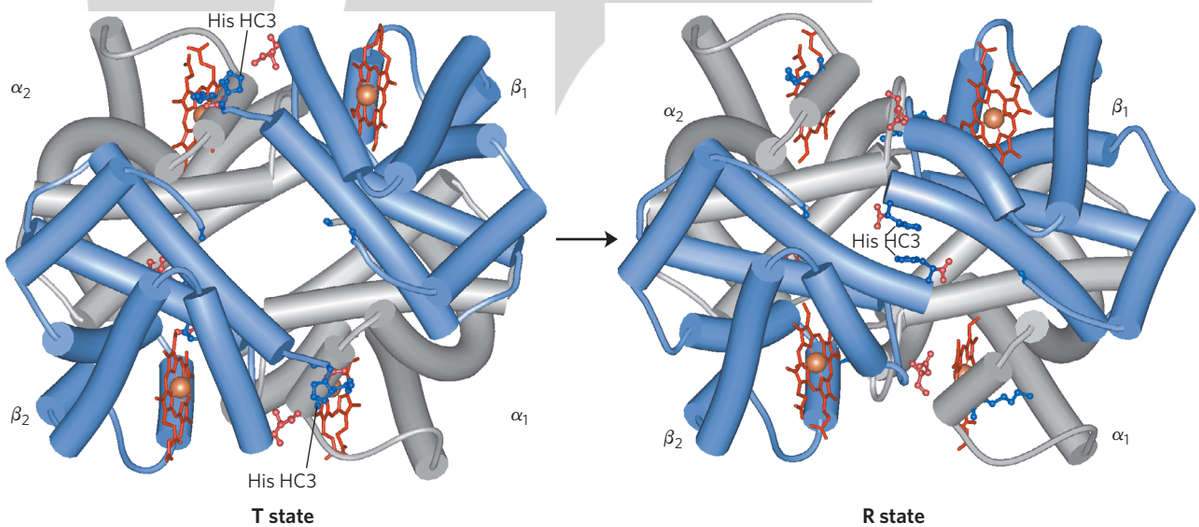


FIGURE 5-10 The T → R transition. In these depictions of deoxyhemoglobin, as in Figure 5-9, the β subunits are blue and the α subunits are gray. Positively charged side chains and chain termini involved in ion pairs are shown in blue, their negatively charged partners in red. The Lys C5 of each α subunit and Asp FG1 of each β subunit are visible but not labeled (compare Fig. 5-9a). Note that the molecule is oriented slightly differently than in Figure 5-9. The transition from the T state to the R state shifts the subunit pairs substantially, affecting certain ion pairs. Most noticeably, the His HC3 residues at the carboxyl termini of the β subunits, which are involved in ion pairs in the T state, rotate in the R state toward the center of the molecule, where they are no longer in ion pairs. Another dramatic result of the T → R transition is a narrowing of the pocket between the β subunits. [Sources: T state: PDB ID 1HGA, R. Liddington et al., *J. Mol. Biol.* 228:551, 1992. R state: PDB ID 1BBB, M. M. Silva et al., *J. Biol. Chem.* 267:17,248, 1992.]

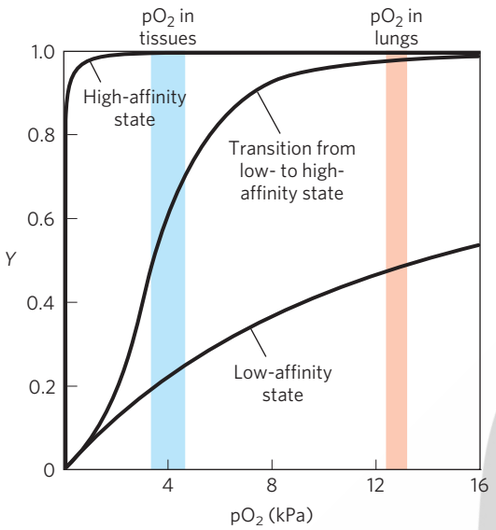


FIGURE 5-12 A sigmoid (cooperative) binding curve. A sigmoid binding curve can be viewed as a hybrid curve reflecting a transition from a low-affinity to a high-affinity state. Because of its cooperative binding, as manifested by a sigmoid binding curve, hemoglobin is more sensitive to the small differences in O_2 concentration between the tissues and the lungs, allowing it to bind oxygen in the lungs (where pO_2 is high) and release it in the tissues (where pO_2 is low).

Hemoglobin solves the problem by undergoing a transition from a low-affinity state (the T state) to a high-affinity state (the R state) as more O_2 molecules are bound. As a result, hemoglobin has a hybrid S-shaped, or sigmoid, binding curve for oxygen (Fig. 5-12). A single-subunit protein with a single ligand-binding site cannot produce a sigmoid binding curve—even if binding elicits a conformational change—because each molecule of ligand binds independently and cannot affect ligand binding to another molecule. In contrast, O_2 binding to individual subunits of hemoglobin can alter the affinity for O_2 in adjacent subunits. The first molecule of O_2 that interacts with deoxyhemoglobin binds weakly, because it binds to a subunit in the T state. Its binding, however, leads to conformational changes that are communicated to adjacent subunits, making it easier for additional molecules of O_2 to bind. In effect, the T $\rightarrow$ R transition occurs more readily in the second subunit once O_2 is bound to the first subunit. The last (fourth) O_2 molecule binds to a heme in a subunit that is already in the R state, and hence it binds with much higher affinity than the first molecule.

An **allosteric protein** is one in which the binding of a ligand to one site affects the binding properties of another site on the same protein. The term "allosteric" derives from the Greek *allos*, "other," and *stereos*, "solid" or "shape." Allosteric proteins are those having "other shapes," or conformations, induced by the binding of ligands referred to as **modulators**. The conformational changes induced by the modulator(s) interconvert more-active and less-active forms of the protein. The modulators for allosteric proteins may be either inhibitors or activators. When the normal ligand and modulator are identical, the interaction is termed **homotropic**. When the modulator is a molecule other than the normal ligand, the interaction is **heterotropic**. Some proteins have two or more modulators and therefore can have both homotropic and heterotropic interactions.

Cooperative binding of a ligand to a multimeric protein, such as we observe with the binding of O_2 to hemoglobin, is a form of allosteric binding. The binding of one ligand affects the affinities of any remaining unfilled binding sites, and O_2 can be considered as both a ligand and an activating homotropic modulator. There is only one binding site for O_2 on each subunit, so the allosteric effects giving rise to cooperativity are mediated by conformational changes transmitted from one subunit to another by subunit-subunit interactions. A sigmoid binding curve is diagnostic of cooperative binding. It permits a much more sensitive response to ligand concentration and is important to the function of many multisubunit proteins. The principle of allostery extends readily to regulatory enzymes, as we shall see in Chapter 6.

Cooperative conformational changes depend on variations in the structural stability of different parts of a protein, as described in Chapter 4. The binding sites of an allosteric protein typically consist of stable segments in proximity to relatively unstable segments, with the latter capable of frequent changes in conformation or intrinsic disorder **(Fig. 5-13)**. When a ligand binds, the moving parts of the protein's binding site may be stabilized in a particular conformation, affecting the conformation of adjacent polypeptide subunits. If the entire binding site were highly stable, then few structural changes could occur in this site or be propagated to other parts of the protein when a ligand bound.

As is the case with myoglobin, ligands other than oxygen can bind to hemoglobin. An important example is carbon monoxide, which binds to hemoglobin about 250 times better than does oxygen (the critical hydrogen bond between O_2 and the distal His is not quite as strong in human hemoglobin as it is in most mammalian myoglobins, so the binding of O_2 relative to CO is not augmented quite as much). Human exposure to CO can have tragic consequences (Box 5-1).

Cooperative Ligand Binding Can Be Described Quantitatively

Cooperative binding of oxygen by hemoglobin was first analyzed by Archibald Hill in 1910. From this work came a general approach to the study of cooperative ligand binding to multisubunit proteins.

For a protein with n binding sites, the equilibrium of Equation 5-1 becomes

$$\mathrm{P} + n\mathrm{L} \rightleftharpoons \mathrm{PL}_n \qquad (5\text{-}12)$$

and the expression for the association constant becomes

$$K_\mathrm{a} = \frac{[\mathrm{PL}_n]}{[\mathrm{P}][\mathrm{L}]^n} \qquad (5\text{-}13)$$

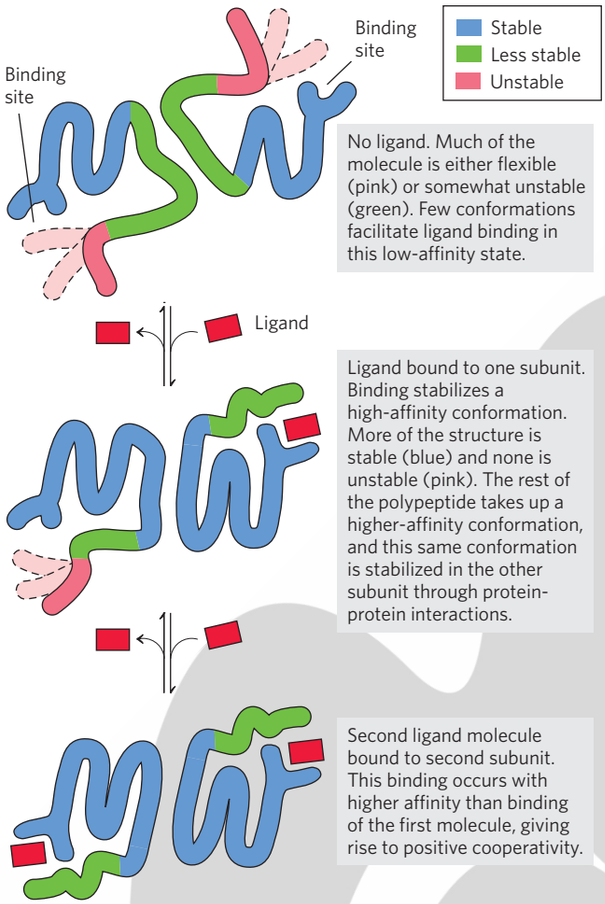


FIGURE 5-13 Structural changes in a multisubunit protein undergoing cooperative binding to ligand. Structural stability is not uniform throughout a protein molecule. Shown here is a hypothetical dimeric protein, with regions of high (blue), medium (green), and low (pink) stability. The ligand-binding sites are composed of both high- and low-stability segments, so affinity for ligand is relatively low. The conformational changes that occur as ligand binds convert the protein from a low- to a high-affinity state, a form of induced fit.

The expression for Y (see Eqn 5-8) is

$$Y = \frac{[\mathrm{L}]^n}{[\mathrm{L}]^n + K_\mathrm{d}} \qquad (5\text{-}14)$$

Rearranging, then taking the log of both sides, yields

$$\frac{Y}{1-Y} = \frac{[\mathrm{L}]^n}{K_\mathrm{d}} \qquad (5\text{-}15)$$

$$\log\left(\frac{Y}{1-Y}\right) = n \log [\mathrm{L}] - \log K_\mathrm{d} \qquad (5\text{-}16)$$

where $K_\mathrm{d} = [\mathrm{L}]_{0.5}^n$

Equation 5-16 is the **Hill equation**, and a plot of log $[Y/(1 - Y)]$ versus log [L] is called a **Hill plot**. Based on the equation, the Hill plot should have a slope of n. However, the experimentally determined slope actually reflects not the number of binding sites but the degree of interaction between them. The slope of a Hill plot is therefore denoted by n_H, the **Hill coefficient**, which is a measure of the degree of cooperativity. If n_H equals 1, ligand binding is not cooperative, a situation that can arise even in a multisubunit protein if the subunits do not communicate. An n_H of greater than 1 indicates positive cooperativity in ligand binding. This is the situation observed in hemoglobin, in which the binding of one molecule of ligand facilitates the binding of others. The theoretical upper limit for n_H is reached when $n_\mathrm{H} = n$. In this case the binding would be completely cooperative: all binding sites on the protein would bind ligand simultaneously, and no protein molecules partially saturated with ligand would be present under any conditions. This limit is never reached in practice, and the measured value of n_H is always less than the actual number of ligand-binding sites in the protein.

An n_H of less than 1 indicates negative cooperativity, in which the binding of one molecule of ligand *impedes* the binding of others. Well-documented cases of negative cooperativity are rare.

To adapt the Hill equation to the binding of oxygen to hemoglobin we must again substitute pO_2 for [L] and P_{50}^n for K_d:

$$\log\left(\frac{Y}{1-Y}\right) = n \log pO_2 - n \log P_{50} \qquad (5\text{-}17)$$

Hill plots for myoglobin and hemoglobin are given in **Figure 5-14**.

Two Models Suggest Mechanisms for Cooperative Binding

Biochemists now know a great deal about the T and R states of hemoglobin, but much remains to be learned about how the T → R transition occurs. Two models for

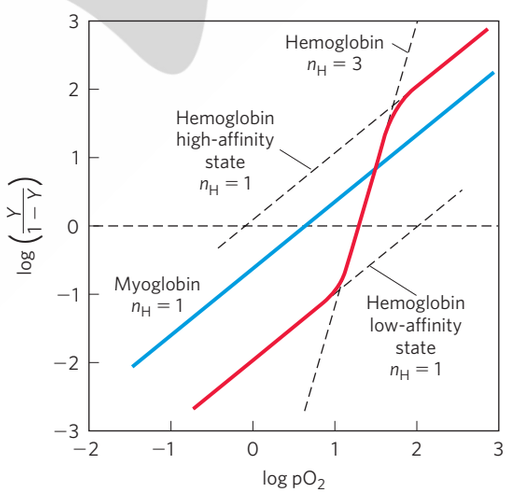


FIGURE 5-14 Hill plots for oxygen binding to myoglobin and hemoglobin. When $n_\mathrm{H} = 1$, there is no evident cooperativity. The maximum degree of cooperativity observed for hemoglobin corresponds approximately to $n_\mathrm{H} = 3$. Note that while this indicates a high level of cooperativity, n_H is less than n, the number of O_2-binding sites in hemoglobin. This is normal for a protein that exhibits allosteric binding behavior.

BOX 5-1 MEDICINE Carbon Monoxide: A Stealthy Killer

Lake Powell, Arizona, August 2000. A family was vacationing on a rented houseboat. They turned on the electrical generator to power an air conditioner and a television. About 15 minutes later, two brothers, aged 8 and 11, jumped off the swim deck at the stern. Situated immediately below the deck was the exhaust port for the generator. Within two minutes, both boys were overcome by the carbon monoxide in the exhaust, which had become concentrated in the space under the deck. Both drowned. These deaths, along with a series of deaths in the 1990s that were linked to houseboats of similar design, eventually led to the recall and redesign of the generator exhaust assembly.

Carbon monoxide (CO), a colorless, odorless gas, is responsible for more than half of yearly deaths due to poisoning worldwide. CO has an approximately 250-fold greater affinity for hemoglobin than does oxygen. Consequently, relatively low levels of CO can have substantial and tragic effects. When CO combines with hemoglobin, the complex is referred to as carboxyhemoglobin, or COHb.

Some CO is produced by natural processes, but locally high levels generally result only from human activities. Engine and furnace exhausts are important sources, as CO is a byproduct of the incomplete combustion of fossil fuels. In the United States alone, nearly 4,000 people succumb to CO poisoning each year, both accidentally and intentionally. Many of the accidental deaths involve undetected CO buildup in enclosed spaces, such as when a household furnace malfunctions or leaks, venting CO into a home. However, CO poisoning can also occur in open spaces, as unsuspecting people at work or play inhale the exhaust from generators, outboard motors, tractor engines, recreational vehicles, or lawn mowers.

Carbon monoxide levels in the atmosphere are rarely dangerous, ranging from less than 0.05 part per million (ppm) in remote and uninhabited areas to 3 to 4 ppm in some cities of the northern hemisphere. In the United States, the government-mandated (Occupational Safety and Health Administration, OSHA) limit for CO at worksites is 50 ppm for people working an eight-hour shift. The tight binding of CO to hemoglobin means that COHb can accumulate over time as people are exposed to a constant low-level source of CO.

In an average, healthy individual, 1% or less of the total hemoglobin is complexed as COHb. Since CO is a product of tobacco smoke, many smokers have COHb levels in the range of 3% to 8% of total hemoglobin, and the levels can rise to 15% for chain-smokers. COHb levels equilibrate at 50% in people who breathe air containing 570 ppm of CO for several hours. Reliable methods have been developed that relate CO content in the atmosphere to COHb levels in the blood (Fig. 1). In tests of houseboats with a generator exhaust like the one responsible for the Lake Powell deaths, CO levels reached 6,000 to 30,000 ppm under the swim deck, and atmospheric O_2 levels under the deck declined from 21% to 12%. Even above the swim deck, CO levels of up to 7,200 ppm were detected, high enough to cause death within a few minutes.

How is a human affected by COHb? At levels of less than 10% of total hemoglobin, symptoms are rarely observed. At 15%, the individual experiences mild headaches. At 20% to 30%, the headache is severe and is generally accompanied by nausea, dizziness, confusion,

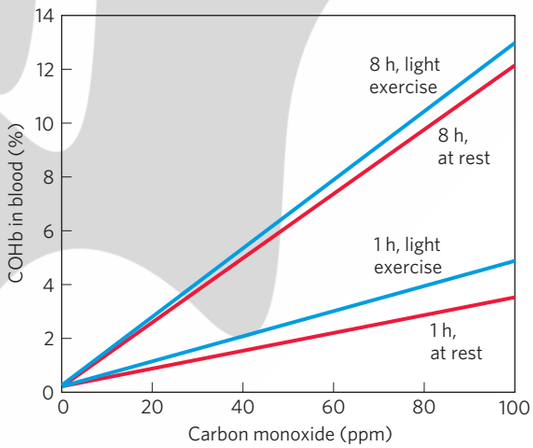


FIGURE 1 Relationship between levels of COHb in blood and concentration of CO in the surrounding air. Four different conditions of exposure are shown, comparing the effects of short versus extended exposure, and exposure at rest versus exposure during light exercise. [Source: Data from R. F. Coburn et al., *J. Clin. Invest.* 44:1899, 1965.]

the cooperative binding of ligands to proteins with multiple binding sites have greatly influenced thinking about this problem.

The first model was proposed by Jacques Monod, Jeffries Wyman, and Jean-Pierre Changeux in 1965, and is called the **MWC model** or the **concerted model (Fig. 5-15a)**. The concerted model assumes that the subunits of a cooperatively binding protein are functionally identical, that each subunit can exist in (at least) two conformations, and that all subunits undergo the transition from one conformation to the other simultaneously. In this model, no protein has individual subunits in different conformations. The two conformations are in equilibrium. The ligand can bind to either conformation but binds much more tightly to the R state. Successive binding of ligand molecules to the low-affinity conformation (which is more stable in the absence of ligand) makes a transition to the high-affinity conformation more likely.

In the second model, the **sequential model** (Fig. 5-15b), proposed in 1966 by Daniel Koshland and

disorientation, and some visual disturbances; these symptoms are generally reversed if the individual is treated with oxygen. At COHb levels of 30% to 50%, the neurological symptoms become more severe, and at levels near 50%, the individual loses consciousness and can sink into coma. Respiratory failure may follow. With prolonged exposure, some damage becomes permanent. Death normally occurs when COHb levels rise above 60%. Autopsy on the boys who died at Lake Powell revealed COHb levels of 59% and 52%.

Binding of CO to hemoglobin is affected by many factors, including exercise (Fig. 1) and changes in air pressure related to altitude. Because of their higher base levels of COHb, smokers exposed to a source of CO often develop symptoms faster than nonsmokers. Individuals with heart, lung, or blood diseases that reduce the availability of oxygen to tissues may also experience symptoms at lower levels of CO exposure. Fetuses are at particular risk for CO poisoning, because fetal hemoglobin has a somewhat higher affinity for CO than adult hemoglobin. Cases of CO exposure have been recorded in which the fetus died but the woman recovered.

It may seem surprising that the loss of half of one's hemoglobin to COHb can prove fatal—we know that people with any of several anemic conditions manage to function reasonably well with half the usual complement of active hemoglobin. However, the binding of CO to hemoglobin does more than remove protein from the pool available to bind oxygen. It also affects the affinity of the remaining hemoglobin subunits for oxygen. As CO binds to one or two subunits of a hemoglobin tetramer, the affinity for O_2 is increased substantially in the remaining subunits (Fig. 2). Thus, a hemoglobin tetramer with two bound CO molecules can efficiently bind O_2 in the lungs—but it releases very little of it in the tissues. Oxygen deprivation in the tissues rapidly becomes severe. To add to the problem, the effects of CO are not limited to interference with hemoglobin function. CO binds to other heme proteins and a variety of metalloproteins. The effects of these interactions are not yet well understood, but they may be responsible for some of the longer-term effects of acute but nonfatal CO poisoning.

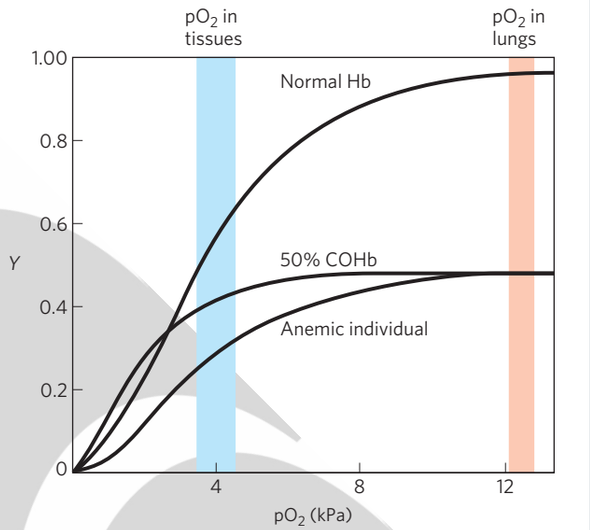


FIGURE 2 Several oxygen-binding curves: for normal hemoglobin, hemoglobin from an anemic individual with only 50% of her hemoglobin functional, and hemoglobin from an individual with 50% of his hemoglobin subunits complexed with CO. The pO_2 in human lungs and tissues is indicated. [Source: Data from F. J. W. Roughton and R. C. Darling, *Am. J. Physiol.* 141:17, 1944.]

When CO poisoning is suspected, rapid removal of the person from the CO source is essential, but this does not always result in rapid recovery. When an individual is moved from the CO-polluted site to a normal, outdoor atmosphere, O_2 begins to replace the CO in hemoglobin—but the COHb level drops only slowly. The half-time is 2 to 6.5 hours, depending on individual and environmental factors. If 100% oxygen is administered with a mask, the rate of exchange can be increased about fourfold; the half-time for O_2-CO exchange can be reduced to tens of minutes if 100% oxygen at a pressure of 3 atm (303 kPa) is supplied. Thus, rapid treatment by a properly equipped medical team is critical.

Carbon monoxide detectors in all homes are highly recommended. This is a simple and inexpensive measure to avoid possible tragedy. After completing the research for this box, we immediately purchased several new CO detectors for our homes.

colleagues, ligand binding can induce a change of conformation in an individual subunit. A conformational change in one subunit makes a similar change in an adjacent subunit, as well as the binding of a second ligand molecule, more likely. There are more potential intermediate states in this model than in the concerted model. The two models are not mutually exclusive; the concerted model may be viewed as the "all-or-none" limiting case of the sequential model. In Chapter 6 we use these models to investigate allosteric enzymes.

Hemoglobin Also Transports H^+ and CO_2

In addition to carrying nearly all the oxygen required by cells from the lungs to the tissues, hemoglobin carries two end products of cellular respiration—H^+ and CO_2—from the tissues to the lungs and the kidneys, where they are excreted. The CO_2, produced by oxidation of organic fuels in mitochondria, is hydrated to form bicarbonate:

$$CO_2 + H_2O \rightleftharpoons H^+ + HCO_3^-$$

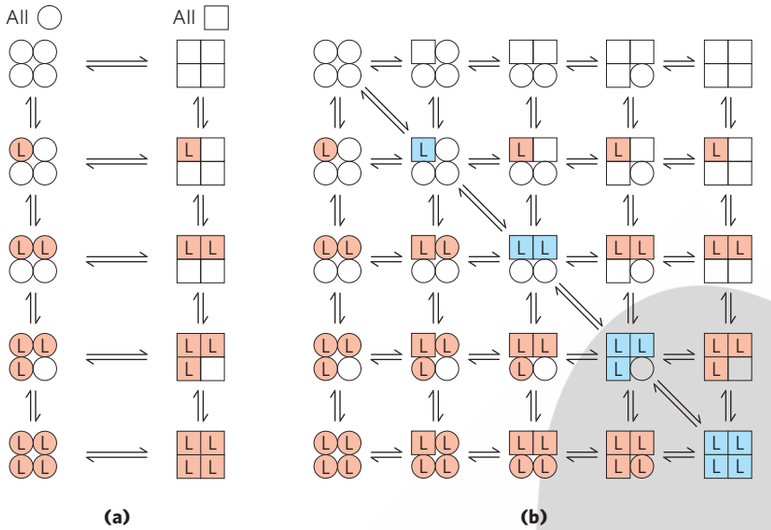


FIGURE 5-15 Two general models for the interconversion of inactive and active forms of a protein during cooperative ligand binding. Although the models may be applied to any protein—including any enzyme (Chapter 6)—that exhibits cooperative binding, we show here four subunits because the model was originally proposed for hemoglobin. **(a)** In the concerted, or all-or-none, model (MWC model), all subunits are postulated to be in the same conformation, either all ○ (low affinity or inactive) or all □ (high affinity or active). Depending on the equilibrium, K_{eq}, between ○ and □ forms, the binding of one or more ligand molecules (L) will pull the equilibrium toward the ○ form. Subunits with bound L are shaded. **(b)** In the sequential model, each individual subunit can be in either the ○ or □ form. A very large number of conformations is thus possible. Most subunits spend most of their time in the states shaded in blue.

This reaction is catalyzed by **carbonic anhydrase**, an enzyme particularly abundant in erythrocytes. Carbon dioxide is not very soluble in aqueous solution, and bubbles of CO_2 would form in the tissues and blood if it were not converted to bicarbonate. As you can see from the reaction catalyzed by carbonic anhydrase, the hydration of CO_2 results in an increase in the H^+ concentration (a decrease in pH) in the tissues. The binding of oxygen by hemoglobin is profoundly influenced by pH and CO_2 concentration, so the interconversion of CO_2 and bicarbonate is of great importance to the regulation of oxygen binding and release in the blood.

Hemoglobin transports about 40% of the total H^+ and 15% to 20% of the CO_2 formed in the tissues to the lungs and kidneys. (The remainder of the H^+ is absorbed by the plasma's bicarbonate buffer; the remainder of the CO_2 is transported as dissolved HCO_3^- and CO_2.) The binding of H^+ and CO_2 is inversely related to the binding of oxygen. At the relatively low pH and high CO_2 concentration of peripheral tissues, the affinity of hemoglobin for oxygen decreases as H^+ and CO_2 are bound, and O_2 is released to the tissues. Conversely, in the capillaries of the lung, as CO_2 is excreted and the blood pH consequently rises, the affinity of hemoglobin for oxygen increases and the protein binds more O_2 for transport to the peripheral tissues. This effect of pH and CO_2 concentration on the binding and release of oxygen by hemoglobin is called the **Bohr effect**, after Christian Bohr, the Danish physiologist (and father of physicist Niels Bohr) who discovered it in 1904.

The binding equilibrium for hemoglobin and one molecule of oxygen can be designated by the reaction

$$Hb + O_2 \rightleftharpoons HbO_2$$

but this is not a complete statement. To account for the effect of H^+ concentration on this binding equilibrium, we rewrite the reaction as

$$HHb^+ + O_2 \rightleftharpoons HbO_2 + H^+$$

where HHb^+ denotes a protonated form of hemoglobin. This equation tells us that the O_2-saturation curve of hemoglobin is influenced by the H^+ concentration **(Fig. 5-16)**. Both O_2 and H^+ are bound by hemoglobin, but with inverse affinity. When the oxygen concentration is high, as in the lungs, hemoglobin binds O_2 and releases protons. When the oxygen concentration is low, as in the peripheral tissues, H^+ is bound and O_2 is released.

Oxygen and H^+ are not bound at the same sites in hemoglobin. Oxygen binds to the iron atoms of the hemes, whereas H^+ binds to any of several amino acid residues in the protein. A major contribution to the Bohr effect is made by His^{146} (His HC3) of the β subunits. When protonated, this residue forms one of the ion pairs—to Asp^{94} (Asp FG1)—that helps stabilize deoxyhemoglobin in the T state (Fig. 5-9). The ion pair stabilizes the protonated form of His HC3, giving this residue

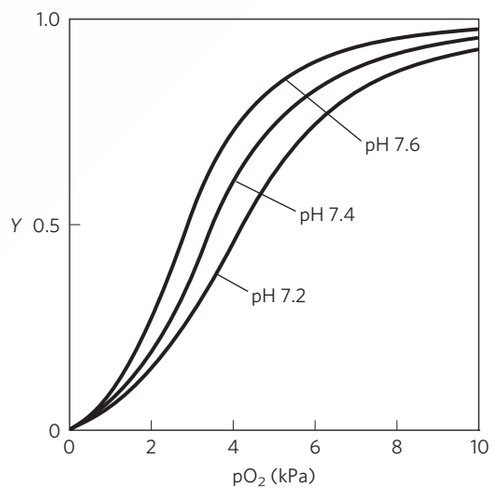
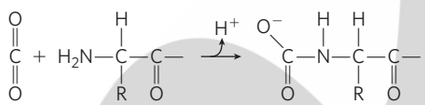


FIGURE 5-16 Effect of pH on oxygen binding to hemoglobin. The pH of blood is 7.6 in the lungs and 7.2 in the tissues. Experimental measurements on hemoglobin binding are often performed at pH 7.4.

an abnormally high pK_a in the T state. The pK_a falls to its normal value of 6.0 in the R state because the ion pair cannot form, and this residue is largely unprotonated in oxyhemoglobin at pH 7.6, the blood pH in the lungs. As the concentration of H^+ rises, protonation of His HC3 promotes release of oxygen by favoring a transition to the T state. Protonation of the amino-terminal residues of the α subunits, certain other His residues, and perhaps other groups has a similar effect.

Thus we see that the four polypeptide chains of hemoglobin communicate with each other not only about O_2 binding to their heme groups but also about H^+ binding to specific amino acid residues. And there is still more to the story. Hemoglobin also binds CO_2, again in a manner inversely related to the binding of oxygen. Carbon dioxide binds as a carbamate group to the α-amino group at the amino-terminal end of each globin chain, forming carbaminohemoglobin:

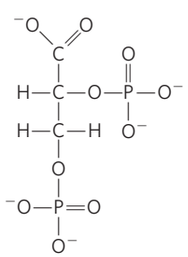


This reaction produces H^+, contributing to the Bohr effect. The bound carbamates also form additional salt bridges (not shown in Fig. 5-9) that help to stabilize the T state and promote the release of oxygen.

When the concentration of carbon dioxide is high, as in peripheral tissues, some CO_2 binds to hemoglobin and the affinity for O_2 decreases, causing its release. Conversely, when hemoglobin reaches the lungs, the high oxygen concentration promotes binding of O_2 and release of CO_2. It is the capacity to communicate ligand-binding information from one polypeptide subunit to the others that makes the hemoglobin molecule so beautifully adapted to integrating the transport of O_2, CO_2, and H^+ by erythrocytes.

Oxygen Binding to Hemoglobin Is Regulated by 2,3-Bisphosphoglycerate

The interaction of **2,3-bisphosphoglycerate (BPG)** with hemoglobin molecules further refines the function of hemoglobin, and provides an example of heterotropic allosteric modulation.


2,3-Bisphosphoglycerate

BPG is present in relatively high concentrations in erythrocytes. When hemoglobin is isolated, it contains substantial amounts of bound BPG, which can be difficult to remove completely. In fact, the O_2-binding curves for hemoglobin that we have examined to this point were obtained in the presence of bound BPG. 2,3-Bisphosphoglycerate is known to greatly reduce the affinity of hemoglobin for oxygen—there is an inverse relationship between the binding of O_2 and the binding of BPG. We can therefore describe another binding process for hemoglobin:

$$HbBPG + O_2 \rightleftharpoons HbO_2 + BPG$$

BPG binds at a site distant from the oxygen-binding site and regulates the O_2-binding affinity of hemoglobin in relation to the pO_2 in the lungs. BPG is important in the physiological adaptation to the lower pO_2 at high altitudes. For a healthy human at sea level, the binding of O_2 to hemoglobin is regulated such that the amount of O_2 delivered to the tissues is nearly 40% of the maximum that could be carried by the blood **(Fig. 5-17)**. Imagine that this person is suddenly transported from sea level to

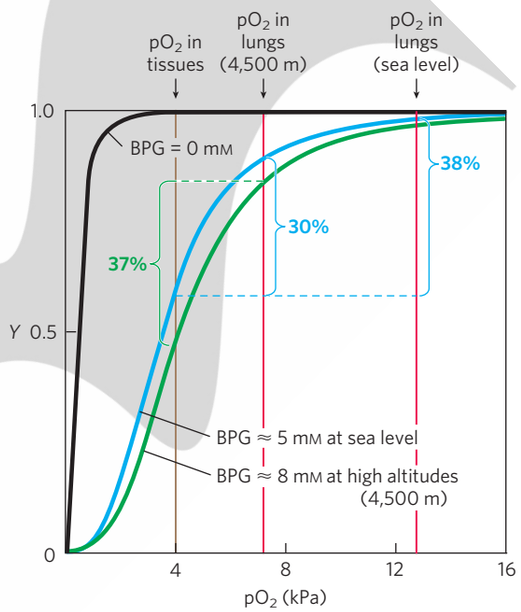


FIGURE 5-17 Effect of 2,3-bisphosphoglycerate on oxygen binding to hemoglobin. The BPG concentration in normal human blood is about 5 mM at sea level and about 8 mM at high altitudes. Note that hemoglobin binds to oxygen quite tightly when BPG is entirely absent, and the binding curve seems to be hyperbolic. In reality, the measured Hill coefficient for O_2-binding cooperativity decreases only slightly (from 3 to about 2.5) when BPG is removed from hemoglobin, but the rising part of the sigmoid curve is confined to a very small region close to the origin. At sea level, hemoglobin is nearly saturated with O_2 in the lungs, but is just over 60% saturated in the tissues, so the amount of O_2 released in the tissues is about 38% of the maximum that can be carried in the blood. At high altitudes, O_2 delivery declines by about one-fourth, to 30% of maximum. An increase in BPG concentration, however, decreases the affinity of hemoglobin for O_2, so approximately 37% of what can be carried is again delivered to the tissues.

an altitude of 4,500 meters, where the pO_2 is considerably lower. The delivery of O_2 to the tissues is now reduced. However, after just a few hours at the higher altitude, the BPG concentration in the blood has begun to rise, leading to a decrease in the affinity of hemoglobin for oxygen. This adjustment in the BPG level has only a small effect on the binding of O_2 in the lungs but a considerable effect on the release of O_2 in the tissues. As a result, the delivery of oxygen to the tissues is restored to nearly 40% of the O_2 that can be transported by the blood. The situation is reversed when the person returns to sea level. The BPG concentration in erythrocytes also increases in people suffering from **hypoxia**, lowered oxygenation of peripheral tissues due to inadequate functioning of the lungs or circulatory system.

The site of BPG binding to hemoglobin is the cavity between the β subunits in the T state **(Fig. 5-18)**. This cavity is lined with positively charged amino acid residues that interact with the negatively charged groups of BPG. Unlike O_2, only one molecule of BPG is bound to each hemoglobin tetramer. BPG lowers hemoglobin's affinity for oxygen by stabilizing the T state. The transition to the R state narrows the binding pocket for BPG, precluding BPG binding. In the absence of BPG, hemoglobin is converted to the R state more easily.

Regulation of oxygen binding to hemoglobin by BPG has an important role in fetal development. Because a fetus must extract oxygen from its mother's blood, fetal hemoglobin must have greater affinity than the maternal hemoglobin for O_2. The fetus synthesizes γ subunits rather than β subunits, forming $\alpha_2\gamma_2$ hemoglobin. This tetramer has a much lower affinity for BPG than normal adult hemoglobin, and a correspondingly higher affinity for O_2.

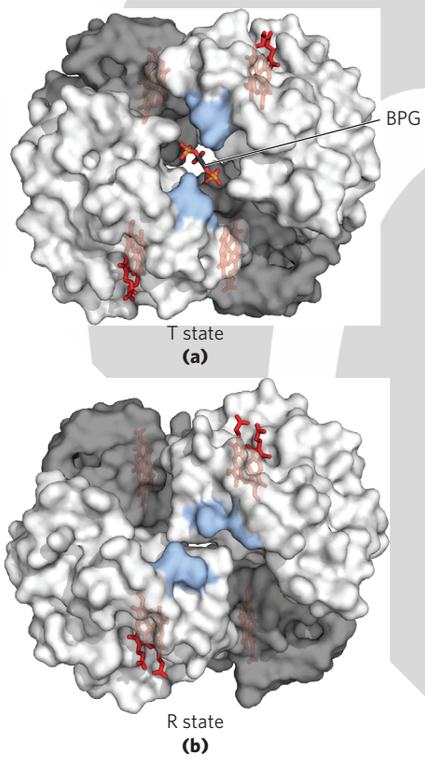


FIGURE 5-18 Binding of 2,3-bisphosphoglycerate to deoxyhemoglobin. (a) BPG binding stabilizes the T state of deoxyhemoglobin. The negative charges of BPG interact with several positively charged groups (shown in blue in this surface contour image) that surround the pocket between the β subunits on the surface of deoxyhemoglobin in the T state. **(b)** The binding pocket for BPG disappears on oxygenation, following transition to the R state. (Compare with Fig. 5-10.) [Sources: (a) PDB ID 1B86, V. Richard et al., *J. Mol. Biol.* 233:270, 1993. (b) PDB ID 1BBB, M. M. Silva et al., *J. Biol. Chem.* 267:17,248, 1992.]

Sickle Cell Anemia Is a Molecular Disease of Hemoglobin

The hereditary human disease sickle cell anemia demonstrates strikingly the importance of amino acid sequence in determining the secondary, tertiary, and quaternary structures of globular proteins, and thus their biological functions. Almost 500 genetic variants of hemoglobin are known to occur in the human population; all but a few are quite rare. Most variations consist of differences in a single amino acid residue. The effects on hemoglobin structure and function are often minor but can sometimes be extraordinary. Each hemoglobin variation is the product of an altered gene. Variant genes are called alleles. Because humans generally have two copies of each gene, an individual may have two copies of one allele (thus being homozygous for that gene) or one copy of each of two different alleles (thus heterozygous).

Sickle cell anemia occurs in individuals who inherit the allele for sickle cell hemoglobin from both parents. The erythrocytes of these individuals are fewer and also abnormal. In addition to an unusually large number of immature cells, the blood contains many long, thin, sickle-shaped erythrocytes **(Fig. 5-19)**. When hemoglobin from sickle

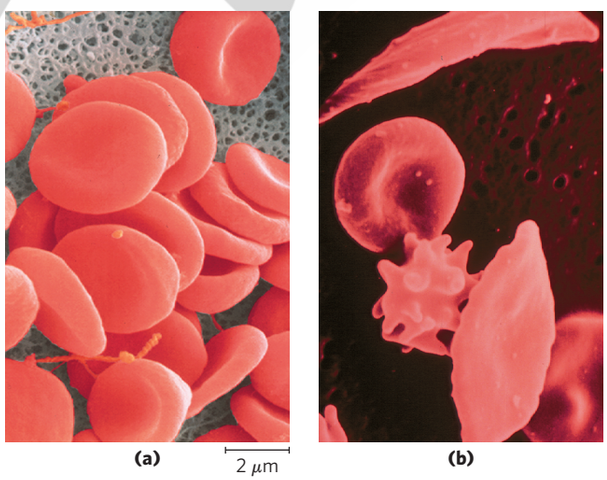


FIGURE 5-19 A comparison of **(a)** uniform, cup-shaped, normal erythrocytes and **(b)** the variably shaped erythrocytes seen in sickle-cell anemia, which range from normal to spiny or sickle-shaped. [Sources: (a) A. Syred/Science Source. (b) Jackie Lewin, Royal Free Hospital/Science Source.]

cells (called hemoglobin S, or HbS) is deoxygenated, it becomes insoluble and forms polymers that aggregate into tubular fibers **(Fig. 5-20)**. Normal hemoglobin (hemoglobin A, or HbA) remains soluble on deoxygenation. The insoluble fibers of deoxygenated HbS cause the deformed, sickle shape of the erythrocytes, and the proportion of sickled cells increases greatly as blood is deoxygenated.

The altered properties of HbS result from a single amino acid substitution, a Val instead of a Glu residue at position 6 in the two β chains. The R group of valine has no electric charge, whereas glutamate has a negative charge at pH 7.4. Hemoglobin S therefore has two fewer negative charges than HbA (one fewer on each β chain). Replacement of the Glu residue by Val creates a "sticky" hydrophobic contact point at position 6 of the β chain, which is on the outer surface of the molecule. These sticky spots cause deoxyHbS molecules to associate abnormally with each other, forming the long, fibrous aggregates characteristic of this disorder.

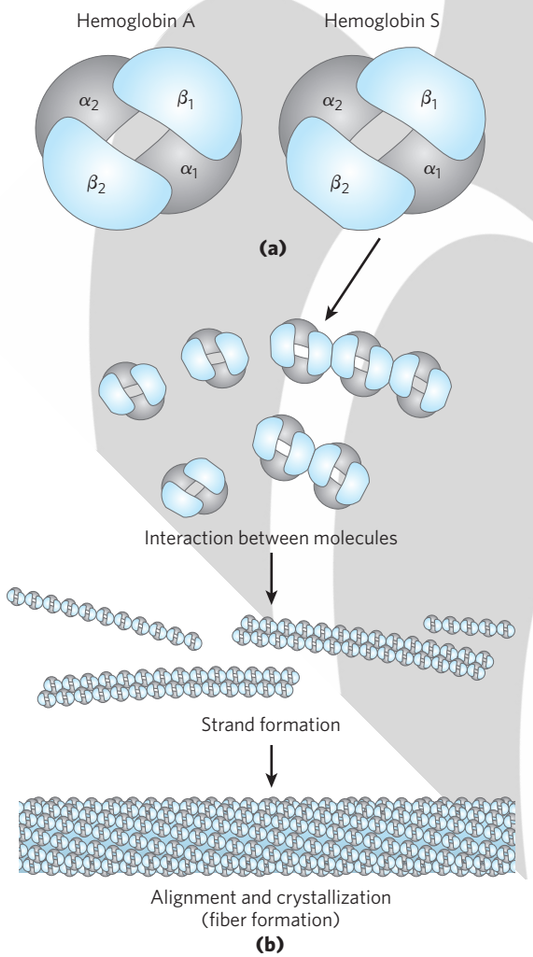


FIGURE 5-20 Normal and sickle-cell hemoglobin. **(a)** Subtle differences between the conformations of HbA and HbS result from a single amino acid change in the β chains. **(b)** As a result of this change, deoxyHbS has a hydrophobic patch on its surface, which causes the molecules to aggregate into strands that align into insoluble fibers.

Sickle cell anemia is life-threatening and painful. People with this disease suffer repeated crises brought on by physical exertion. They become weak, dizzy, and short of breath, and they also experience heart murmurs and an increased pulse rate. The hemoglobin content of their blood is only about half the normal value of 15 to 16 g/100 mL, because sickled cells are very fragile and rupture easily; this results in anemia ("lack of blood"). An even more serious consequence is that capillaries become blocked by the long, abnormally shaped cells, causing severe pain and interfering with normal organ function—a major factor in the early death of many people with the disease.

Without medical treatment, people with sickle cell anemia usually die in childhood. Curiously, the frequency of the sickle cell allele in populations is unusually high in certain parts of Africa. Investigation into this matter led to the finding that when heterozygous, the allele confers a small but significant resistance to lethal forms of malaria. The heterozygous individuals experience a milder condition called sickle cell trait; only about 1% of their erythrocytes become sickled on deoxygenation. These individuals may live completely normal lives if they avoid vigorous exercise and other stresses on the circulatory system. Natural selection has resulted in an allele population that balances the deleterious effects of the homozygous condition against the resistance to malaria afforded by the heterozygous condition. ■

SUMMARY 5.1 Reversible Binding of a Protein to a Ligand: Oxygen-Binding Proteins

■ Protein function often entails interactions with other molecules. A protein binds a molecule, known as a ligand, at its binding site. Proteins may undergo conformational changes when a ligand binds, a process called induced fit. In a multisubunit protein, the binding of a ligand to one subunit may affect ligand binding to other subunits. Ligand binding can be regulated.

■ Myoglobin contains a heme prosthetic group, which binds oxygen. Heme consists of a single atom of Fe^{2+} coordinated within a porphyrin. Oxygen binds to myoglobin reversibly; this simple reversible binding can be described by an association constant K_a or a dissociation constant K_d. For a monomeric protein such as myoglobin, the fraction of binding sites occupied by a ligand is a hyperbolic function of ligand concentration.

■ Normal adult hemoglobin has four heme-containing subunits, two α and two β, similar in structure to each other and to myoglobin. Hemoglobin exists in two interchangeable structural states, T and R. The T state is most stable when oxygen is not bound. Oxygen binding promotes transition to the R state.

■ Oxygen binding to hemoglobin is both allosteric and cooperative. As O_2 binds to one binding site, the hemoglobin undergoes conformational changes that affect the other binding sites—an example of allosteric

behavior. Conformational changes between the T and R states, mediated by subunit-subunit interactions, result in cooperative binding; this is described by a sigmoid binding curve and can be analyzed by a Hill plot.

- Two major models have been proposed to explain the cooperative binding of ligands to multisubunit proteins: the concerted model and the sequential model.
- Hemoglobin also binds H^+ and CO_2, resulting in the formation of ion pairs that stabilize the T state and lessen the protein's affinity for O_2 (the Bohr effect). Oxygen binding to hemoglobin is also modulated by 2,3-bisphosphoglycerate, which binds to and stabilizes the T state.
- Sickle cell anemia is a genetic disease caused by a single amino acid substitution (Glu^6 to Val^6) in each β chain of hemoglobin. The change produces a hydrophobic patch on the surface of the hemoglobin that causes the molecules to aggregate into bundles of fibers. This homozygous condition results in serious medical complications.

5.2 Complementary Interactions between Proteins and Ligands: The Immune System and Immunoglobulins

We have seen how the conformations of oxygen-binding proteins affect and are affected by the binding of small ligands (O_2 or CO) to the heme group. However, most protein-ligand interactions do not involve a prosthetic group. Instead, the binding site for a ligand is more often like the hemoglobin binding site for BPG—a cleft in the protein lined with amino acid residues, arranged to make the binding interaction highly specific. Effective discrimination between ligands is the norm at binding sites, even when the ligands have only minor structural differences.

All vertebrates have an immune system capable of distinguishing molecular "self" from "nonself" and then destroying what is identified as nonself. In this way, the immune system eliminates viruses, bacteria, and other pathogens and molecules that may pose a threat to the organism. On a physiological level, the **immune response** is an intricate and coordinated set of interactions among many classes of proteins, molecules, and cell types. At the level of individual proteins, the immune response demonstrates how an acutely sensitive and specific biochemical system is built upon the reversible binding of ligands to proteins.

The Immune Response Includes a Specialized Array of Cells and Proteins

Immunity is brought about by a variety of **leukocytes** (white blood cells), including **macrophages** and **lymphocytes**, all of which develop from undifferentiated stem cells in the bone marrow. Leukocytes can leave the bloodstream and patrol the tissues, each cell producing one or more proteins capable of recognizing and binding to molecules that might signal an infection.

The immune response consists of two complementary systems, the humoral and cellular immune systems. The **humoral immune system** (Latin *humor*, "fluid") is directed at bacterial infections and extracellular viruses (those found in the body fluids), but can also respond to individual foreign proteins. The **cellular immune system** destroys host cells infected by viruses and also destroys some parasites and foreign tissues.

At the heart of the humoral immune response are soluble proteins called **antibodies** or **immunoglobulins**, often abbreviated **Ig**. Immunoglobulins bind bacteria, viruses, or large molecules identified as foreign and target them for destruction. Making up 20% of blood protein, the immunoglobulins are produced by **B lymphocytes**, or **B cells**, so named because they complete their development in the *b*one marrow.

The agents at the heart of the cellular immune response are a class of **T lymphocytes**, or **T cells** (so called because the latter stages of their development occur in the *t*hymus), known as **cytotoxic T cells** (**T_C cells**, also called killer T cells). Recognition of infected cells or parasites involves proteins called **T-cell receptors** on the surface of T_C cells. Receptors are proteins, usually found on the outer surface of cells and extending through the plasma membrane, that recognize and bind extracellular ligands, thus triggering changes inside the cell.

In addition to cytotoxic T cells, there are **helper T cells (T_H cells)**, whose function it is to produce soluble signaling proteins called cytokines, which include the interleukins. T_H cells interact with macrophages. The T_H cells participate only indirectly in the destruction of infected cells and pathogens, stimulating the selective proliferation of those T_C and B cells that can bind to a particular antigen. This process, called **clonal selection**, increases the number of immune system cells that can respond to a particular pathogen. The importance of T_H cells is dramatically illustrated by the epidemic produced by HIV (human immunodeficiency virus), the virus that causes AIDS (acquired immune deficiency syndrome). T_H cells are the primary targets of HIV infection; elimination of these cells progressively incapacitates the entire immune system. Table 5-2 summarizes the functions of some leukocytes of the immune system.

Each recognition protein of the immune system, either a T-cell receptor or an antibody produced by a B cell, specifically binds some particular chemical structure, distinguishing it from virtually all others. Humans are capable of producing more than 10^8 different antibodies with distinct binding specificities. Given this extraordinary diversity, any chemical structure on the surface of a virus or invading cell will most likely be recognized and bound by one or more antibodies. Antibody diversity is derived from random reassembly of a set of immunoglobulin gene segments through genetic recombination mechanisms that are discussed in Chapter 25 (see Fig. 25-43).

A specialized lexicon is used to describe the unique interactions between antibodies or T-cell receptors and

TABLE 5-2 Some Types of Leukocytes Associated with the Immune System

Cell type	Function
Macrophages	Ingest large particles and cells by phagocytosis
B lymphocytes (B cells)	Produce and secrete antibodies
T lymphocytes (T cells)	
Cytotoxic (Killer) T cells (T_C)	Interact with infected host cells through receptors on T-cell surface
Helper T cells (T_H)	Interact with macrophages and secrete cytokines (interleukins) that stimulate T_C, T_H, and B cells to proliferate.

the molecules they bind. Any molecule or pathogen capable of eliciting an immune response is called an **antigen**. An antigen may be a virus, a bacterial cell wall, or an individual protein or other macromolecule. A complex antigen may be bound by several different antibodies. An individual antibody or T-cell receptor binds only a particular molecular structure within the antigen, called its **antigenic determinant** or **epitope**.

It would be unproductive for the immune system to respond to small molecules that are common intermediates and products of cellular metabolism. Molecules of M_r <5,000 are generally not antigenic. However, when small molecules are covalently attached to large proteins in the laboratory, they can be used to elicit an immune response. These small molecules are called **haptens**. The antibodies produced in response to protein-linked haptens will then bind to the same small molecules in their free form. Such antibodies are sometimes used in the development of analytical tests described later in this chapter or as a specific ligand in affinity chromatography (see Fig. 3-17c). We now turn to a more detailed description of antibodies and their binding properties.

Antibodies Have Two Identical Antigen-Binding Sites

Immunoglobulin G (IgG) is the major class of antibody molecule and one of the most abundant proteins in the blood serum. IgG has four polypeptide chains: two large ones, called heavy chains, and two light chains, linked by noncovalent and disulfide bonds into a complex of M_r 150,000. The heavy chains of an IgG molecule interact at one end, then branch to interact separately with the light chains, forming a Y-shaped molecule **(Fig. 5-21)**.

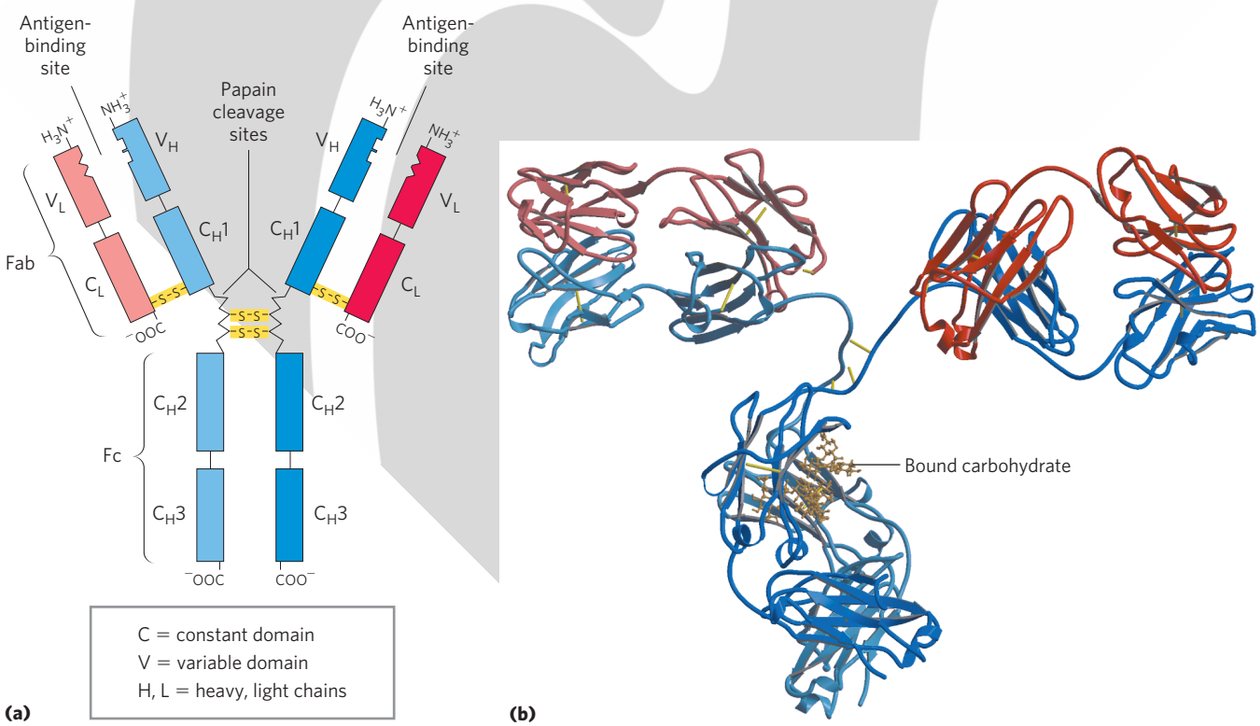


FIGURE 5-21 **Immunoglobulin G. (a)** Pairs of heavy and light chains combine to form a Y-shaped molecule. Two antigen-binding sites are formed by the combination of variable domains from one light (V_L) and one heavy (V_H) chain. Cleavage with papain separates the Fab and Fc portions of the protein in the hinge region. The Fc portion also contains bound carbohydrate (shown in (b)). **(b)** A ribbon model of the first complete IgG molecule to be crystallized and structurally analyzed. Although the molecule has two identical heavy chains (two shades of blue) and two identical light chains (two shades of red), it crystallized in the asymmetric conformation shown here. Conformational flexibility may be important to the function of immunoglobulins. [Source: (b) PDB ID 1IGT, L. J. Harris et al., *Biochemistry* 36:1581, 1997.]

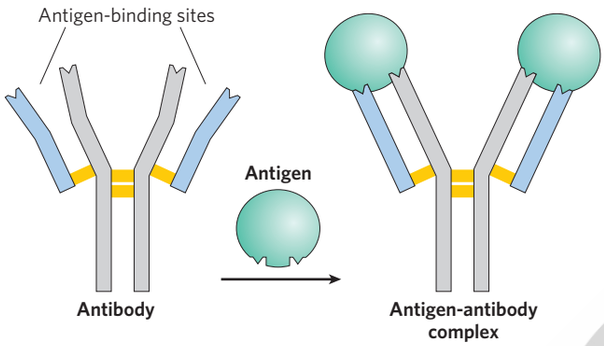


FIGURE 5-22 Binding of IgG to an antigen. To generate an optimal fit for the antigen, the binding sites of IgG often undergo slight conformational changes. Such induced fit is common to many protein-ligand interactions.

At the "hinges" separating the base of an IgG molecule from its branches, the immunoglobulin can be cleaved with proteases. Cleavage with the protease papain liberates the basal fragment, called **Fc** because it usually *c*rystallizes readily, and the two branches, called **Fab**, the *a*ntigen-*b*inding fragments. Each branch has a single antigen-binding site.

The fundamental structure of immunoglobulins was first established by Gerald Edelman and Rodney Porter. Each chain is made up of identifiable domains. Some are constant in sequence and structure from one IgG to the next; others are variable. The constant domains have a characteristic structure known as the **immunoglobulin fold**, a well-conserved structural motif in the all-β class of proteins (Chapter 4). There are three of these constant domains in each heavy chain and one in each light chain. The heavy and light chains also have one variable domain each, in which most of the variability in amino acid sequence is found. The variable domains associate to create the antigen-binding site (Fig. 5-21), allowing formation of an antigen-antibody complex **(Fig. 5-22)**.

In many vertebrates, IgG is but one of five classes of immunoglobulins. Each class has a characteristic type of heavy chain, denoted α, δ, ε, γ, and μ for IgA, IgD, IgE, IgG, and IgM, respectively. Two types of light chain, κ and λ, occur in all classes of immunoglobulins. The overall structures of **IgD** and **IgE** are similar to that of IgG. **IgM** occurs either in a monomeric, membrane-bound form or in a secreted form that is a cross-linked pentamer of this basic structure **(Fig. 5-23)**. **IgA**, found principally in secretions such as saliva, tears, and milk, can be a monomer, dimer, or trimer. IgM is the first antibody to be made by B lymphocytes and the major antibody in the early stages of a primary immune response. Some B cells soon begin to produce IgD (with the same antigen-binding site as the IgM produced by the same cell), but the particular function of IgD is less clear.

The IgG described above is the major antibody in secondary immune responses, which are initiated by a class of B cells called memory B cells. As part of the

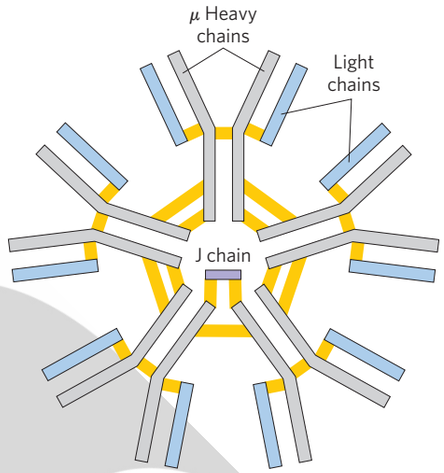


FIGURE 5-23 IgM pentamer of immunoglobulin units. The pentamer is cross-linked with disulfide bonds (yellow). The J chain is a polypeptide of M_r 20,000 found in both IgA and IgM.

organism's ongoing immunity to antigens already encountered and dealt with, IgG is the most abundant immunoglobulin in the blood. When IgG binds to an invading bacterium or virus, it activates certain leukocytes such as macrophages to engulf and destroy the invader, and also activates some other parts of the immune response. Receptors on the macrophage surface recognize and bind the Fc region of IgG. When these Fc receptors bind an antibody-pathogen complex, the macrophage engulfs the complex by phagocytosis **(Fig. 5-24)**.

IgE plays an important role in the allergic response, interacting with basophils (phagocytic leukocytes) in the blood and with histamine-secreting cells called mast cells, which are widely distributed in tissues. This immunoglobulin binds, through its Fc region, to special Fc receptors on the basophils or mast cells. In this form, IgE serves as a receptor for antigen. If antigen is bound, the cells are induced to secrete histamine and other biologically active amines that cause the dilation and increased permeability of blood vessels.

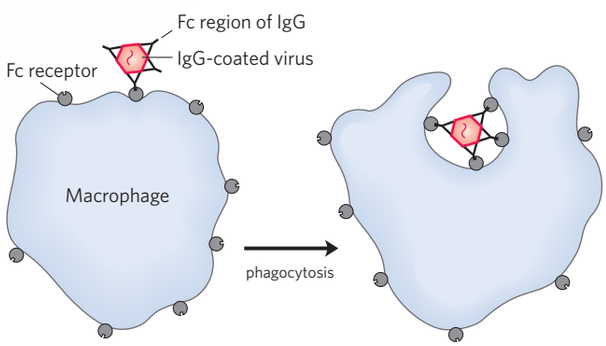
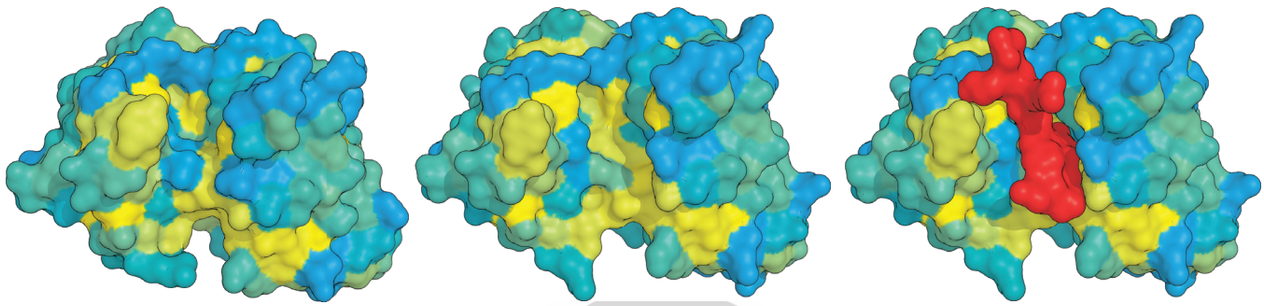


FIGURE 5-24 Phagocytosis of an antibody-bound virus by a macrophage. The Fc regions of antibodies bound to the virus now bind to Fc receptors on the surface of a macrophage, triggering the macrophage to engulf and destroy the virus.



(a) Conformation with no antigen bound **(b)** Antigen bound (but not shown) **(c)** Antigen bound (shown)

FIGURE 5-25 Induced fit in the binding of an antigen to IgG. The Fab fragment of an IgG molecule is shown here with the surface contour colored to represent hydrophobicity. Hydrophobic surfaces are yellow, hydrophilic surfaces are blue, with shades of blue to green to yellow in between. **(a)** View of the Fab fragment in the absence of antigen (a small peptide derived from HIV), looking down on the antigen binding site. **(b)** The same view, but with the Fab fragment in the "bound" conformation with the antigen omitted to provide an unobstructed view of the altered binding site. Note how the hydrophobic binding cavity has enlarged and several groups have shifted position. **(c)** The same view as (b) but with the antigen (red) in the binding site. [Sources: (a) PDB ID 1GGC, R. L. Stanfield et al., *Structure* 1:83, 1993. (b, c) PDB ID 1GGI, J. M. Rini et al., *Proc. Natl. Acad. Sci. USA* 90:6325, 1993.]

These effects on the blood vessels are thought to facilitate the movement of immune system cells and proteins to sites of inflammation. They also produce the symptoms normally associated with allergies. Pollen or other allergens are recognized as foreign, triggering an immune response normally reserved for pathogens. ■

Antibodies Bind Tightly and Specifically to Antigen

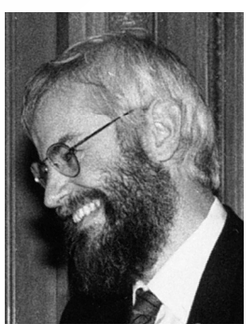
The binding specificity of an antibody is determined by the amino acid residues in the variable domains of its heavy and light chains. Many residues in these domains are variable, but not equally so. Some, particularly those lining the antigen-binding site, are hypervariable—especially likely to differ. Specificity is conferred by chemical complementarity between the antigen and its specific binding site, in terms of shape and the location of charged, nonpolar, and hydrogen-bonding groups. For example, a binding site with a negatively charged group may bind an antigen with a positive charge in the complementary position. In many instances, complementarity is achieved interactively as the structures of antigen and binding site influence each other as they come closer together. Conformational changes in the antibody and/or the antigen then allow the complementary groups to interact fully. This is an example of induced fit. The complex of a peptide derived from HIV (a model antigen) and an Fab molecule, shown in **Figure 5-25**, illustrates some of these properties. The changes in structure observed on antigen binding are particularly striking in this example.

A typical antibody-antigen interaction is quite strong, characterized by K_d values as low as 10^{-10} M (recall that a lower K_d corresponds to a stronger binding interaction; see Table 5-1). The K_d reflects the energy derived from the hydrophobic effect and the various ionic, hydrogen-bonding, and van der Waals interactions that stabilize the binding. The binding energy required to produce a K_d of 10^{-10} M is about 65 kJ/mol.

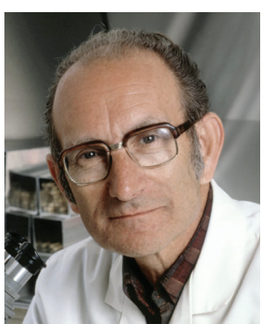
The Antibody-Antigen Interaction Is the Basis for a Variety of Important Analytical Procedures

The extraordinary binding affinity and specificity of antibodies make them valuable analytical reagents. Two types of antibody preparations are in use: polyclonal and monoclonal. **Polyclonal antibodies** are those produced by many different B lymphocytes responding to one antigen, such as a protein injected into an animal. Cells in the population of B lymphocytes produce antibodies that bind specific, different epitopes within the antigen. Thus, polyclonal preparations contain a mixture of antibodies that recognize different parts of the protein. **Monoclonal antibodies**, in contrast, are synthesized by a population of identical B cells (a **clone**) grown in cell culture. These antibodies are homogeneous, all recognizing the same epitope. The techniques for producing monoclonal antibodies were developed by Georges Köhler and Cesar Milstein.

The specificity of antibodies has practical uses. A selected antibody can be covalently attached to a resin and used in a chromatography column of the type shown in Figure 3-17c. When a mixture of proteins is added to the column, the antibody specifically binds its



Georges Köhler, 1946–1995
[Source: Bettman/Corbis.]



Cesar Milstein, 1927–2002
[Source: Corbin O'Grady Studio/Science Source.]

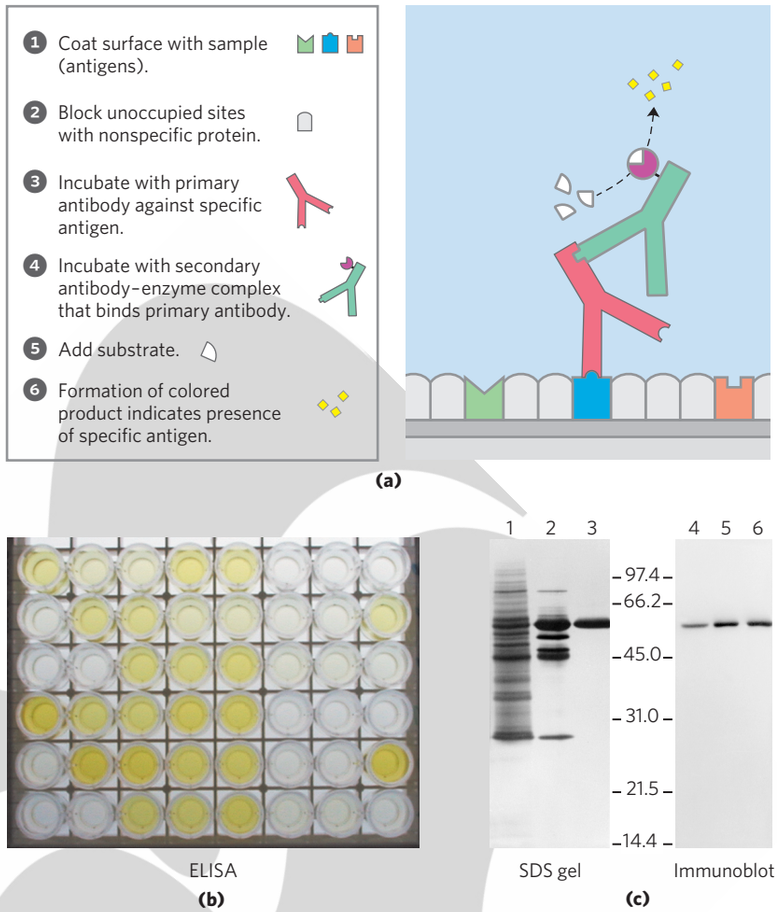


FIGURE 5-26 Antibody techniques. The specific reaction of an antibody with its antigen is the basis of several techniques that identify and quantify a specific protein in a complex sample. **(a)** A schematic representation of the general method. **(b)** An ELISA to test for the presence of herpes simplex virus (HSV) antibodies in blood samples. Wells were coated with an HSV antigen, to which antibodies against HSV will bind. The second antibody is anti-human IgG linked to horseradish peroxidase. Following completion of the steps shown in (a), blood samples with greater amounts of HSV antibody turn brighter yellow. **(c)** An immunoblot. Lanes 1 to 3 are from an SDS gel; samples from successive stages in the purification of a protein kinase were separated and stained with Coomassie blue. Lanes 4 to 6 show the same samples, but these were electrophoretically transferred to a nitrocellulose membrane after separation on an SDS gel. The membrane was then "probed" with antibody against the protein kinase. The numbers between the SDS gel and the immunoblot indicate M_r in thousands. [Sources: (b, c) State of Wisconsin Lab of Hygiene, Madison, WI.]

target protein and retains it on the column while other proteins are washed through. The target protein can then be eluted from the resin by a salt solution or some other agent. This is a powerful protein analytical tool.

In another versatile analytical technique, an antibody is attached to a radioactive label or some other reagent that makes it easy to detect. When the antibody binds the target protein, the label reveals the presence of the protein in a solution or its location in a gel, or even in a living cell. Several variations of this procedure are illustrated in **Figure 5-26**.

An **ELISA** (enzyme-linked immunosorbent assay) can be used to rapidly screen for and quantify an antigen in a sample (Fig. 5-26b). Proteins in the sample are adsorbed to an inert surface, usually a 96-well polystyrene plate. The surface is washed with a solution of an inexpensive nonspecific protein (often casein from nonfat dry milk powder) to block proteins introduced in subsequent steps from adsorbing to unoccupied sites. The surface is then treated with a solution containing the primary antibody—an antibody against the protein of interest. Unbound antibody is washed away, and the surface is treated with a solution containing a secondary antibody—antibody against the primary antibody—linked to an enzyme that catalyzes a reaction that forms a colored product. After unbound secondary antibody is washed away, the substrate of the antibody-linked enzyme is added. Product formation (monitored as color intensity) is proportional to the concentration of the protein of interest in the sample.

In an **immunoblot assay**, also called a **Western blot** (Fig. 5-26c), proteins that have been separated by gel electrophoresis are transferred electrophoretically to a nitrocellulose membrane. The membrane is blocked (as described above for ELISA), then treated successively with primary antibody, secondary antibody linked to enzyme, and substrate. A colored precipitate forms only along the band containing the protein of interest. Immunoblotting allows the detection of a minor component in a sample and provides an approximation of its molecular weight.

We will encounter other aspects of antibodies in later chapters. They are extremely important in medicine and can tell us much about the structure of proteins and the action of genes.

SUMMARY 5.2 Complementary Interactions between Proteins and Ligands: The Immune System and Immunoglobulins

■ The immune response is mediated by interactions among an array of specialized leukocytes and their associated proteins. T lymphocytes produce T-cell receptors. B lymphocytes produce immunoglobulins. In a process called clonal selection, helper T cells induce the proliferation of B cells and cytotoxic T cells that

produce immunoglobulins or proliferation of T-cell receptors that bind to a specific antigen.

- Humans have five classes of immunoglobulins, each with different biological functions. The most abundant class is IgG, a Y-shaped protein with two heavy and two light chains. The domains near the upper ends of the Y are hypervariable within the broad population of IgGs and form two antigen-binding sites.
- A given immunoglobulin generally binds to only a part, called the epitope, of a large antigen. Binding often involves a conformational change in the IgG, an induced fit to the antigen.
- The exquisite binding specificity of immunoglobulins is exploited in analytical techniques such as ELISA and immunoblotting.

5.3 Protein Interactions Modulated by Chemical Energy: Actin, Myosin, and Molecular Motors

Organisms move. Cells move. Organelles and macromolecules within cells move. Most of these movements arise from the activity of a fascinating class of protein-based molecular motors. Fueled by chemical energy, usually derived from ATP, large aggregates of motor proteins undergo cyclic conformational changes that accumulate into a unified, directional force—the tiny force that pulls apart chromosomes in a dividing cell, and the immense force that levers a pouncing, quarter-ton jungle cat into the air.

The interactions among motor proteins, as you might predict, feature complementary arrangements of ionic, hydrogen-bonding, and hydrophobic groups at protein binding sites. In motor proteins, however, the resulting interactions achieve exceptionally high levels of spatial and temporal organization.

Motor proteins underlie the migration of organelles along microtubules, the motion of eukaryotic and bacterial flagella, the movement of some proteins along DNA, and the contraction of muscles. Proteins called kinesins and dyneins move along microtubules in cells, pulling along organelles or reorganizing chromosomes during cell division. An interaction of dynein with microtubules brings about the motion of eukaryotic flagella and cilia. Flagellar motion in bacteria involves a complex rotational motor at the base of the flagellum (see Fig. 19-41). Helicases, polymerases, and other proteins move along DNA as they carry out their functions in DNA metabolism (Chapter 25). Here, we focus on the well-studied example of the contractile proteins of vertebrate skeletal muscle as a paradigm for how proteins translate chemical energy into motion.

The Major Proteins of Muscle Are Myosin and Actin

The contractile force of muscle is generated by the interaction of two proteins, myosin and actin. These proteins are arranged in filaments that undergo transient interactions and slide past each other to bring about contraction. Together, actin and myosin make up more than 80% of the protein mass of muscle.

Myosin (M_r 520,000) has six subunits: two heavy chains (each of M_r 220,000) and four light chains (each of M_r 20,000). The heavy chains account for much of the overall structure. At their carboxyl termini, they are arranged as extended α helices, wrapped around each other in a fibrous, left-handed coiled coil similar to that of α-keratin **(Fig. 5-27a)**. At its amino terminus, each heavy chain has a large globular domain containing a site where ATP is hydrolyzed. The light chains are associated with the globular domains. When myosin is treated briefly with the protease trypsin, much of the fibrous tail is cleaved off, dividing the protein into components called light and heavy meromyosin (Fig. 5-27b). The globular domain—called myosin subfragment 1, or S1, or simply the myosin head group—is liberated from heavy meromyosin by cleavage with papain, leaving myosin subfragment 2, or S2. The S1 fragment is the motor domain that makes muscle contraction possible. S1 fragments can be crystallized, and their overall structure, as determined by Ivan Rayment and Hazel Holden, is shown in Figure 5-27c.

In muscle cells, molecules of myosin aggregate to form structures called **thick filaments (Fig. 5-28a)**. These rodlike structures are the core of the contractile unit. Within a thick filament, several hundred myosin molecules are arranged with their fibrous "tails" associated to form a long bipolar structure. The globular domains project from either end of this structure, in regular stacked arrays.

The second major muscle protein, **actin**, is abundant in almost all eukaryotic cells. In muscle, molecules of monomeric actin, called G-actin (*g*lobular actin; M_r 42,000), associate to form a long polymer called F-actin (*f*ilamentous actin). The **thin filament** consists of F-actin (Fig. 5-28b), along with the proteins troponin and tropomyosin (discussed below). The filamentous parts of thin filaments assemble as successive monomeric actin molecules add to one end. On addition, each monomer binds ATP, then hydrolyzes it to ADP, so every actin molecule in the filament is complexed to ADP. This ATP hydrolysis by actin functions only in the assembly of the filaments; it does not contribute directly to the energy expended in muscle contraction. Each actin monomer in the thin filament can bind tightly and specifically to one myosin head group (Fig. 5-28c).

Additional Proteins Organize the Thin and Thick Filaments into Ordered Structures

Skeletal muscle consists of parallel bundles of **muscle fibers**, each fiber a single, very large, multinucleated cell, 20 to 100 μm in diameter, formed from many cells fused together; a single fiber often spans the length of the muscle. Each fiber contains about 1,000 **myofibrils**, 2 μm in diameter, each consisting of a vast number of regularly arrayed thick and thin filaments complexed to

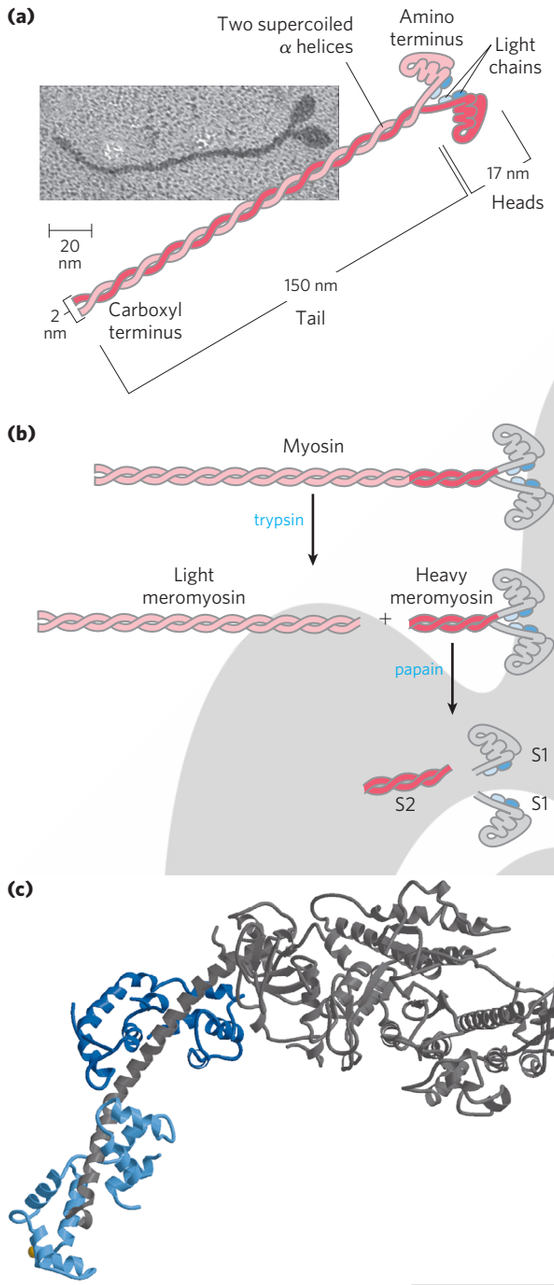


FIGURE 5-27 Myosin. (a) Myosin has two heavy chains (in two shades of red), the carboxyl termini forming an extended coiled coil (tail) and the amino termini having globular domains (heads). Two light chains (blue) are associated with each myosin head. **(b)** Cleavage with trypsin and papain separates the myosin heads (S1 fragments) from the tails (S2 fragments). **(c)** Ribbon representation of the myosin S1 fragment. The heavy chain is in gray, the two light chains in two shades of blue. [Sources: (a) Takeshi Katayama, et al. "Stimulatory effects of arachidonic acid on myosin ATPase activity and contraction of smooth muscle via myosin motor domain," *Am. J. Physiol. Heart Circ. Physiol.* Vol 298, Issue 2, pp. H505-H514, February 2010, Fig. 6b. **(c)** Courtesy of Ivan Rayment, University of Wisconsin–Madison, Enzyme Institute and Department of Biochemistry; PDB ID 2MYS, I. Rayment et al., *Science* 261:50, 1993.]

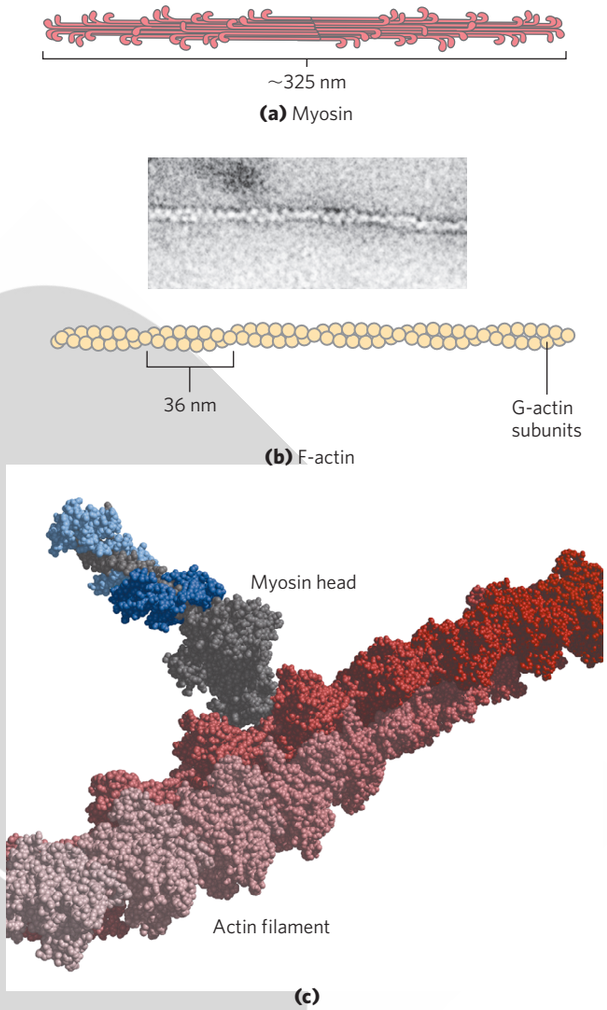


FIGURE 5-28 The major components of muscle. (a) Myosin aggregates to form a bipolar structure called a thick filament. **(b)** F-actin is a filamentous assemblage of G-actin monomers that polymerize two by two, giving the appearance of two filaments spiraling about one another in a right-handed fashion. **(c)** Space-filling model of an actin filament (shades of red) with one myosin head (gray and two shades of blue) bound to an actin monomer within the filament. [Sources: (b) Dr. Roger W. Craig PhD, University of Massachusetts Medical School. (c) Courtesy of Ivan Rayment, University of Wisconsin–Madison, Enzyme Institute and Department of Biochemistry; PDB ID 2MYS, I. Rayment et al., *Science* 261:50, 1993.]

other proteins **(Fig. 5-29)**. A system of flat membranous vesicles called the **sarcoplasmic reticulum** surrounds each myofibril. Examined under the electron microscope, muscle fibers reveal alternating regions of high and low electron density, called the **A bands** and **I bands** (Fig. 5-29b, c). The A and I bands arise from the arrangement of thick and thin filaments, which are aligned and partially overlapping. The I band is the region of the bundle that in cross section would contain only thin filaments. The darker A band stretches the length of the thick filament

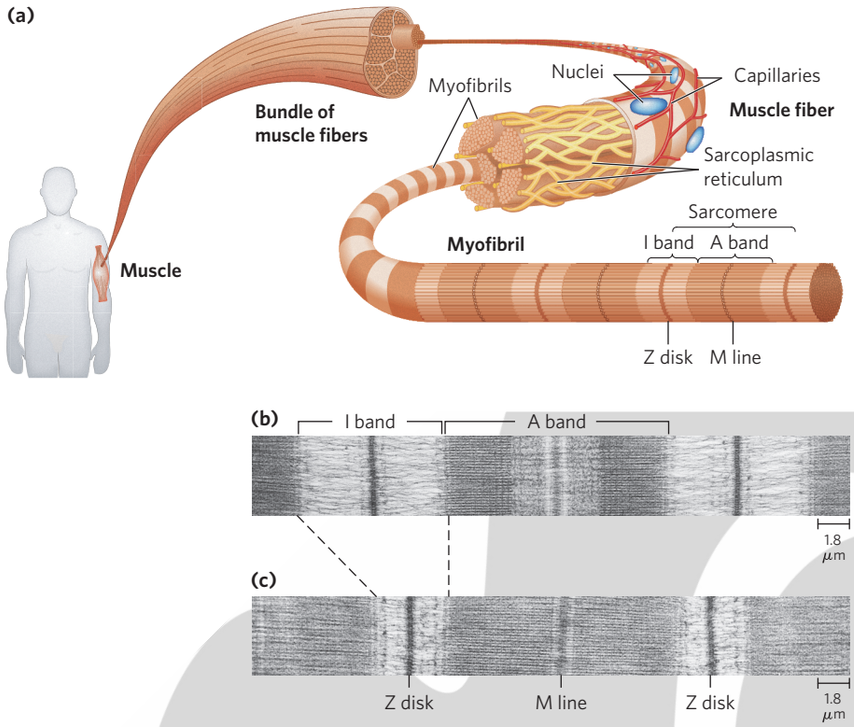
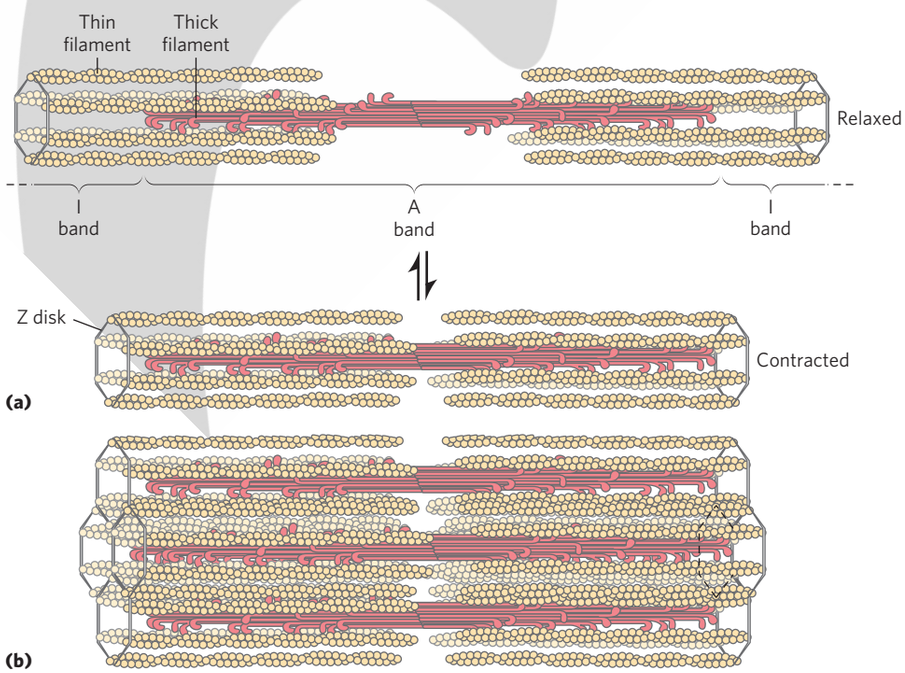


FIGURE 5-29 Skeletal muscle. **(a)** Muscle fibers consist of single, elongated, multinucleated cells that arise from the fusion of many precursor cells. The fibers are made up of many myofibrils (only six are shown here for simplicity) surrounded by the membranous sarcoplasmic reticulum. The organization of thick and thin filaments in a myofibril gives it a striated appearance. When muscle contracts, the I bands narrow and the Z disks move closer together, as seen in electron micrographs of **(b)** relaxed and **(c)** contracted muscle. [Source: (b, c) James E. Dennis/Phototake.]

and includes the region where parallel thick and thin filaments overlap. Bisecting the I band is a thin structure called the **Z disk**, perpendicular to the thin filaments and serving as an anchor to which the thin filaments are attached. The A band, too, is bisected by a thin line, the **M line** or M disk, a region of high electron density in the middle of the thick filaments. The entire contractile unit, consisting of bundles of thick filaments interleaved at either end with bundles of thin filaments, is called the **sarcomere**. The arrangement of interleaved bundles allows the thick and thin filaments to slide past each other (by a mechanism discussed below), causing a progressive shortening of each sarcomere **(Fig. 5-30)**.

The thin actin filaments are attached at one end to the Z disk in a regular pattern. The assembly includes the minor muscle proteins **α-actinin**, **desmin**, and **vimentin**.

FIGURE 5-30 Muscle contraction. Thick filaments are bipolar structures created by the association of many myosin molecules. **(a)** Muscle contraction occurs by the sliding of the thick and thin filaments past each other so that the Z disks in neighboring I bands draw closer together. **(b)** The thick and thin filaments are interleaved such that each thick filament is surrounded by six thin filaments.



Thin filaments also contain a large protein called **nebulin** (~7,000 amino acid residues), thought to be structured as an α helix that is long enough to span the length of the filament. The M line similarly organizes the thick filaments. It contains the proteins **paramyosin**, **C-protein**, and **M-protein**. Another class of proteins called **titins**, the largest single polypeptide chains discovered thus far (the titin of human cardiac muscle has 26,926 amino acid residues), link the thick filaments to the Z disk, providing additional organization to the overall structure. Among their structural functions, the proteins nebulin and titin are believed to act as "molecular rulers," regulating the length of the thin and thick filaments, respectively. Titin extends from the Z disk to the M line, regulating the length of the sarcomere itself and preventing overextension of the muscle. The characteristic sarcomere length varies from one muscle tissue to the next in a vertebrate, largely due to the different titin variants in the tissues.

Myosin Thick Filaments Slide along Actin Thin Filaments

The interaction between actin and myosin, like that between all proteins and ligands, involves weak bonds. When ATP is not bound to myosin, a face on the myosin head group binds tightly to actin **(Fig. 5-31)**. When ATP binds to myosin and is hydrolyzed to ADP and phosphate, a coordinated and cyclic series of conformational changes occurs in which myosin releases the F-actin subunit and binds another subunit farther along the thin filament.

The cycle has four major steps (Fig. 5-31). In step 1, ATP binds to myosin and a cleft in the myosin molecule opens, disrupting the actin-myosin interaction so that the bound actin is released. ATP is then hydrolyzed in step 2, causing a conformational change in the protein to a "high-energy" state that moves the myosin head and changes its orientation in relation to the actin thin filament. Myosin then binds weakly to an F-actin subunit closer to the Z disk than the one just released. As the phosphate product of ATP hydrolysis is released from myosin in step 3, another conformational change occurs in which the myosin cleft closes, strengthening the myosin-actin binding. This is followed quickly by step 4, a "power stroke" during which the conformation of the myosin head returns to the original resting state, its orientation relative to the bound actin changing so as to pull the tail of the myosin toward the Z disk. ADP is then released to complete the cycle. Each cycle generates about 3 to 4 pN (piconewtons) of force and moves the thick filament 5 to 10 nm relative to the thin filament.

Because there are many myosin heads in a thick filament, at any given moment some (probably 1% to 3%) are bound to thin filaments. This prevents thick filaments from slipping backward when an individual myosin head releases the actin subunit to which it was bound. The thick filament thus actively slides forward past the adjacent thin filaments. This process, coordinated among the many sarcomeres in a muscle fiber, brings about muscle contraction.

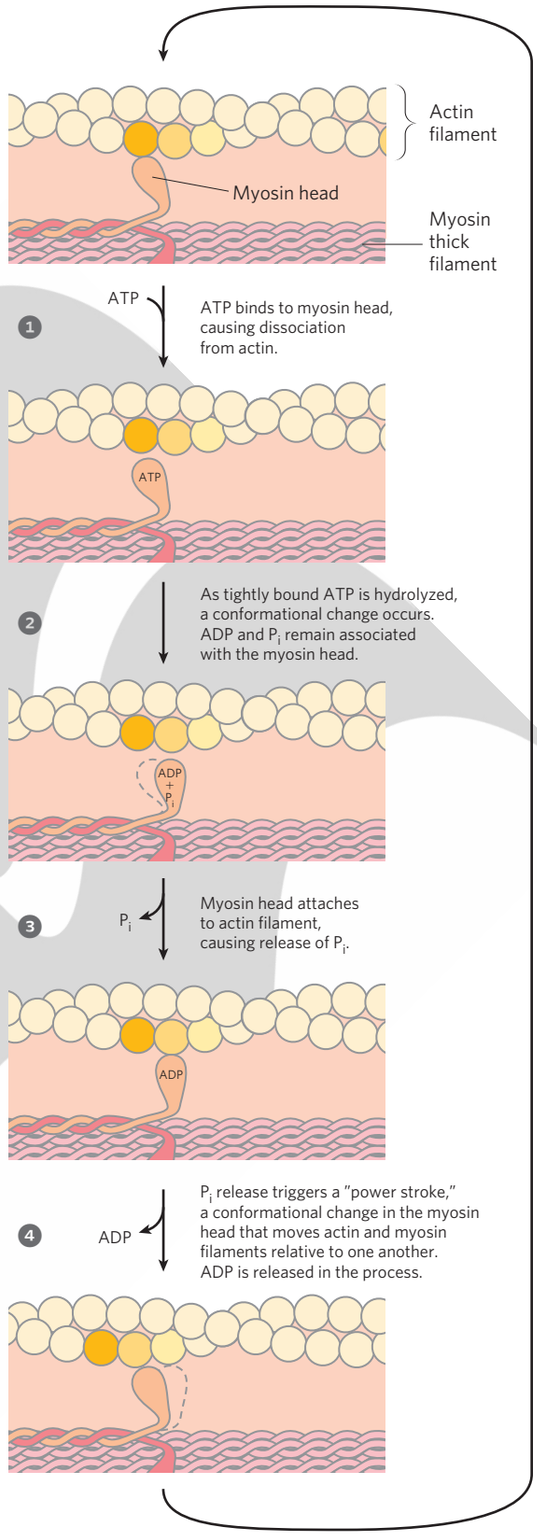


FIGURE 5-31 Molecular mechanism of muscle contraction. Conformational changes in the myosin head that are coupled to stages in the ATP hydrolytic cycle cause myosin to successively dissociate from one actin subunit, then associate with another farther along the actin filament. In this way, the myosin heads slide along the thin filaments, drawing the thick filament array into the thin filament array (see Fig. 5-30).

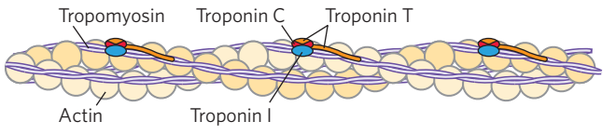


FIGURE 5-32 Regulation of muscle contraction by tropomyosin and troponin. Tropomyosin and troponin are bound to F-actin in the thin filaments. In the relaxed muscle, these two proteins are arranged around the actin filaments so as to block the binding sites for myosin. Tropomyosin is a two-stranded coiled coil of α helices, the same structural motif as in α-keratin (see Fig. 4-11). It forms head-to-tail polymers twisting around the two actin chains. Troponin is attached to the actin-tropomyosin complex at regular intervals of 38.5 nm. Troponin consists of three different subunits: I, C, and T. Troponin I prevents binding of the myosin head to actin; troponin C has a binding site for Ca^{2+}; and troponin T links the entire troponin complex to tropomyosin. When the muscle receives a neural signal to initiate contraction, Ca^{2+} is released from the sarcoplasmic reticulum (see Fig. 5-29a) and binds to troponin C. This causes a conformational change in troponin C, which alters the positions of troponin I and tropomyosin so as to relieve the inhibition by troponin I and allow muscle contraction.

The interaction between actin and myosin must be regulated so that contraction occurs only in response to appropriate signals from the nervous system. The regulation is mediated by a complex of two proteins, **tropomyosin** and **troponin (Fig. 5-32)**. Tropomyosin binds to the thin filament, blocking the attachment sites for the myosin head groups. Troponin is a Ca^{2+}-binding protein. A nerve impulse causes release of Ca^{2+} ions from the sarcoplasmic reticulum. The released Ca^{2+} binds to troponin (another protein-ligand interaction) and causes a conformational change in the tropomyosin-troponin complexes, exposing the myosin-binding sites on the thin filaments. Contraction follows.

Working skeletal muscle requires two types of molecular functions that are common in proteins—binding and catalysis. The actin-myosin interaction, a protein-ligand interaction like that of immunoglobulins with antigens, is reversible and leaves the participants unchanged. When ATP binds myosin, however, it is hydrolyzed to ADP and P_i. Myosin is not only an actin-binding protein, it is also an ATPase—an enzyme. The function of enzymes in catalyzing chemical transformations is the topic of the next chapter.

SUMMARY 5.3 Protein Interactions Modulated by Chemical Energy: Actin, Myosin, and Molecular Motors

■ Protein-ligand interactions achieve a special degree of spatial and temporal organization in motor proteins. Muscle contraction results from choreographed interactions between myosin and actin, coupled to the hydrolysis of ATP by myosin.

■ Myosin consists of two heavy and four light chains, forming a fibrous coiled coil (tail) domain and a globular (head) domain. Myosin molecules are organized into thick filaments, which slide past thin filaments composed largely of actin. ATP hydrolysis in myosin is coupled to a series of conformational changes in the myosin head, leading to dissociation of myosin from one F-actin subunit and its eventual reassociation with another, farther along the thin filament. The myosin thus slides along the actin filaments.

■ Muscle contraction is stimulated by the release of Ca^{2+} from the sarcoplasmic reticulum. The Ca^{2+} binds to the protein troponin, leading to a conformational change in a troponin-tropomyosin complex that triggers the cycle of actin-myosin interactions.

Key Terms

Terms in bold are defined in the glossary.

ligand 157
binding site 157
induced fit 157
hemoglobin 158
heme 158
porphyrin 158
heme protein 158
globins 159
equilibrium expression 160
association constant, K_a 160
dissociation constant, K_d 160
allosteric protein 166
modulator 166
Hill equation 167
Bohr effect 170
immune response 174
lymphocytes 174
antibody 174
immunoglobulin 174
B lymphocyte or **B cell** 174
T lymphocyte or **T cell** 174
antigen 175
epitope 175
hapten 175
immunoglobulin fold 176
polyclonal antibodies 177
monoclonal antibodies 177
ELISA 178
immunoblotting 178
Western blotting 178
myosin 179
actin 179
sarcomere 179

Problems

1. Relationship between Affinity and Dissociation Constant Protein A has a binding site for ligand X with a K_d of 10^{-6} M. Protein B has a binding site for ligand X with a K_d of 10^{-9} M. Which protein has a higher affinity for ligand X? Explain your reasoning. Convert the K_d to K_a for both proteins.

2. Negative Cooperativity Which of the following situations would produce a Hill plot with $n_H < 1.0$? Explain your reasoning in each case.

(a) The protein has multiple subunits, each with a single ligand-binding site. Binding of ligand to one site decreases the binding affinity of other sites for the ligand.

(b) The protein is a single polypeptide with two ligand-binding sites, each having a different affinity for the ligand.

(c) The protein is a single polypeptide with a single ligand-binding site. As purified, the protein preparation is heterogeneous, containing some protein molecules that are partially denatured and thus have a lower binding affinity for the ligand.

3. Hemoglobin's Affinity for Oxygen What is the effect of the following changes on the O_2 affinity of hemoglobin? (a) A drop in the pH of blood plasma from 7.4 to 7.2. (b) A decrease in the partial pressure of CO_2 in the lungs from 6 kPa (holding one's breath) to 2 kPa (normal breathing). (c) An increase in the BPG level from 5 mM (normal altitudes) to 8 mM (high altitudes). (d) An increase in CO from 1.0 part per million (ppm) in a normal indoor atmosphere to 30 ppm in a home that has a malfunctioning or leaking furnace.

4. Reversible Ligand Binding I The protein calcineurin binds to the protein calmodulin with an association rate of $8.9 \times 10^3\ M^{-1}s^{-1}$ and an overall dissociation constant, K_d, of 10 nM. Calculate the dissociation rate, k_d, including appropriate units.

5. Reversible Ligand Binding II A binding protein binds to a ligand L with a K_d of 400 nM. What is the concentration of ligand when Y is (a) 0.25, (b) 0.6, (c) 0.95?

6. Reversible Ligand Binding III Three membrane receptor proteins bind tightly to a hormone. Based on the data in the table below, (a) what is the K_d for hormone binding by protein 2? (Include appropriate units.) (b) Which of these proteins binds *most* tightly to this hormone?

Hormone concentration (nM)	*Y*		
	Protein 1	**Protein 2**	**Protein 3**
0.2	0.048	0.29	0.17
0.5	0.11	0.5	0.33
1	0.2	0.67	0.5
4	0.5	0.89	0.8
10	0.71	0.95	0.91
20	0.83	0.97	0.95
50	0.93	0.99	0.98

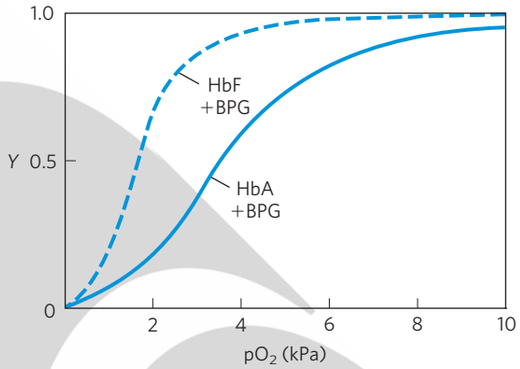
7. Cooperativity in Hemoglobin Under appropriate conditions, hemoglobin dissociates into its four subunits. The isolated α subunit binds oxygen, but the O_2-saturation curve is hyperbolic rather than sigmoid. In addition, the binding of oxygen to the isolated α subunit is not affected by the presence of H^+, CO_2, or BPG. What do these observations indicate about the source of the cooperativity in hemoglobin?

8. Comparison of Fetal and Maternal Hemoglobins Studies of oxygen transport in pregnant mammals show that the O_2-saturation curves of fetal and maternal blood are markedly different when measured under the same conditions. Fetal erythrocytes contain a structural variant of hemoglobin, HbF, consisting of two α and two γ subunits ($\alpha_2\gamma_2$), whereas maternal erythrocytes contain HbA ($\alpha_2\beta_2$).

(a) Which hemoglobin has a higher affinity for oxygen under physiological conditions, HbA or HbF? Explain.

(b) What is the physiological significance of the different O_2 affinities?

(c) When all the BPG is carefully removed from samples of HbA and HbF, the measured O_2-saturation curves (and consequently the O_2 affinities) are displaced to the left. However, HbA now has a greater affinity for oxygen than does HbF. When BPG is reintroduced, the O_2-saturation curves return to normal, as shown in the graph. What is the effect of BPG on the O_2 affinity of hemoglobin? How can the above information be used to explain the different O_2 affinities of fetal and maternal hemoglobin?



9. Hemoglobin Variants There are almost 500 naturally occurring variants of hemoglobin. Most are the result of a single amino acid substitution in a globin polypeptide chain. Some variants produce clinical illness, though not all variants have deleterious effects. A brief sample follows.

HbS (sickle cell Hb): substitutes a Val for a Glu on the surface
Hb Cowtown: eliminates an ion pair involved in T-state stabilization
Hb Memphis: substitutes one uncharged polar residue for another of similar size on the surface
Hb Bibba: substitutes a Pro for a Leu involved in an α helix
Hb Milwaukee: substitutes a Glu for a Val
Hb Providence: substitutes an Asn for a Lys that normally projects into the central cavity of the tetramer
Hb Philly: substitutes a Phe for a Tyr, disrupting hydrogen bonding at the $\alpha_1\beta_1$ interface

Explain your choices for each of the following:

(a) The Hb variant *least* likely to cause pathological symptoms.

(b) The variant(s) most likely to show pI values different from that of HbA on an isoelectric focusing gel.

(c) The variant(s) most likely to show a decrease in BPG binding and an increase in the overall affinity of the hemoglobin for oxygen.

10. Oxygen Binding and Hemoglobin Structure A team of biochemists uses genetic engineering to modify the interface region between hemoglobin subunits. The resulting hemoglobin variants exist in solution primarily as $\alpha\beta$ dimers (few, if any, $\alpha_2\beta_2$ tetramers form). Are these variants likely to bind oxygen more weakly or more tightly? Explain your answer.

11. Reversible (but Tight) Binding to an Antibody An antibody binds to an antigen with a K_d of 5×10^{-8} M. At what concentration of antigen will Y be (a) 0.2, (b) 0.5, (c) 0.6, (d) 0.8?

12. Using Antibodies to Probe Structure-Function Relationships in Proteins A monoclonal antibody binds to

G-actin but not to F-actin. What does this tell you about the epitope recognized by the antibody?

13. The Immune System and Vaccines A host organism needs time, often days, to mount an immune response against a new antigen, but memory cells permit a rapid response to pathogens previously encountered. A vaccine to protect against a particular viral infection often consists of weakened or killed virus or isolated proteins from a viral protein coat. When injected into a person, the vaccine generally does not cause an infection and illness, but it effectively "teaches" the immune system what the viral particles look like, stimulating the production of memory cells. On subsequent infection, these cells can bind to the virus and trigger a rapid immune response. Some pathogens, including HIV, have developed mechanisms to evade the immune system, making it difficult or impossible to develop effective vaccines against them. What strategy could a pathogen use to evade the immune system? Assume that a host's antibodies and/or T-cell receptors are available to bind to any structure that might appear on the surface of a pathogen and that, once bound, the pathogen is destroyed.

14. How We Become a "Stiff" When a vertebrate dies, its muscles stiffen as they are deprived of ATP, a state called rigor mortis. Using your knowledge of the catalytic cycle of myosin in muscle contraction, explain the molecular basis of the rigor state.

15. Sarcomeres from Another Point of View The symmetry of thick and thin filaments in a sarcomere is such that six thin filaments ordinarily surround each thick filament in a hexagonal array. Draw a cross section (transverse cut) of a myofibril at the following points: (a) at the M line; (b) through the I band; (c) through the dense region of the A band; (d) through the less dense region of the A band, adjacent to the M line (see Fig. 5-29b, c).

Biochemistry Online

16. Lysozyme and Antibodies To fully appreciate how proteins function in a cell, it is helpful to have a three-dimensional view of how proteins interact with other cellular components. Fortunately, this is possible using Web-based protein databases and three-dimensional molecular viewing utilities such as JSmol, a free and user-friendly molecular viewer that is compatible with most browsers and operating systems.

In this exercise, you will examine the interactions between the enzyme lysozyme (Chapter 4) and the Fab portion of the anti-lysozyme antibody. Use the PDB identifier 1FDL to explore the structure of the IgG1 Fab fragment–lysozyme complex (antibody-antigen complex). To answer the following questions, use the information on the Structure Summary page at the Protein Data Bank (www.pdb.org), and view the structure using JSmol or a similar viewer.

(a) Which chains in the three-dimensional model correspond to the antibody fragment and which correspond to the antigen, lysozyme?

(b) What type of secondary structure predominates in this Fab fragment?

(c) How many amino acid residues are in the heavy and light chains of the Fab fragment? In lysozyme? Estimate the percentage of the lysozyme that interacts with the antigen-binding site of the antibody fragment.

(d) Identify the specific amino acid residues in lysozyme and in the variable regions of the Fab heavy and light chains that are situated at the antigen-antibody interface. Are the residues contiguous in the primary sequence of the polypeptide chains?

17. Exploring Antibodies in the Protein Data Bank Use the PDB Molecule of the Month article at www.rcsb.org/pdb/101/motm.do?momID=21 to complete the following exercises.

(a) How many specific antigen-binding sites are there on the first immunoglobulin image on the Web page (image derived from PDB ID 1IGT)?

(b) When a virus enters your lungs, how long does it take for you to produce one or more antibodies that bind to it?

(c) Approximately how many types of different antibodies are present in your blood?

(d) Explore the structure of the immunoglobulin molecule (PDB ID 1IGT) on the Web page by clicking the link in the article or by going directly to www.rcsb.org/pdb/explore/explore.do?structureId=1igt. Use one of the structure viewers provided on the PDB site to create a ribbon structure for this immunoglobulin. Identify the two light chains and two heavy chains, and give them different colors.

Data Analysis Problem

18. Protein Function During the 1980s, the structures of actin and myosin were known only at the resolution shown in Figure 5-28a, b. Although researchers knew that the S1 portion of myosin bound to actin and hydrolyzed ATP, there was a substantial debate about where in the myosin molecule the contractile force was generated. At the time, two competing models were proposed for the mechanism of force generation in myosin.

In the "hinge" model, S1 bound to actin, but the pulling force was generated by contraction of the "hinge region" in the myosin tail. The hinge region is in the heavy meromyosin portion of the myosin molecule, near where trypsin cleaves off light meromyosin (see Fig. 5-27b); this is roughly the point labeled "Two supercoiled α helices" in Figure 5-27a. In the "S1" model, the pulling force was generated in the S1 "head" itself and the tail was just for structural support.

Many experiments were performed but provided no conclusive evidence. Then, in 1987, James Spudich and his colleagues at Stanford University published a study that, although not conclusive, went a long way toward resolving this controversy.

Recombinant DNA techniques were not sufficiently developed to address this issue in vivo, so Spudich and colleagues used an interesting in vitro motility assay. The alga *Nitella* has extremely long cells, often several centimeters long and about 1 mm in diameter. These cells have actin fibers that run along their long axes, and the cells can be cut open along their length to expose the actin fibers. Spudich and his group had observed that plastic beads coated with myosin would "walk" along these fibers in the presence of ATP, just as myosin would do in contracting muscle.

For these experiments, the researchers used a more well-defined method for attaching the myosin to the beads. The "beads" were clumps of killed bacterial (*Staphylococcus aureus*) cells. These cells have a protein on their surface that binds to the Fc region of antibody molecules (Fig. 5-21a). The antibodies, in turn, bind to several (unknown) places along the tail of the myosin molecule. When bead-antibody-myosin complexes were prepared with intact myosin molecules, they would move along *Nitella* actin fibers in the presence of ATP.

(a) Sketch a diagram showing what a bead-antibody-myosin complex might look like at the molecular level.

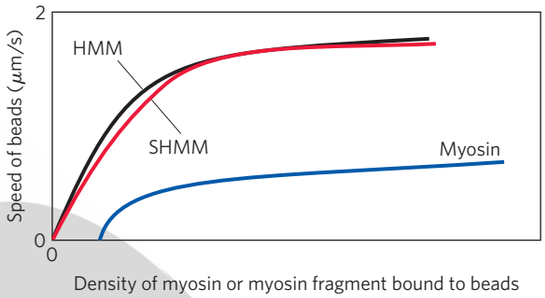
(b) Why was ATP required for the beads to move along the actin fibers?

(c) Spudich and coworkers used antibodies that bound to the myosin tail. Why would this experiment have failed if they had used an antibody that bound to the part of S1 that normally bound to actin? Why would this experiment have failed if they had used an antibody that bound to actin?

To help focus on the part of myosin responsible for force production, Spudich and colleagues used trypsin to produce two partial myosin molecules (Fig. 5-27b): (1) heavy meromyosin (HMM), made by briefly digesting myosin with trypsin; HMM consists of S1 and the part of the tail that includes the hinge; and (2) short heavy meromyosin (SHMM), made from a more extensive digestion of HMM with trypsin; SHMM consists of S1 and a shorter part of the tail that does not include the hinge. Brief digestion of myosin with trypsin produces HMM and light meromyosin, by cleavage of a single specific peptide bond in the myosin molecule.

(d) Why might trypsin attack this peptide bond first rather than other peptide bonds in myosin?

Spudich and colleagues prepared bead-antibody-myosin complexes with varying amounts of myosin, HMM, and SHMM and measured their speed of movement along *Nitella* actin fibers in the presence of ATP. The graph below sketches their results.



(e) Which model ("S1" or "hinge") is consistent with these results? Explain your reasoning.

(f) Provide a plausible explanation for the increased speed of the beads with increasing myosin density.

(g) Provide a plausible explanation for the plateauing of the speed of the beads at high myosin density.

The more extensive trypsin digestion required to produce SHMM had a side effect: another specific cleavage of the myosin polypeptide backbone in addition to the cleavage in the tail. This second cleavage was in the S1 head.

(h) Why is it surprising that SHMM was still capable of moving beads along the actin fibers?

(i) As it turns out, the tertiary structure of the S1 head remains intact in SHMM. Provide a plausible explanation of how the protein remains intact and functional even though the polypeptide backbone has been cleaved and is no longer continuous.

Reference

Hynes, T.R., S.M. Block, B.T. White, and J.A. Spudich. 1987. Movement of myosin fragments in vitro: domains involved in force production. *Cell* 48:953–963.

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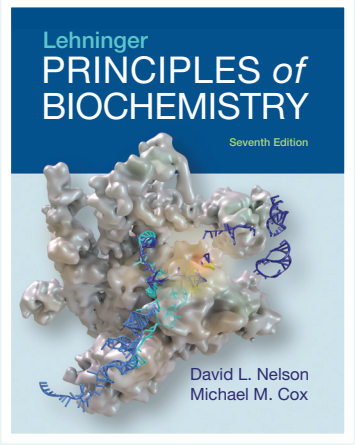

INSIDE: SAMPLE CHAPTER 5 PROTEIN FUNCTION

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