

chapter 13

PRINCIPLES OF BIOENERGETICS

- 13.1 Bioenergetics and Thermodynamics 490
- 13.2 Phosphoryl Group Transfers and ATP 496
- 13.3 Biological Oxidation-Reduction Reactions 507

The total energy of the universe is constant; the total entropy is continually increasing.

—Rudolf Clausius, *The Mechanical Theory of Heat with Its Applications to the Steam-Engine and to the Physical Properties of Bodies*, 1865 (trans. 1867)

The isomorphism of entropy and information establishes a link between the two forms of power: the power to do and the power to direct what is done.

—François Jacob, *La logique du vivant: une histoire de l'hérédité* (The Logic of Life: A History of Heredity), 1970

Living cells and organisms must perform work to stay alive, to grow, and to reproduce. The ability to harness energy and to channel it into biological work is a fundamental property of all living organisms; it must have been acquired very early in cellular evolution. Modern organisms carry out a remarkable variety of energy transductions, conversions of one form of energy to another. They use the chemical energy in fuels to bring about the synthesis of complex, highly ordered macromolecules from simple precursors. They also convert the chemical energy of fuels into concentration gradients and electrical gradients, into motion and heat, and, in a few organisms such as fireflies and some deep-sea fish, into light. Photosynthetic organisms transduce light energy into all these other forms of energy.

The chemical mechanisms that underlie biological energy transductions have fascinated and challenged biologists for centuries. Antoine Lavoisier, before he lost his head in the French Revolution, recognized that animals somehow transform chemical fuels (foods) into

heat and that this process of respiration is essential to life. He observed that

... in general, respiration is nothing but a slow combustion of carbon and hydrogen, which is entirely similar to that which occurs in a lighted lamp or candle, and that, from this point of view, animals that respire are true combustible bodies that burn

and consume themselves ... One may say that this analogy between combustion and respiration has not escaped the notice of the poets, or rather the philosophers of antiquity, and which they had expounded and interpreted. This fire stolen from heaven, this torch of Prometheus, does not only represent an ingenious and poetic idea, it is a faithful picture of the operations of nature, at least for animals that breathe; one may therefore say, with the ancients, that the torch of life lights itself at the moment the infant breathes for the first time, and it does not extinguish itself except at death.*

In this century, biochemical studies have revealed much of the chemistry underlying that “torch of life.” Biological energy transductions obey the same physical laws that govern all other natural processes. It is therefore essential for a student of biochemistry to understand these laws and how they apply to the flow of energy in the biosphere. In this chapter we first review the laws of thermodynamics and the quantitative relationships among free energy, enthalpy, and entropy. We then describe the special role of ATP in biological



Antoine Lavoisier,
1743–1794

*From a memoir by Armand Seguin and Antoine Lavoisier, dated 1789, quoted in Lavoisier, A. (1862) *Oeuvres de Lavoisier*; Imprimerie Impériale, Paris.

energy exchanges. Finally, we consider the importance of oxidation-reduction reactions in living cells, the energetics of electron-transfer reactions, and the electron carriers commonly employed as cofactors of the enzymes that catalyze these reactions.

13.1 Bioenergetics and Thermodynamics

Bioenergetics is the quantitative study of the energy transductions that occur in living cells and of the nature and function of the chemical processes underlying these transductions. Although many of the principles of thermodynamics have been introduced in earlier chapters and may be familiar to you, a review of the quantitative aspects of these principles is useful here.

Biological Energy Transformations Obey the Laws of Thermodynamics

Many quantitative observations made by physicists and chemists on the interconversion of different forms of energy led, in the nineteenth century, to the formulation of two fundamental laws of thermodynamics. The first law is the principle of the conservation of energy: *for any physical or chemical change, the total amount of energy in the universe remains constant; energy may change form or it may be transported from one region to another, but it cannot be created or destroyed.* The second law of thermodynamics, which can be stated in several forms, says that the universe always tends toward increasing disorder: *in all natural processes, the entropy of the universe increases.*

Living organisms consist of collections of molecules much more highly organized than the surrounding materials from which they are constructed, and organisms maintain and produce order, seemingly oblivious to the second law of thermodynamics. But living organisms do

not violate the second law; they operate strictly within it. To discuss the application of the second law to biological systems, we must first define those systems and their surroundings.

The reacting system is the collection of matter that is undergoing a particular chemical or physical process; it may be an organism, a cell, or two reacting compounds. The reacting system and its surroundings together constitute the universe. In the laboratory, some chemical or physical processes can be carried out in isolated or closed systems, in which no material or energy is exchanged with the surroundings. Living cells and organisms, however, are open systems, exchanging both material and energy with their surroundings; living systems are never at equilibrium with their surroundings, and the constant transactions between system and surroundings explain how organisms can create order within themselves while operating within the second law of thermodynamics.

In Chapter 1 (p. 23) we defined three thermodynamic quantities that describe the energy changes occurring in a chemical reaction:

Gibbs free energy, G , expresses the amount of energy capable of doing work during a reaction at constant temperature and pressure. When a reaction proceeds with the release of free energy (that is, when the system changes so as to possess less free energy), the free-energy change, ΔG , has a negative value and the reaction is said to be exergonic. In endergonic reactions, the system gains free energy and ΔG is positive.

Enthalpy, H , is the heat content of the reacting system. It reflects the number and kinds of chemical bonds in the reactants and products. When a chemical reaction releases heat, it is said to be exothermic; the heat content of the products is less than that of the reactants and ΔH has, by convention, a negative value. Reacting systems that take up heat from their surroundings are endothermic and have positive values of ΔH .

Entropy, S , is a quantitative expression for the randomness or disorder in a system (see Box 1-3). When the products of a reaction are less complex and more disordered than the reactants, the reaction is said to proceed with a gain in entropy.

The units of ΔG and ΔH are joules/mole or calories/mole (recall that 1 cal = 4.184 J); units of entropy are joules/mole · Kelvin (J/mol · K) (Table 13-1).

Under the conditions existing in biological systems (including constant temperature and pressure), changes in free energy, enthalpy, and entropy are related to each other quantitatively by the equation

$$\Delta G = \Delta H - T\Delta S \quad (13-1)$$

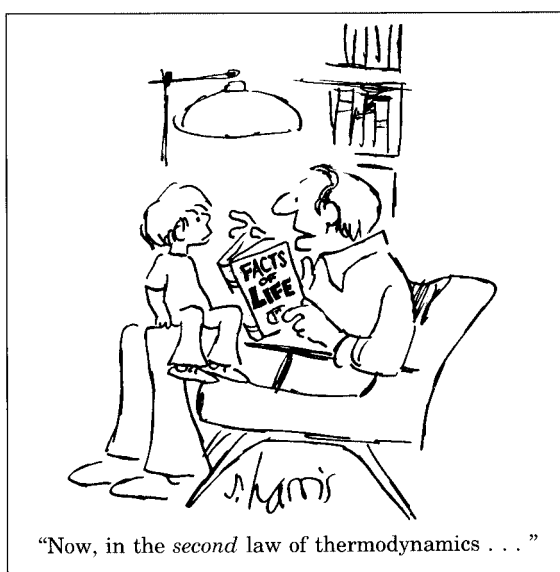


TABLE 13–1 Some Physical Constants and Units Used in Thermodynamics

Boltzmann constant, k = 1.381×10^{-23} J/K
Avogadro's number, N = 6.022×10^{23} mol ⁻¹
Faraday constant, \mathcal{F} = 96,480 J/V · mol
Gas constant, R = 8.315 J/mol · K (= 1.987 cal/mol · K)
Units of ΔG and ΔH are J/mol (or cal/mol)
Units of ΔS are J/mol · K (or cal/mol · K)
1 cal = 4.184 J
Units of absolute temperature, T , are Kelvin, K
25 °C = 298 K
At 25 °C, RT = 2.479 kJ/mol (= 0.592 kcal/mol)

in which ΔG is the change in Gibbs free energy of the reacting system, ΔH is the change in enthalpy of the system, T is the absolute temperature, and ΔS is the change in entropy of the system. By convention, ΔS has a positive sign when entropy increases and ΔH , as noted above, has a negative sign when heat is released by the system to its surroundings. Either of these conditions, which are typical of favorable processes, tend to make ΔG negative. In fact, ΔG of a spontaneously reacting system is always negative.

The second law of thermodynamics states that the entropy of the universe increases during all chemical and physical processes, but it does not require that the entropy increase take place in the reacting system itself. The order produced within cells as they grow and divide is more than compensated for by the disorder they create in their surroundings in the course of growth and division (see Box 1–3, case 2). In short, living organisms preserve their internal order by taking from the surroundings free energy in the form of nutrients or sunlight, and returning to their surroundings an equal amount of energy as heat and entropy.

Cells Require Sources of Free Energy

Cells are isothermal systems—they function at essentially constant temperature (they also function at constant pressure). Heat flow is not a source of energy for cells, because heat can do work only as it passes to a zone or object at a lower temperature. The energy that cells can and must use is free energy, described by the Gibbs free-energy function G , which allows prediction of the direction of chemical reactions, their exact equilibrium position, and the amount of work they can in theory perform at constant temperature and pressure. Heterotrophic cells acquire free energy from nutrient molecules, and photosynthetic cells acquire it from absorbed solar radiation. Both kinds of cells transform this

free energy into ATP and other energy-rich compounds capable of providing energy for biological work at constant temperature.

The Standard Free-Energy Change Is Directly Related to the Equilibrium Constant

The composition of a reacting system (a mixture of chemical reactants and products) tends to continue changing until equilibrium is reached. At the equilibrium concentration of reactants and products, the rates of the forward and reverse reactions are exactly equal and no further net change occurs in the system. The concentrations of reactants and products at equilibrium define the equilibrium constant, K_{eq} (p. 26). In the general reaction $aA + bB \rightleftharpoons cC + dD$, where a , b , c , and d are the number of molecules of A, B, C, and D participating, the equilibrium constant is given by

$$K_{eq} = \frac{[C]^c[D]^d}{[A]^a[B]^b}$$
 (13–2)

where [A], [B], [C], and [D] are the molar concentrations of the reaction components at the point of equilibrium.

When a reacting system is not at equilibrium, the tendency to move toward equilibrium represents a driving force, the magnitude of which can be expressed as the free-energy change for the reaction, ΔG . Under standard conditions (298 K = 25 °C), when reactants and products are initially present at 1 M concentrations or, for gases, at partial pressures of 101.3 kilopascals (kPa), or 1 atm, the force driving the system toward equilibrium is defined as the standard free-energy change, ΔG° . By this definition, the standard state for reactions that involve hydrogen ions is $[H^+] = 1$ M, or pH 0. Most biochemical reactions, however, occur in well-buffered aqueous solutions near pH 7; both the pH and the concentration of water (55.5 M) are essentially constant. For convenience of calculations, biochemists therefore define a different standard state, in which the concentration of H^+ is 10^{-7} M (pH 7) and that of water is 55.5 M; for reactions that involve Mg^{2+} (including most in which ATP is a reactant), its concentration in solution is commonly taken to be constant at 1 mM. Physical constants based on this biochemical standard state are called **standard transformed constants** and are written with a prime (such as $\Delta G'^\circ$ and K'_{eq}) to distinguish them from the untransformed constants used by chemists and physicists. (Notice that most other textbooks use the symbol $\Delta G'^\circ$ rather than ΔG° . Our use of $\Delta G'^\circ$, recommended by an international committee of chemists and biochemists, is intended to emphasize that the transformed free energy G' is the criterion for equilibrium.) By convention, when H_2O , H^+ , and/or Mg^{2+} are reactants or products, their concentrations are not included in equations such as Equation 13–2 but are instead incorporated into the constants K'_{eq} and $\Delta G'^\circ$.

Just as K'_{eq} is a physical constant characteristic for each reaction, so too is $\Delta G'^{\circ}$ a constant. As we noted in Chapter 6, there is a simple relationship between K'_{eq} and $\Delta G'^{\circ}$:

$$\Delta G'^{\circ} = -RT \ln K'_{\text{eq}}$$

The standard free-energy change of a chemical reaction is simply an alternative mathematical way of expressing its equilibrium constant. Table 13–2 shows the relationship between $\Delta G'^{\circ}$ and K'_{eq} . If the equilibrium constant for a given chemical reaction is 1.0, the standard free-energy change of that reaction is 0.0 (the natural logarithm of 1.0 is zero). If K'_{eq} of a reaction is greater than 1.0, its $\Delta G'^{\circ}$ is negative. If K'_{eq} is less than 1.0, $\Delta G'^{\circ}$ is positive. Because the relationship between $\Delta G'^{\circ}$ and K'_{eq} is exponential, relatively small changes in $\Delta G'^{\circ}$ correspond to large changes in K'_{eq} .

It may be helpful to think of the standard free-energy change in another way. $\Delta G'^{\circ}$ is the difference between the free-energy content of the products and the free-energy content of the reactants, under standard conditions. When $\Delta G'^{\circ}$ is negative, the products contain less free energy than the reactants and the reaction will proceed spontaneously under standard conditions; all chemical reactions tend to go in the direction that results in a decrease in the free energy of the system. A positive value of $\Delta G'^{\circ}$ means that the products of the reaction contain more free energy than the reactants, and this reaction will tend to go in the reverse direction if we start with 1.0 M concentrations of all components (standard conditions). Table 13–3 summarizes these points.

TABLE 13–2 Relationship between the Equilibrium Constants and Standard Free-Energy Changes of Chemical Reactions

K'_{eq}	$\Delta G'^{\circ}$	
	(kJ/mol)	(kcal/mol)*
10^3	−17.1	−4.1
10^2	−11.4	−2.7
10^1	−5.7	−1.4
1	0.0	0.0
10^{-1}	5.7	1.4
10^{-2}	11.4	2.7
10^{-3}	17.1	4.1
10^{-4}	22.8	5.5
10^{-5}	28.5	6.8
10^{-6}	34.2	8.2

*Although joules and kilojoules are the standard units of energy and are used throughout this text, biochemists sometimes express $\Delta G'^{\circ}$ values in kilocalories per mole. We have therefore included values in both kilojoules and kilocalories in this table and in Tables 13–4 and 13–6. To convert kilojoules to kilocalories, divide the number of kilojoules by 4.184.

TABLE 13–3 Relationships among K'_{eq} , $\Delta G'^{\circ}$, and the Direction of Chemical Reactions under Standard Conditions

When K'_{eq} is . . .	$\Delta G'^{\circ}$ is . . .	Starting with all components at 1 M, the reaction . . .
>1.0	negative	proceeds forward
1.0	zero	is at equilibrium
<1.0	positive	proceeds in reverse

As an example, let's make a simple calculation of the standard free-energy change of the reaction catalyzed by the enzyme phosphoglucomutase:



Chemical analysis shows that whether we start with, say, 20 mM glucose 1-phosphate (but no glucose 6-phosphate) or with 20 mM glucose 6-phosphate (but no glucose 1-phosphate), the final equilibrium mixture at 25 °C and pH 7.0 will be the same: 1 mM glucose 1-phosphate and 19 mM glucose 6-phosphate. (Remember that enzymes do not affect the point of equilibrium of a reaction; they merely hasten its attainment.) From these data we can calculate the equilibrium constant:

$$K'_{\text{eq}} = \frac{[\text{glucose 6-phosphate}]}{[\text{glucose 1-phosphate}]} = \frac{19 \text{ mM}}{1 \text{ mM}} = 19$$

From this value of K'_{eq} we can calculate the standard free-energy change:

$$\begin{aligned} \Delta G'^{\circ} &= -RT \ln K'_{\text{eq}} \\ &= -(8.315 \text{ J/mol} \cdot \text{K})(298 \text{ K})(\ln 19) \\ &= -7.3 \text{ kJ/mol} \end{aligned}$$

Because the standard free-energy change is negative, when the reaction starts with 1.0 M glucose 1-phosphate and 1.0 M glucose 6-phosphate, the conversion of glucose 1-phosphate to glucose 6-phosphate proceeds with a loss (release) of free energy. For the reverse reaction (the conversion of glucose 6-phosphate to glucose 1-phosphate), $\Delta G'^{\circ}$ has the same magnitude but the opposite sign.

Table 13–4 gives the standard free-energy changes for some representative chemical reactions. Note that hydrolysis of simple esters, amides, peptides, and glycosides, as well as rearrangements and eliminations, proceed with relatively small standard free-energy changes, whereas hydrolysis of acid anhydrides is accompanied by relatively large decreases in standard free energy. The complete oxidation of organic compounds such as glucose or palmitate to CO_2 and H_2O , which in cells requires many steps, results in very large decreases in standard free energy. However, standard free-energy

TABLE 13–4 Standard Free-Energy Changes of Some Chemical Reactions at pH 7.0 and 25 °C (298 K)

Reaction type	$\Delta G'^{\circ}$	
	(kJ/mol)	(kcal/mol)
Hydrolysis reactions		
Acid anhydrides		
Acetic anhydride + H ₂ O \longrightarrow 2 acetate	−91.1	−21.8
ATP + H ₂ O \longrightarrow ADP + P _i	−30.5	−7.3
ATP + H ₂ O \longrightarrow AMP + PP _i	−45.6	−10.9
PP _i + H ₂ O \longrightarrow 2P _i	−19.2	−4.6
UDP-glucose + H ₂ O \longrightarrow UMP + glucose 1-phosphate	−43.0	−10.3
Esters		
Ethyl acetate + H ₂ O \longrightarrow ethanol + acetate	−19.6	−4.7
Glucose 6-phosphate + H ₂ O \longrightarrow glucose + P _i	−13.8	−3.3
Amides and peptides		
Glutamine + H ₂ O \longrightarrow glutamate + NH ₄ ⁺	−14.2	−3.4
Glycylglycine + H ₂ O \longrightarrow 2 glycine	−9.2	−2.2
Glycosides		
Maltose + H ₂ O \longrightarrow 2 glucose	−15.5	−3.7
Lactose + H ₂ O \longrightarrow glucose + galactose	−15.9	−3.8
Rearrangements		
Glucose 1-phosphate \longrightarrow glucose 6-phosphate	−7.3	−1.7
Fructose 6-phosphate \longrightarrow glucose 6-phosphate	−1.7	−0.4
Elimination of water		
Malate \longrightarrow fumarate + H ₂ O	3.1	0.8
Oxidations with molecular oxygen		
Glucose + 6O ₂ \longrightarrow 6CO ₂ + 6H ₂ O	−2,840	−686
Palmitate + 23O ₂ \longrightarrow 16CO ₂ + 16H ₂ O	−9,770	−2,338

changes such as those in Table 13–4 indicate how much free energy is available from a reaction under *standard conditions*. To describe the energy released under the conditions existing in cells, an expression for the *actual* free-energy change is essential.

Actual Free-Energy Changes Depend on Reactant and Product Concentrations

We must be careful to distinguish between two different quantities: the free-energy change, ΔG , and the standard free-energy change, $\Delta G'^{\circ}$. Each chemical reaction has a characteristic standard free-energy change, which may be positive, negative, or zero, depending on the equilibrium constant of the reaction. The standard free-

energy change tells us in which direction and how far a given reaction must go to reach equilibrium *when the initial concentration of each component is 1.0 M*, the pH is 7.0, the temperature is 25 °C, and the pressure is 101.3 kPa. Thus $\Delta G'^{\circ}$ is a constant: it has a characteristic, unchanging value for a given reaction. But the *actual* free-energy change, ΔG , is a function of reactant and product concentrations and of the temperature prevailing during the reaction, which will not necessarily match the standard conditions as defined above. Moreover, the ΔG of any reaction proceeding spontaneously toward its equilibrium is always negative, becomes less negative as the reaction proceeds, and is zero at the point of equilibrium, indicating that no more work can be done by the reaction.

ΔG and $\Delta G'^{\circ}$ for any reaction $A + B \rightleftharpoons C + D$ are related by the equation

$$\Delta G = \Delta G'^{\circ} + RT \ln \frac{[C][D]}{[A][B]} \quad (13-3)$$

in which the terms in red are those *actually prevailing* in the system under observation. The concentration terms in this equation express the effects commonly called mass action, and the term $[C][D]/[A][B]$ is called the **mass-action ratio, Q** . As an example, let us suppose that the reaction $A + B \rightleftharpoons C + D$ is taking place at the standard conditions of temperature (25 °C) and pressure (101.3 kPa) but that the concentrations of A, B, C, and D are *not* equal and none of the components is present at the standard concentration of 1.0 M. To determine the actual free-energy change, ΔG , under these nonstandard conditions of concentration as the reaction proceeds from left to right, we simply enter the *actual* concentrations of A, B, C, and D in Equation 13-3; the values of R , T , and $\Delta G'^{\circ}$ are the standard values. ΔG is negative and approaches zero as the reaction proceeds because the actual concentrations of A and B decrease and the concentrations of C and D increase. Notice that when a reaction is at equilibrium—when there is no force driving the reaction in either direction and ΔG is zero—Equation 13-3 reduces to

$$0 = \Delta G = \Delta G'^{\circ} + RT \ln \frac{[C]_{\text{eq}}[D]_{\text{eq}}}{[A]_{\text{eq}}[B]_{\text{eq}}}$$

or

$$\Delta G'^{\circ} = -RT \ln K'_{\text{eq}}$$

which is the equation relating the standard free-energy change and equilibrium constant given earlier.

The criterion for spontaneity of a reaction is the value of ΔG , not $\Delta G'^{\circ}$. A reaction with a positive $\Delta G'^{\circ}$ can go in the forward direction *if ΔG is negative*. This is possible if the term $RT \ln ([\text{products}]/[\text{reactants}])$ in Equation 13-3 is negative and has a larger absolute value than $\Delta G'^{\circ}$. For example, the immediate removal of the products of a reaction can keep the ratio $[\text{products}]/[\text{reactants}]$ well below 1, such that the term $RT \ln ([\text{products}]/[\text{reactants}])$ has a large, negative value.

$\Delta G'^{\circ}$ and ΔG are expressions of the *maximum* amount of free energy that a given reaction can *theoretically* deliver—an amount of energy that could be realized only if a perfectly efficient device were available to trap or harness it. Given that no such device is possible (some free energy is always lost to entropy during any process), the amount of work done by the reaction at constant temperature and pressure is always less than the theoretical amount.

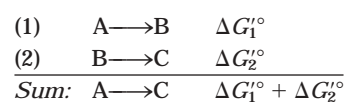
Another important point is that some thermodynamically favorable reactions (that is, reactions for which $\Delta G'^{\circ}$ is large and negative) do not occur at meas-

urable rates. For example, combustion of firewood to CO_2 and H_2O is very favorable thermodynamically, but firewood remains stable for years because the activation energy (see Figs 6-2 and 6-3) for the combustion reaction is higher than the energy available at room temperature. If the necessary activation energy is provided (with a lighted match, for example), combustion will begin, converting the wood to the more stable products CO_2 and H_2O and releasing energy as heat and light. The heat released by this exothermic reaction provides the activation energy for combustion of neighboring regions of the firewood; the process is self-perpetuating.

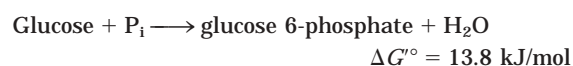
In living cells, reactions that would be extremely slow *if uncatalyzed* are caused to proceed, not by supplying additional heat but by lowering the activation energy with an enzyme. An enzyme provides an alternative reaction pathway with a lower activation energy than the uncatalyzed reaction, so that at room temperature a large fraction of the substrate molecules have enough thermal energy to overcome the activation barrier, and the reaction rate increases dramatically. *The free-energy change for a reaction is independent of the pathway by which the reaction occurs*; it depends only on the nature and concentration of the initial reactants and the final products. Enzymes cannot, therefore, change equilibrium constants; but they can and do increase the *rate* at which a reaction proceeds in the direction dictated by thermodynamics.

Standard Free-Energy Changes Are Additive

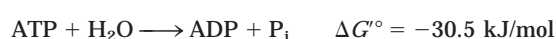
In the case of two sequential chemical reactions, $A \rightleftharpoons B$ and $B \rightleftharpoons C$, each reaction has its own equilibrium constant and each has its characteristic standard free-energy change, $\Delta G'_1{}^{\circ}$ and $\Delta G'_2{}^{\circ}$. As the two reactions are sequential, B cancels out to give the overall reaction $A \rightleftharpoons C$, which has its own equilibrium constant and thus its own standard free-energy change, $\Delta G'_{\text{total}}{}^{\circ}$. *The $\Delta G'^{\circ}$ values of sequential chemical reactions are additive*. For the overall reaction $A \rightleftharpoons C$, $\Delta G'_{\text{total}}{}^{\circ}$ is the sum of the individual standard free-energy changes, $\Delta G'_1{}^{\circ}$ and $\Delta G'_2{}^{\circ}$, of the two reactions: $\Delta G'_{\text{total}}{}^{\circ} = \Delta G'_1{}^{\circ} + \Delta G'_2{}^{\circ}$.



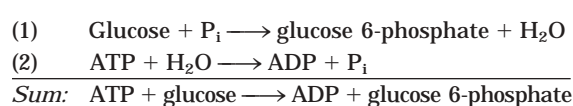
This principle of bioenergetics explains how a thermodynamically unfavorable (endergonic) reaction can be driven in the forward direction by coupling it to a highly exergonic reaction through a common intermediate. For example, the synthesis of glucose 6-phosphate is the first step in the utilization of glucose by many organisms:



The positive value of $\Delta G'^{\circ}$ predicts that under standard conditions the reaction will tend not to proceed spontaneously in the direction written. Another cellular reaction, the hydrolysis of ATP to ADP and P_i , is very exergonic:



These two reactions share the common intermediates P_i and H_2O and may be expressed as sequential reactions:



The overall standard free-energy change is obtained by adding the $\Delta G'^{\circ}$ values for individual reactions:

$$\Delta G'^{\circ} = 13.8 \text{ kJ/mol} + (-30.5 \text{ kJ/mol}) = -16.7 \text{ kJ/mol}$$

The overall reaction is exergonic. In this case, energy stored in ATP is used to drive the synthesis of glucose 6-phosphate, even though its formation from glucose and inorganic phosphate (P_i) is endergonic. The *pathway* of glucose 6-phosphate formation by phosphoryl transfer from ATP is different from reactions (1) and (2) above, but the net result is the same as the sum of the two reactions. In thermodynamic calculations, all that matters is the state of the system at the beginning of the process and its state at the end; the route between the initial and final states is immaterial.

We have said that $\Delta G'^{\circ}$ is a way of expressing the equilibrium constant for a reaction. For reaction (1) above,

$$K'_{\text{eq}_1} = \frac{[\text{glucose 6-phosphate}]}{[\text{glucose}][P_i]} = 3.9 \times 10^{-3} \text{ M}^{-1}$$

Notice that H_2O is not included in this expression, as its concentration (55.5 M) is assumed to remain unchanged by the reaction. The equilibrium constant for the hydrolysis of ATP is

$$K'_{\text{eq}_2} = \frac{[\text{ADP}][P_i]}{[\text{ATP}]} = 2.0 \times 10^5 \text{ M}$$

The equilibrium constant for the two coupled reactions is

$$\begin{aligned} K'_{\text{eq}_3} &= \frac{[\text{glucose 6-phosphate}][\text{ADP}][P_i]}{[\text{glucose}][P_i][\text{ATP}]} \\ &= (K'_{\text{eq}_1})(K'_{\text{eq}_2}) = (3.9 \times 10^{-3} \text{ M}^{-1})(2.0 \times 10^5 \text{ M}) \\ &= 7.8 \times 10^2 \end{aligned}$$

This calculation illustrates an important point about equilibrium constants: although the $\Delta G'^{\circ}$ values for two reactions that sum to a third are *additive*, the K'_{eq} for a reaction that is the sum of two reactions is the *product* of their individual K'_{eq} values. Equilibrium constants are *multiplicative*. By coupling ATP hydrolysis to glu-

cose 6-phosphate synthesis, the K'_{eq} for formation of glucose 6-phosphate has been raised by a factor of about 2×10^5 .

This common-intermediate strategy is employed by all living cells in the synthesis of metabolic intermediates and cellular components. Obviously, the strategy works only if compounds such as ATP are continuously available. In the following chapters we consider several of the most important cellular pathways for producing ATP.

SUMMARY 13.1 Bioenergetics and Thermodynamics

- Living cells constantly perform work. They require energy for maintaining their highly organized structures, synthesizing cellular components, generating electric currents, and many other processes.
- Bioenergetics is the quantitative study of energy relationships and energy conversions in biological systems. Biological energy transformations obey the laws of thermodynamics.
- All chemical reactions are influenced by two forces: the tendency to achieve the most stable bonding state (for which enthalpy, H , is a useful expression) and the tendency to achieve the highest degree of randomness, expressed as entropy, S . The net driving force in a reaction is ΔG , the free-energy change, which represents the net effect of these two factors: $\Delta G = \Delta H - T\Delta S$.
- The standard transformed free-energy change, $\Delta G'^{\circ}$, is a physical constant that is characteristic for a given reaction and can be calculated from the equilibrium constant for the reaction: $\Delta G'^{\circ} = -RT \ln K'_{\text{eq}}$.
- The actual free-energy change, ΔG , is a variable that depends on $\Delta G'^{\circ}$ and on the concentrations of reactants and products: $\Delta G = \Delta G'^{\circ} + RT \ln ([\text{products}]/[\text{reactants}])$.
- When ΔG is large and negative, the reaction tends to go in the forward direction; when ΔG is large and positive, the reaction tends to go in the reverse direction; and when $\Delta G = 0$, the system is at equilibrium.
- The free-energy change for a reaction is independent of the pathway by which the reaction occurs. Free-energy changes are additive; the net chemical reaction that results from successive reactions sharing a common intermediate has an overall free-energy change that is the sum of the ΔG values for the individual reactions.

13.2 Phosphoryl Group Transfers and ATP

Having developed some fundamental principles of energy changes in chemical systems, we can now examine the energy cycle in cells and the special role of ATP as the energy currency that links catabolism and anabolism (see Fig. 1–28). Heterotrophic cells obtain free energy in a chemical form by the catabolism of nutrient molecules, and they use that energy to make ATP from ADP and P_i . ATP then donates some of its chemical energy to endergonic processes such as the synthesis of metabolic intermediates and macromolecules from smaller precursors, the transport of substances across membranes against concentration gradients, and mechanical motion. This donation of energy from ATP generally involves the covalent participation of ATP in the reaction that is to be driven, with the eventual result that ATP is converted to ADP and P_i or, in some reactions, to AMP and 2 P_i . We discuss here the chemical basis for the large free-energy changes that accompany hydrolysis of ATP and other high-energy phosphate compounds, and we show that most cases of energy donation by ATP involve group transfer, not simple hydrolysis of ATP. To illustrate the range of energy transductions in which ATP provides the energy, we consider the synthesis of information-rich macromolecules, the transport of solutes across membranes, and motion produced by muscle contraction.

The Free-Energy Change for ATP Hydrolysis Is Large and Negative

Figure 13–1 summarizes the chemical basis for the relatively large, negative, standard free energy of hydrolysis of ATP. The hydrolytic cleavage of the terminal phosphoric acid anhydride (phosphoanhydride) bond in ATP separates one of the three negatively charged phosphates and thus relieves some of the electrostatic repulsion in ATP; the P_i (HPO_4^{2-}) released is stabilized by the formation of several resonance forms not possible in ATP; and ADP^{2-} , the other direct product of hydrolysis, immediately ionizes, releasing H^+ into a medium of very low $[H^+]$ ($\sim 10^{-7}$ M). Because the concentrations of the direct products of ATP hydrolysis are, in the cell, far below the concentrations at equilibrium (Table 13–5), mass action favors the hydrolysis reaction in the cell.

Although the hydrolysis of ATP is highly exergonic ($\Delta G^\circ = -30.5$ kJ/mol), the molecule is kinetically stable at pH 7 because the activation energy for ATP hydrolysis is relatively high. Rapid cleavage of the phosphoanhydride bonds occurs only when catalyzed by an enzyme.

The free-energy change for ATP hydrolysis is -30.5 kJ/mol under standard conditions, but the *actual* free energy of hydrolysis (ΔG) of ATP in living cells is very different: the cellular concentrations of ATP, ADP,

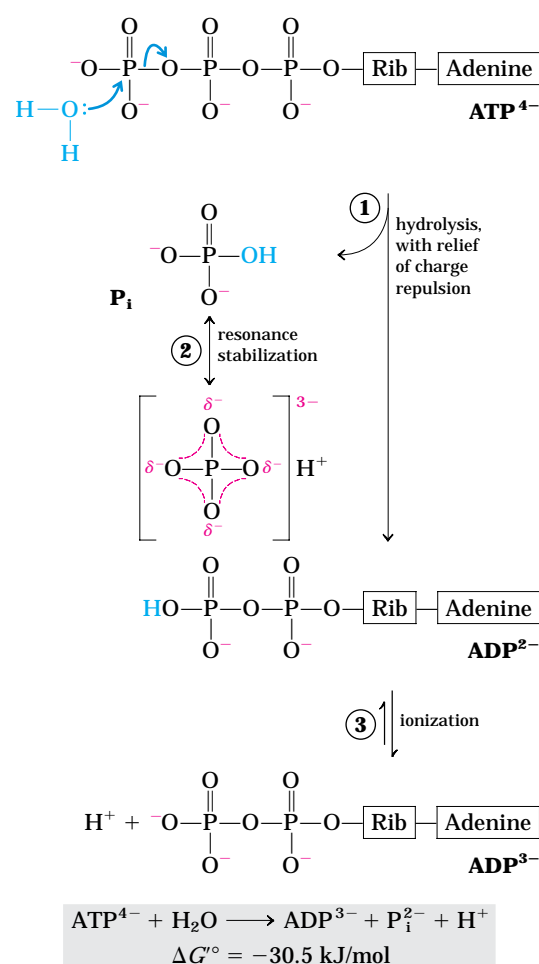


FIGURE 13–1 Chemical basis for the large free-energy change associated with ATP hydrolysis. ① The charge separation that results from hydrolysis relieves electrostatic repulsion among the four negative charges on ATP. ② The product inorganic phosphate (P_i) is stabilized by formation of a resonance hybrid, in which each of the four phosphorus–oxygen bonds has the same degree of double-bond character and the hydrogen ion is not permanently associated with any one of the oxygens. (Some degree of resonance stabilization also occurs in phosphates involved in ester or anhydride linkages, but fewer resonance forms are possible than for P_i .) ③ The product ADP^{2-} immediately ionizes, releasing a proton into a medium of very low $[H^+]$ (pH 7). A fourth factor (not shown) that favors ATP hydrolysis is the greater degree of solvation (hydration) of the products P_i and ADP relative to ATP, which further stabilizes the products relative to the reactants.

and P_i are not identical and are much lower than the 1.0 M of standard conditions (Table 13–5). Furthermore, Mg^{2+} in the cytosol binds to ATP and ADP (Fig. 13–2), and for most enzymatic reactions that involve ATP as phosphoryl group donor, the true substrate is $MgATP^{2-}$. The relevant ΔG° is therefore that for $MgATP^{2-}$ hydrolysis. Box 13–1 shows how ΔG for ATP hydrolysis in the intact erythrocyte can be calculated from the data in Table 13–5. In intact cells, ΔG for ATP hydrolysis, usually designated ΔG_p , is much more negative than

TABLE 13–5 Adenine Nucleotide, Inorganic Phosphate, and Phosphocreatine Concentrations in Some Cells

	Concentration (mM)*				
	ATP	ADP [†]	AMP	P _i	PCr
Rat hepatocyte	3.38	1.32	0.29	4.8	0
Rat myocyte	8.05	0.93	0.04	8.05	28
Rat neuron	2.59	0.73	0.06	2.72	4.7
Human erythrocyte	2.25	0.25	0.02	1.65	0
<i>E. coli</i> cell	7.90	1.04	0.82	7.9	0

*For erythrocytes the concentrations are those of the cytosol (human erythrocytes lack a nucleus and mitochondria). In the other types of cells the data are for the entire cell contents, although the cytosol and the mitochondria have very different concentrations of ADP. PCr is phosphocreatine, discussed on p. 489.

[†]This value reflects total concentration; the true value for free ADP may be much lower (see Box 13–1).

$\Delta G'^{\circ}$, ranging from -50 to -65 kJ/mol. ΔG_p is often called the **phosphorylation potential**. In the following discussions we use the standard free-energy change for ATP hydrolysis, because this allows comparison, on the same basis, with the energetics of other cellular reactions. Remember, however, that in living cells ΔG is the relevant quantity—for ATP hydrolysis and all other reactions—and may be quite different from $\Delta G'^{\circ}$.

Other Phosphorylated Compounds and Thioesters Also Have Large Free Energies of Hydrolysis

Phosphoenolpyruvate (Fig. 13–3) contains a phosphate ester bond that undergoes hydrolysis to yield the enol form of pyruvate, and this direct product can immediately tautomerize to the more stable keto form of pyruvate. Because the reactant (phosphoenolpyruvate) has only one form (enol) and the product (pyruvate) has two possible forms, the product is stabilized relative to the reactant. This is the greatest contributing factor to the high standard free energy of hydrolysis of phosphoenolpyruvate: $\Delta G'^{\circ} = -61.9$ kJ/mol.

Another three-carbon compound, 1,3-bisphosphoglycerate (Fig. 13–4), contains an anhydride bond between the carboxyl group at C-1 and phosphoric acid. Hydrolysis of this acyl phosphate is accompanied by a large, negative, standard free-energy change ($\Delta G'^{\circ} =$

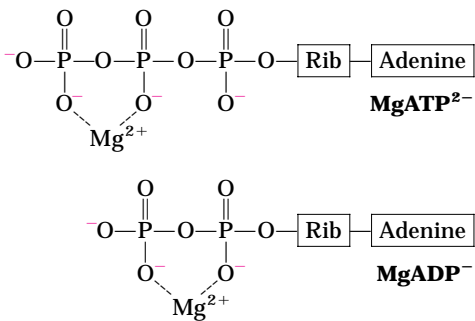


FIGURE 13–2 Mg^{2+} and ATP. Formation of Mg^{2+} complexes partially shields the negative charges and influences the conformation of the phosphate groups in nucleotides such as ATP and ADP.

-49.3 kJ/mol), which can, again, be explained in terms of the structure of reactant and products. When H_2O is added across the anhydride bond of 1,3-bisphosphoglycerate, one of the direct products, 3-phosphoglyceric acid, can immediately lose a proton to give the carboxylate ion, 3-phosphoglycerate, which has two equally probable resonance forms (Fig. 13–4). Removal of the direct product (3-phosphoglyceric acid) and formation of the resonance-stabilized ion favor the forward reaction.

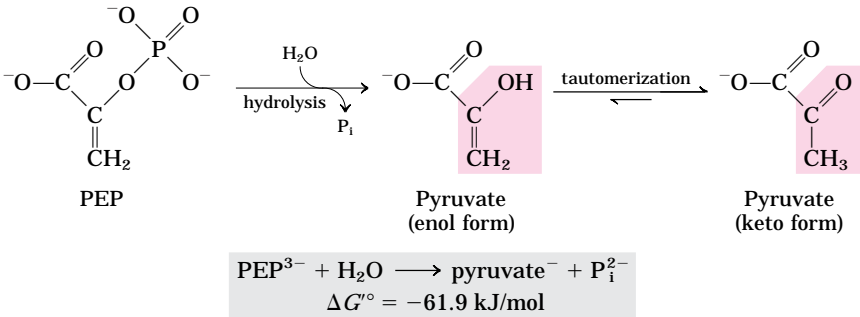


FIGURE 13–3 Hydrolysis of phosphoenolpyruvate (PEP). Catalyzed by pyruvate kinase, this reaction is followed by spontaneous tautomerization of the product, pyruvate. Tautomerization is not possible in PEP, and thus the products of hydrolysis are stabilized relative to the reactants. Resonance stabilization of P_i also occurs, as shown in Figure 13–1.

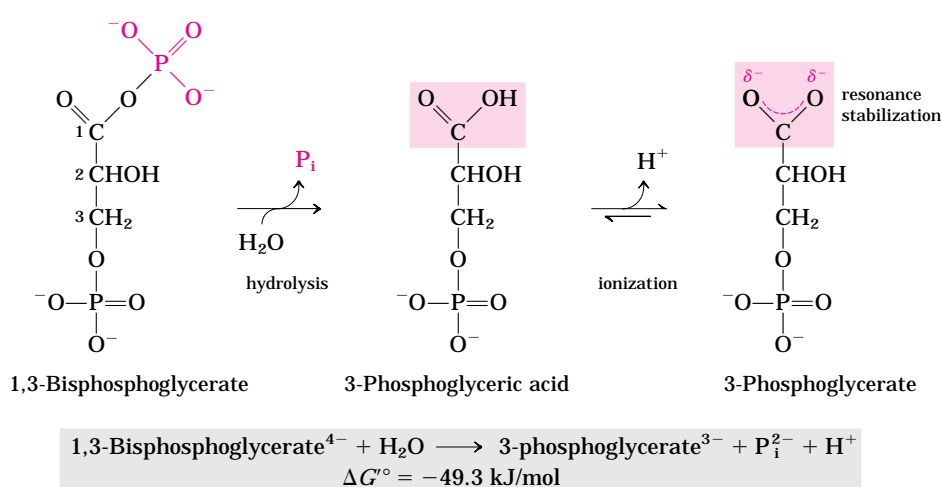


FIGURE 13-4 Hydrolysis of 1,3-bisphosphoglycerate. The direct product of hydrolysis is 3-phosphoglyceric acid, with an undissociated carboxylic acid group, but dissociation occurs immediately. This ionization and the resonance structures it makes possible stabilize the product relative to the reactants. Resonance stabilization of P_i further contributes to the negative free-energy change.

BOX 13-1 WORKING IN BIOCHEMISTRY

The Free Energy of Hydrolysis of ATP within Cells: The Real Cost of Doing Metabolic Business

The standard free energy of hydrolysis of ATP is -30.5 kJ/mol . In the cell, however, the concentrations of ATP, ADP, and P_i are not only unequal but much lower than the standard 1 M concentrations (see Table 13-5). Moreover, the cellular pH may differ somewhat from the standard pH of 7.0. Thus the *actual* free energy of hydrolysis of ATP under intracellular conditions (ΔG_p) differs from the standard free-energy change, $\Delta G'^{\circ}$. We can easily calculate ΔG_p .

In human erythrocytes, for example, the concentrations of ATP, ADP, and P_i are 2.25 , 0.25 , and 1.65 mM , respectively. Let us assume for simplicity that the pH is 7.0 and the temperature is 25°C , the standard pH and temperature. The actual free energy of hydrolysis of ATP in the erythrocyte under these conditions is given by the relationship

$$\Delta G_p = \Delta G'^{\circ} + RT \ln \frac{[\text{ADP}][\text{P}_i]}{[\text{ATP}]}$$

Substituting the appropriate values we obtain

$$\begin{aligned} \Delta G_p &= -30.5 \text{ kJ/mol} + \\ &\left[(8.315 \text{ J/mol} \cdot \text{K})(298 \text{ K}) \ln \frac{(0.25 \times 10^{-3})(1.65 \times 10^{-3})}{2.25 \times 10^{-3}} \right] \\ &= -30.5 \text{ kJ/mol} + (2.48 \text{ kJ/mol}) \ln 1.8 \times 10^{-4} \\ &= -30.5 \text{ kJ/mol} - 21 \text{ kJ/mol} \\ &= -52 \text{ kJ/mol} \end{aligned}$$

Thus ΔG_p , the actual free-energy change for ATP hydrolysis in the intact erythrocyte (-52 kJ/mol), is

much larger than the standard free-energy change (-30.5 kJ/mol). By the same token, the free energy required to *synthesize* ATP from ADP and P_i under the conditions prevailing in the erythrocyte would be 52 kJ/mol .

Because the concentrations of ATP, ADP, and P_i differ from one cell type to another (see Table 13-5), ΔG_p for ATP hydrolysis likewise differs among cells. Moreover, in any given cell, ΔG_p can vary from time to time, depending on the metabolic conditions in the cell and how they influence the concentrations of ATP, ADP, P_i , and H^+ (pH). We can calculate the actual free-energy change for any given metabolic reaction as it occurs in the cell, providing we know the concentrations of all the reactants and products of the reaction and know about the other factors (such as pH, temperature, and concentration of Mg^{2+}) that may affect the $\Delta G'^{\circ}$ and thus the calculated free-energy change, ΔG_p .

To further complicate the issue, the total concentrations of ATP, ADP, P_i , and H^+ may be substantially higher than the *free* concentrations, which are the thermodynamically relevant values. The difference is due to tight binding of ATP, ADP, and P_i to cellular proteins. For example, the concentration of free ADP in resting muscle has been variously estimated at between 1 and $37 \mu\text{M}$. Using the value $25 \mu\text{M}$ in the calculation outlined above, we get a ΔG_p of -58 kJ/mol .

Calculation of the exact value of ΔG_p is perhaps less instructive than the generalization we can make about actual free-energy changes: *in vivo*, the energy released by ATP hydrolysis is greater than the standard free-energy change, $\Delta G'^{\circ}$.

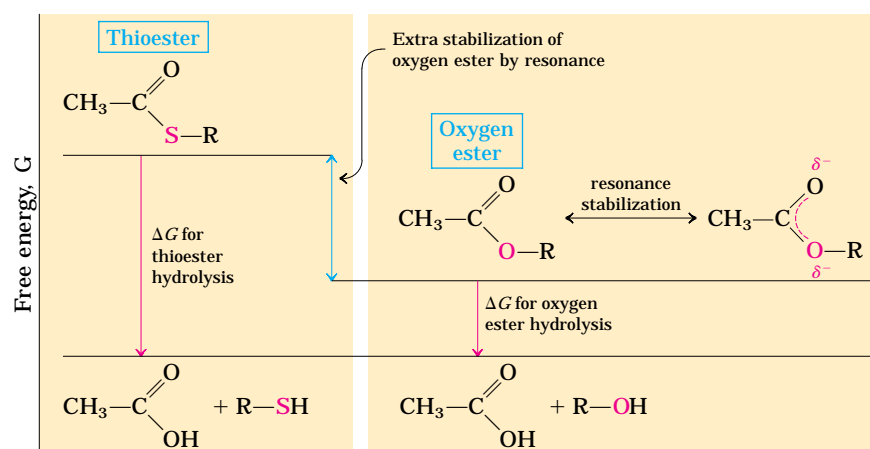


FIGURE 13-7 Free energy of hydrolysis for thioesters and oxygen esters. The products of both types of hydrolysis reaction have about the same free-energy content (G), but the thioester has a higher free-energy content than the oxygen ester. Orbital overlap between the O and C atoms allows resonance stabilization in oxygen esters; orbital overlap between S and C atoms is poorer and provides little resonance stabilization.

ionization, as for ATP, acyl phosphates, and thioesters; (3) the products are stabilized by isomerization (tautomerization), as for phosphoenolpyruvate; and/or (4) the products are stabilized by resonance, as for creatine released from phosphocreatine, carboxylate ion released from acyl phosphates and thioesters, and phosphate (P_i) released from anhydride or ester linkages.

ATP Provides Energy by Group Transfers, Not by Simple Hydrolysis

Throughout this book you will encounter reactions or processes for which ATP supplies energy, and the contribution of ATP to these reactions is commonly indicated as in Figure 13-8a, with a single arrow showing the conversion of ATP to ADP and P_i (or, in some cases, of ATP to AMP and pyrophosphate, PP_i). When written this way, these reactions of ATP appear to be simple hydrolysis reactions in which water displaces P_i (or PP_i), and one is tempted to say that an ATP-dependent reaction is “driven by the hydrolysis of ATP.” This is *not* the case. ATP hydrolysis per se usually accomplishes nothing but the liberation of heat, which cannot drive a chemical process in an isothermal system. A single reaction arrow such as that in Figure 13-8a almost invariably represents a two-step process (Fig. 13-8b) in which part of the ATP molecule, a phosphoryl or pyrophosphoryl group or the adenylate moiety (AMP), is first transferred to a substrate molecule or to an amino acid residue in an enzyme, becoming covalently attached to the substrate or the enzyme and raising its free-energy content. Then, in a second step, the phosphate-containing moiety transferred in the first step is displaced, generating P_i , PP_i , or AMP. Thus ATP participates *covalently* in the enzyme-catalyzed reaction to which it contributes free energy.

Some processes *do* involve direct hydrolysis of ATP (or GTP), however. For example, noncovalent binding of ATP (or of GTP), followed by its hydrolysis to ADP (or GDP) and P_i , can provide the energy to cycle some proteins between two conformations, producing me-

chanical motion. This occurs in muscle contraction and in the movement of enzymes along DNA or of ribosomes along messenger RNA. The energy-dependent reactions catalyzed by helicases, RecA protein, and some topoisomerases (Chapter 25) also involve direct hydrolysis of phosphoanhydride bonds. GTP-binding proteins that act in signaling pathways directly hydrolyze GTP to drive conformational changes that terminate signals

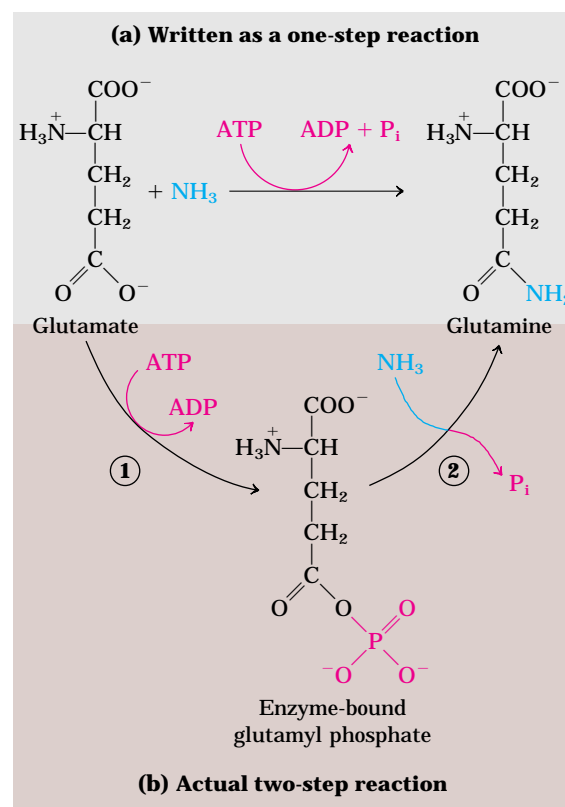


FIGURE 13-8 ATP hydrolysis in two steps. (a) The contribution of ATP to a reaction is often shown as a single step, but is almost always a two-step process. (b) Shown here is the reaction catalyzed by ATP-dependent glutamine synthetase. ① A phosphoryl group is transferred from ATP to glutamate, then ② the phosphoryl group is displaced by NH_3 and released as P_i .

triggered by hormones or by other extracellular factors (Chapter 12).

The phosphate compounds found in living organisms can be divided somewhat arbitrarily into two groups, based on their standard free energies of hydrolysis (Fig. 13-9). “High-energy” compounds have a ΔG° of hydrolysis more negative than -25 kJ/mol; “low-energy” compounds have a less negative ΔG° . Based on this criterion, ATP, with a ΔG° of hydrolysis of -30.5 kJ/mol (-7.3 kcal/mol), is a high-energy compound; glucose 6-phosphate, with a ΔG° of hydrolysis of -13.8 kJ/mol (-3.3 kcal/mol), is a low-energy compound.

The term “high-energy phosphate bond,” long used by biochemists to describe the P—O bond broken in hydrolysis reactions, is incorrect and misleading as it wrongly suggests that the bond itself contains the energy. In fact, the breaking of all chemical bonds requires an *input* of energy. The free energy released by hydrolysis of phosphate compounds does not come from the specific bond that is broken; it results from the products of the reaction having a lower free-energy content than the reactants. For simplicity, we will sometimes use the term “high-energy phosphate compound” when referring to ATP or other phosphate compounds with a large, negative, standard free energy of hydrolysis.

As is evident from the additivity of free-energy changes of sequential reactions, any phosphorylated compound can be synthesized by coupling the synthesis to the breakdown of another phosphorylated compound with a more negative free energy of hydrolysis. For example, because cleavage of P_i from phosphoenolpyruvate (PEP) releases more energy than is needed to drive the condensation of P_i with ADP, the

direct donation of a phosphoryl group from PEP to ADP is thermodynamically feasible:

		ΔG° (kJ/mol)
(1)	$PEP + H_2O \longrightarrow \text{pyruvate} + P_i$	-61.9
(2)	$ADP + P_i \longrightarrow ATP + H_2O$	$+30.5$
Sum:	$PEP + ADP \longrightarrow \text{pyruvate} + ATP$	-31.4

Notice that while the overall reaction above is represented as the algebraic sum of the first two reactions, the overall reaction is actually a third, distinct reaction that does not involve P_i ; PEP donates a *phosphoryl* group *directly* to ADP. We can describe phosphorylated compounds as having a high or low phosphoryl group transfer potential, on the basis of their standard free energies of hydrolysis (as listed in Table 13-6). The phosphoryl group transfer potential of phosphoenolpyruvate is very high, that of ATP is high, and that of glucose 6-phosphate is low (Fig. 13-9).

Much of catabolism is directed toward the synthesis of high-energy phosphate compounds, but their formation is not an end in itself; they are the means of activating a very wide variety of compounds for further chemical transformation. The transfer of a phosphoryl group to a compound effectively puts free energy into that compound, so that it has more free energy to give up during subsequent metabolic transformations. We described above how the synthesis of glucose 6-phosphate is accomplished by phosphoryl group transfer from ATP. In the next chapter we see how this phosphorylation of glucose activates, or “primes,” the glucose for catabolic reactions that occur in nearly every living cell. Because of its intermediate position on the scale of group transfer potential, ATP can carry energy from high-energy

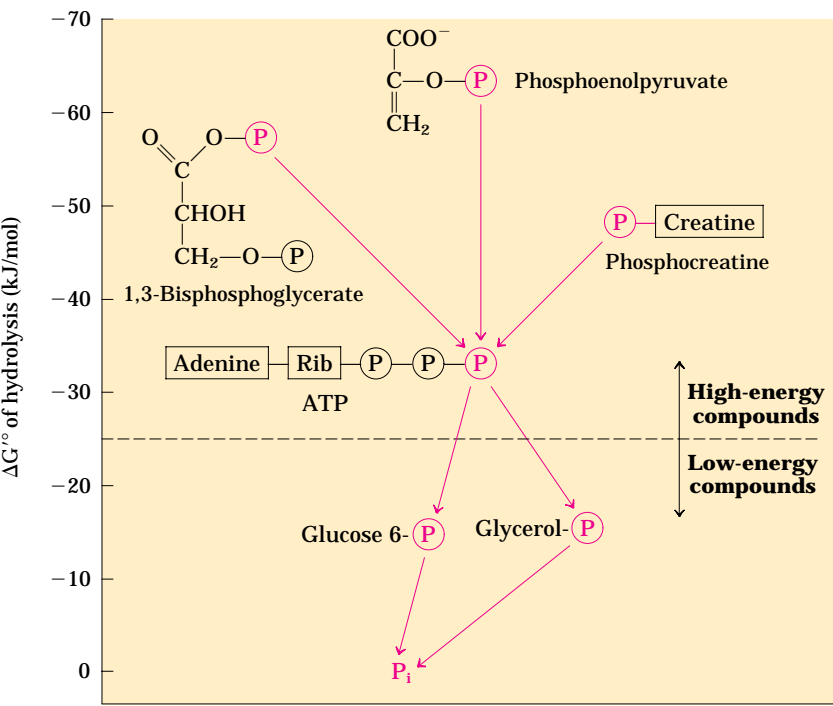


FIGURE 13-9 Ranking of biological phosphate compounds by standard free energies of hydrolysis. This shows the flow of phosphoryl groups, represented by \textcircled{P} , from high-energy phosphoryl donors via ATP to acceptor molecules (such as glucose and glycerol) to form their low-energy phosphate derivatives. This flow of phosphoryl groups, catalyzed by enzymes called kinases, proceeds with an overall loss of free energy under intracellular conditions. Hydrolysis of low-energy phosphate compounds releases P_i , which has an even lower phosphoryl group transfer potential (as defined in the text).

phosphate compounds produced by catabolism to compounds such as glucose, converting them into more reactive species. ATP thus serves as the universal energy currency in all living cells.

One more chemical feature of ATP is crucial to its role in metabolism: although in aqueous solution ATP is thermodynamically unstable and is therefore a good phosphoryl group donor, it is *kinetically* stable. Because of the huge activation energies (200 to 400 kJ/mol) required for uncatalyzed cleavage of its phosphoanhydride bonds, ATP does not spontaneously donate phosphoryl groups to water or to the hundreds of other potential acceptors in the cell. Only when specific enzymes are present to lower the energy of activation does phosphoryl group transfer from ATP proceed. The cell is therefore able to regulate the disposition of the energy carried by ATP by regulating the various enzymes that act on it.

ATP Donates Phosphoryl, Pyrophosphoryl, and Adenylyl Groups

The reactions of ATP are generally S_N2 nucleophilic displacements (p. II.8), in which the nucleophile may be, for example, the oxygen of an alcohol or carboxylate, or a nitrogen of creatine or of the side chain of arginine or histidine. Each of the three phosphates of ATP is susceptible to nucleophilic attack (Fig. 13–10), and each position of attack yields a different type of product.

Nucleophilic attack by an alcohol on the γ phosphate (Fig. 13–10a) displaces ADP and produces a new phosphate ester. Studies with ^{18}O -labeled reactants have shown that the bridge oxygen in the new compound is derived from the alcohol, not from ATP; the group transferred from ATP is a phosphoryl ($-\text{PO}_3^{2-}$), not a phosphate ($-\text{OPO}_3^{2-}$). Phosphoryl group transfer from ATP to glutamate (Fig. 13–8) or to glucose

(p. 218) involves attack at the γ position of the ATP molecule.

Attack at the β phosphate of ATP displaces AMP and transfers a pyrophosphoryl (not pyrophosphate) group to the attacking nucleophile (Fig. 13–10b). For example, the formation of 5′-phosphoribosyl-1-pyrophosphate (p. XXX), a key intermediate in nucleotide synthesis, results from attack of an $-\text{OH}$ of the ribose on the β phosphate.

Nucleophilic attack at the α position of ATP displaces PP_i and transfers adenylyl (5′-AMP) as an adenylyl group (Fig. 13–10c); the reaction is an **adenylylation** (a-den′-i-li-lā′-shun, probably the most ungainly word in the biochemical language). Notice that hydrolysis of the α – β phosphoanhydride bond releases considerably more energy (~ 46 kJ/mol) than hydrolysis of the β – γ bond (~ 31 kJ/mol) (Table 13–6). Furthermore, the PP_i formed as a byproduct of the adenylylation is hydrolyzed to two P_i by the ubiquitous enzyme **inorganic pyrophosphatase**, releasing 19 kJ/mol and thereby providing a further energy “push” for the adenylylation reaction. In effect, both phosphoanhydride bonds of ATP are split in the overall reaction. Adenylylation reactions are therefore thermodynamically very favorable. When the energy of ATP is used to drive a particularly unfavorable metabolic reaction, adenylylation is often the mechanism of energy coupling. Fatty acid activation is a good example of this energy-coupling strategy.

The first step in the activation of a fatty acid—either for energy-yielding oxidation or for use in the synthesis of more complex lipids—is the formation of its thiol ester (see Fig. 17–5). The direct condensation of a fatty acid with coenzyme A is endergonic, but the formation of fatty acyl–CoA is made exergonic by stepwise removal of *two* phosphoryl groups from ATP. First, adenylyl (AMP) is transferred from ATP to the carboxyl group of the fatty acid, forming a mixed anhydride

Three positions on ATP for attack by the nucleophile R^{18}O

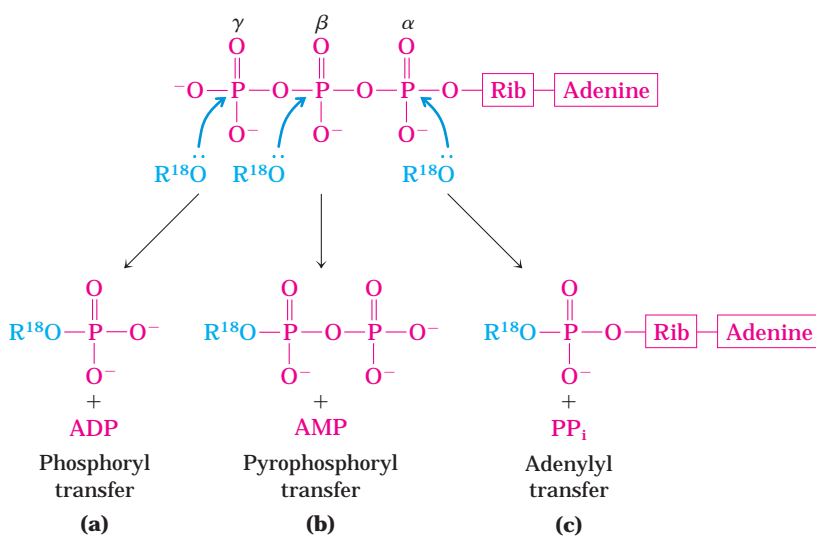
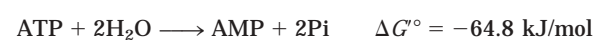


FIGURE 13–10 Nucleophilic displacement reactions of ATP. Any of the three P atoms (α , β , or γ) may serve as the electrophilic target for nucleophilic attack—in this case, by the labeled nucleophile R^{18}O . The nucleophile may be an alcohol (ROH), a carboxyl group (RCOO^-), or a phosphoanhydride (a nucleoside mono- or diphosphate, for example). **(a)** When the oxygen of the nucleophile attacks the γ position, the bridge oxygen of the product is labeled, indicating that the group transferred from ATP is a phosphoryl ($-\text{PO}_3^{2-}$), not a phosphate ($-\text{OPO}_3^{2-}$). **(b)** Attack on the β position displaces AMP and leads to the transfer of a pyrophosphoryl (not pyrophosphate) group to the nucleophile. **(c)** Attack on the α position displaces PP_i and transfers the adenylyl group to the nucleophile.

(fatty acyl adenylate) and liberating PP_i. The thiol group of coenzyme A then displaces the adenylate group and forms a thioester with the fatty acid. The sum of these two reactions is energetically equivalent to the exergonic hydrolysis of ATP to AMP and PP_i ($\Delta G^{\circ} = -45.6$ kJ/mol) and the endergonic formation of fatty acyl-CoA ($\Delta G^{\circ} = 31.4$ kJ/mol). The formation of fatty acyl-CoA is made energetically favorable by hydrolysis of the PP_i by inorganic pyrophosphatase. Thus, in the activation of a fatty acid, both phosphoanhydride bonds of ATP are broken. The resulting ΔG° is the sum of the ΔG° values

for the breakage of these bonds, or $-45.6 \text{ kJ/mol} + (-19.2) \text{ kJ/mol}$:



The activation of amino acids before their polymerization into proteins (see Fig. 27-14) is accomplished by an analogous set of reactions in which a transfer RNA molecule takes the place of coenzyme A. An interesting use of the cleavage of ATP to AMP and PP_i occurs in the firefly, which uses ATP as an energy source to produce light flashes (Box 13-2).

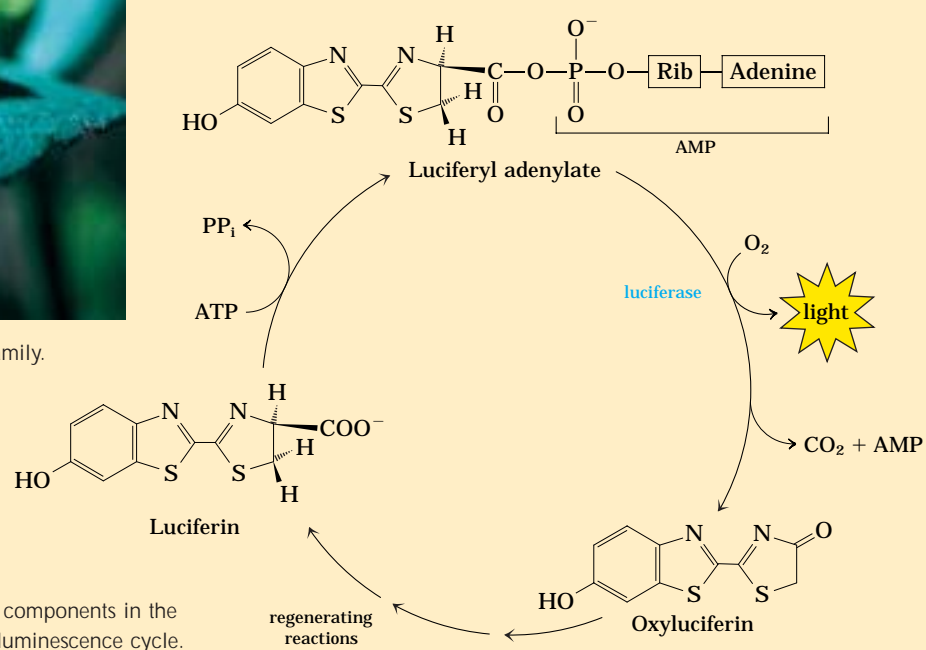
BOX 13-2 THE WORLD OF BIOCHEMISTRY

Firefly Flashes: Glowing Reports of ATP

Bioluminescence requires considerable amounts of energy. In the firefly, ATP is used in a set of reactions that converts chemical energy into light energy. In the 1950s, from many thousands of fireflies collected by children in and around Baltimore, William McElroy and his colleagues at The Johns Hopkins University isolated the principal biochemical components: luciferin, a complex carboxylic acid, and luciferase, an enzyme. The generation of a light flash requires activation of luciferin by an enzymatic reaction involving

pyrophosphate cleavage of ATP to form luciferyl adenylate. In the presence of molecular oxygen and luciferase, the luciferin undergoes a multistep oxidative decarboxylation to oxyluciferin. This process is accompanied by emission of light. The color of the light flash differs with the firefly species and appears to be determined by differences in the structure of the luciferase. Luciferin is regenerated from oxyluciferin in a subsequent series of reactions.

In the laboratory, pure firefly luciferin and luciferase are used to measure minute quantities of ATP by the intensity of the light flash produced. As little as a few picomoles (10^{-12} mol) of ATP can be measured in this way. An enlightening extension of the studies in luciferase was the cloning of the luciferase gene into tobacco plants. When watered with a solution containing luciferin, the plants glowed in the dark (see Fig. 9-29).



The firefly, a beetle of the Lampyridae family.

Assembly of Informational Macromolecules Requires Energy

When simple precursors are assembled into high molecular weight polymers with defined sequences (DNA, RNA, proteins), as described in detail in Part III, energy is required both for the condensation of monomeric units and for the creation of *ordered* sequences. The precursors for DNA and RNA synthesis are nucleoside triphosphates, and polymerization is accompanied by cleavage of the phosphoanhydride linkage between the α and β phosphates, with the release of PP_i (Fig. 13–11). The moieties transferred to the growing polymer in these reactions are adenylate (AMP), guanylate (GMP), cytidylate (CMP), or uridylylate (UMP) for RNA synthesis, and their deoxy analogs (with TMP in place of UMP) for DNA synthesis. As noted above, the activation of amino acids for protein synthesis involves the donation of adenylate groups from ATP, and we shall see in Chapter 27 that several steps of protein synthesis on the ribosome are also accompanied by GTP hydrolysis. In all these cases, the exergonic breakdown of a nucleoside triphosphate is coupled to the endergonic process of synthesizing a polymer of a specific sequence.

ATP Energizes Active Transport and Muscle Contraction

ATP can supply the energy for transporting an ion or a molecule across a membrane into another aqueous compartment where its concentration is higher (see Fig. 11–36). Transport processes are major consumers of energy; in human kidney and brain, for example, as much as two-thirds of the energy consumed at rest is used to pump Na^+ and K^+ across plasma membranes via the Na^+K^+ ATPase. The transport of Na^+ and K^+ is driven by cyclic phosphorylation and dephosphorylation of the transporter protein, with ATP as the phosphoryl group donor (see Fig. 11–37). Na^+ -dependent phosphorylation of the Na^+K^+ ATPase forces a change in the protein's conformation, and K^+ -dependent dephosphorylation favors return to the original conformation. Each cycle in the transport process results in the conversion of ATP to ADP and P_i , and it is the free-energy change of ATP hydrolysis that drives the cyclic changes in protein conformation that result in the electrogenic pumping of Na^+ and K^+ . Note that in this case ATP interacts covalently by phosphoryl group transfer to the enzyme, not the substrate.

In the contractile system of skeletal muscle cells, myosin and actin are specialized to transduce the chemical energy of ATP into motion (see Fig. 5–33). ATP binds tightly but noncovalently to one conformation of myosin, holding the protein in that conformation. When myosin catalyzes the hydrolysis of its bound ATP, the ADP and P_i dissociate from the protein, allowing it to

relax into a second conformation until another molecule of ATP binds. The binding and subsequent hydrolysis of ATP (by myosin ATPase) provide the energy that forces cyclic changes in the conformation of the myosin head. The change in conformation of many individual myosin

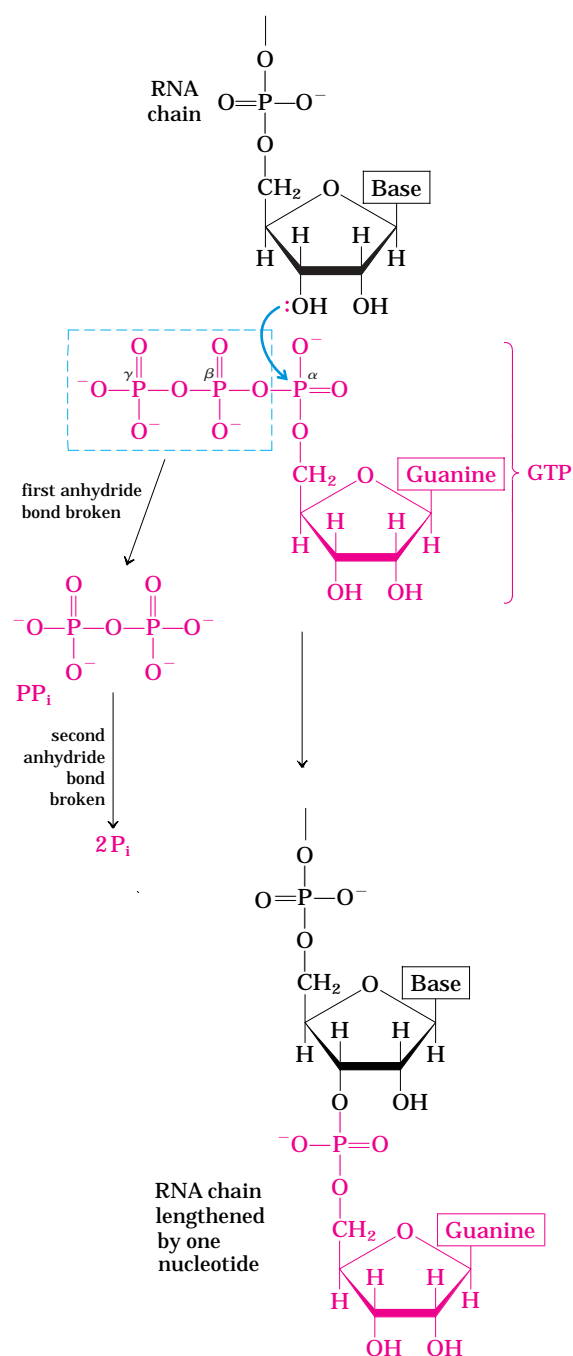


FIGURE 13–11 Nucleoside triphosphates in RNA synthesis. With each nucleoside monophosphate added to the growing chain, one PP_i is released and hydrolyzed to two P_i . The hydrolysis of two phosphoanhydride bonds for each nucleotide added provides the energy for forming the bonds in the RNA polymer and for assembling a specific sequence of nucleotides.

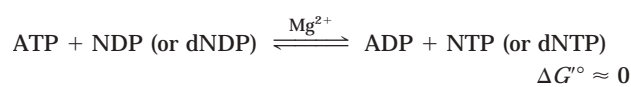
molecules results in the sliding of myosin fibrils along actin filaments (see Fig. 5–32), which translates into macroscopic contraction of the muscle fiber.

As we noted earlier, this production of mechanical motion at the expense of ATP is one of the few cases in which ATP hydrolysis per se, rather than group transfer from ATP, is the source of the chemical energy in a coupled process.

Transphosphorylations between Nucleotides Occur in All Cell Types

Although we have focused on ATP as the cell's energy currency and donor of phosphoryl groups, all other nucleoside triphosphates (GTP, UTP, and CTP) and all the deoxynucleoside triphosphates (dATP, dGTP, dTTP, and dCTP) are energetically equivalent to ATP. The free-energy changes associated with hydrolysis of their phosphoanhydride linkages are very nearly identical with those shown in Table 13–6 for ATP. In preparation for their various biological roles, these other nucleotides are generated and maintained as the nucleoside triphosphate (NTP) forms by phosphoryl group transfer to the corresponding nucleoside diphosphates (NDPs) and monophosphates (NMPs).

ATP is the primary high-energy phosphate compound produced by catabolism, in the processes of glycolysis, oxidative phosphorylation, and, in photosynthetic cells, photophosphorylation. Several enzymes then carry phosphoryl groups from ATP to the other nucleotides. **Nucleoside diphosphate kinase**, found in all cells, catalyzes the reaction



Although this reaction is fully reversible, the relatively high [ATP]/[ADP] ratio in cells normally drives the reaction to the right, with the net formation of NTPs and dNTPs. The enzyme actually catalyzes a two-step phosphoryl transfer, which is a classic case of a double-displacement (Ping-Pong) mechanism (Fig. 13–12; see also Fig. 6–13b). First, phosphoryl group transfer from ATP to an active-site His residue produces a phosphoenzyme

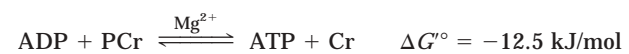
intermediate; then the phosphoryl group is transferred from the P-His residue to an NDP acceptor. Because the enzyme is nonspecific for the base in the NDP and works equally well on dNDPs and NDPs, it can synthesize all NTPs and dNTPs, given the corresponding NDPs and a supply of ATP.

Phosphoryl group transfers from ATP result in an accumulation of ADP; for example, when muscle is contracting vigorously, ADP accumulates and interferes with ATP-dependent contraction. During periods of intense demand for ATP, the cell lowers the ADP concentration, and at the same time acquires ATP, by the action of **adenylate kinase**:



This reaction is fully reversible, so after the intense demand for ATP ends, the enzyme can recycle AMP by converting it to ADP, which can then be phosphorylated to ATP in mitochondria. A similar enzyme, guanylate kinase, converts GMP to GDP at the expense of ATP. By pathways such as these, energy conserved in the catabolic production of ATP is used to supply the cell with all required NTPs and dNTPs.

Phosphocreatine (Fig. 13–5), also called creatine phosphate, serves as a ready source of phosphoryl groups for the quick synthesis of ATP from ADP. The phosphocreatine (PCr) concentration in skeletal muscle is approximately 30 mM, nearly ten times the concentration of ATP, and in other tissues such as smooth muscle, brain, and kidney [PCr] is 5 to 10 mM. The enzyme **creatine kinase** catalyzes the reversible reaction



When a sudden demand for energy depletes ATP, the PCr reservoir is used to replenish ATP at a rate considerably faster than ATP can be synthesized by catabolic pathways. When the demand for energy slackens, ATP produced by catabolism is used to replenish the PCr reservoir by reversal of the creatine kinase reaction. Organisms in the lower phyla employ other PCr-like molecules (collectively called **phosphagens**) as phosphoryl reservoirs.

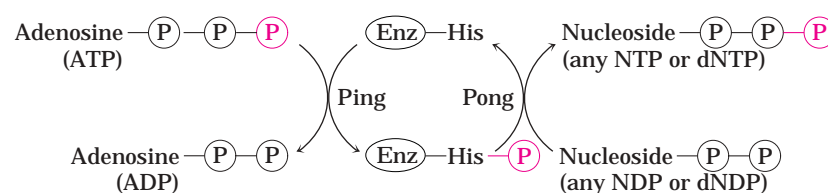
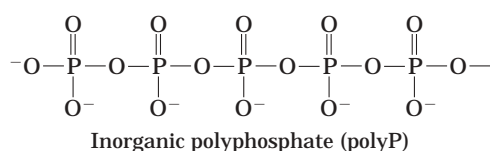


FIGURE 13–12 Ping-Pong mechanism of nucleoside diphosphate kinase. The enzyme binds its first substrate (ATP in our example), and a phosphoryl group is transferred to the side chain of a His residue. ADP departs, and another nucleoside (or deoxynucleoside) diphos-

phate replaces it, and this is converted to the corresponding triphosphate by transfer of the phosphoryl group from the phosphohistidine residue.

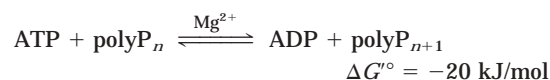
Inorganic Polyphosphate Is a Potential Phosphoryl Group Donor

Inorganic polyphosphate (polyP) is a linear polymer composed of many tens or hundreds of P_i residues linked through phosphoanhydride bonds. This polymer, present in all organisms, may accumulate to high levels in some cells. In yeast, for example, the amount of polyP that accumulates in the vacuoles would represent, if distributed uniformly throughout the cell, a concentration of 200 mM! (Compare this with the concentrations of other phosphoryl donors listed in Table 13–5.)

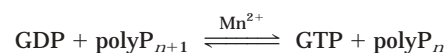


One potential role for polyP is to serve as a phosphagen, a reservoir of phosphoryl groups that can be used to generate ATP, as creatine phosphate is used in muscle. PolyP has about the same phosphoryl group transfer potential as PP_i . The shortest polyphosphate, PP_i ($n = 2$), can serve as the energy source for active transport of H^+ in plant vacuoles. For at least one form of the enzyme phosphofructokinase in plants, PP_i is the phosphoryl group donor, a role played by ATP in animals and microbes (p. XXX). The finding of high concentrations of polyP in volcanic condensates and steam vents suggests that it could have served as an energy source in prebiotic and early cellular evolution.

In prokaryotes, the enzyme **polyphosphate kinase-1** (PPK-1) catalyzes the reversible reaction



by a mechanism involving an enzyme-bound phosphohistidine intermediate (recall the mechanism of nucleoside diphosphate kinase, described above). A second enzyme, **polyphosphate kinase-2** (PPK-2), catalyzes the reversible synthesis of GTP (or ATP) from polyphosphate and GDP (or ADP):



PPK-2 is believed to act primarily in the direction of GTP and ATP synthesis, and PPK-1 in the direction of polyphosphate synthesis. PPK-1 and PPK-2 are present in a wide variety of prokaryotes, including many pathogenic bacteria.

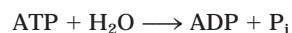
In prokaryotes, elevated levels of polyP have been shown to promote expression of a number of genes involved in adaptation of the organism to conditions of starvation or other threats to survival. In *Escherichia coli*, for example, polyP accumulates when cells are starved for amino acids or P_i , and this accumulation con-

fers a survival advantage. Deletion of the genes for polyphosphate kinases diminishes the ability of certain pathogenic bacteria to invade animal tissues. The enzymes may therefore prove to be vulnerable targets in the development of new antimicrobial drugs.

No gene in yeast encodes a PPK-like protein, but four genes—unrelated to bacterial PPK genes—are necessary for the synthesis of polyphosphate. The mechanism for polyphosphate synthesis in eukaryotes seems to be quite different from that in prokaryotes.

Biochemical and Chemical Equations Are Not Identical

Biochemists write metabolic equations in a simplified way, and this is particularly evident for reactions involving ATP. Phosphorylated compounds can exist in several ionization states and, as we have noted, the different species can bind Mg^{2+} . For example, at pH 7 and 2 mM Mg^{2+} , ATP exists in the forms ATP^{4-} , $HATP^{3-}$, H_2ATP^{2-} , $MgHATP^-$, and Mg_2ATP . In thinking about the biological role of ATP, however, we are not always interested in all this detail, and so we consider ATP as an entity made up of a sum of species, and we write its hydrolysis as the biochemical equation



where ATP, ADP, and P_i are sums of species. The corresponding apparent equilibrium constant, $K'_{eq} = [\text{ADP}][P_i]/[\text{ATP}]$, depends on the pH and the concentration of free Mg^{2+} . Note that H^+ and Mg^{2+} do not appear in the biochemical equation because they are held constant. Thus a biochemical equation does not balance H, Mg, or charge, although it does balance all other elements involved in the reaction (C, N, O, and P in the equation above).

We can write a chemical equation that *does* balance for all elements and for charge. For example, when ATP is hydrolyzed at a pH above 8.5 in the absence of Mg^{2+} , the chemical reaction is represented by



The corresponding equilibrium constant, $K'_{eq} = [\text{ADP}^{3-}][\text{HPO}_4^{2-}][\text{H}^+]/[\text{ATP}^{4-}]$, depends only on temperature, pressure, and ionic strength.

Both ways of writing a metabolic reaction have value in biochemistry. Chemical equations are needed when we want to account for all atoms and charges in a reaction, as when we are considering the mechanism of a chemical reaction. Biochemical equations are used to determine in which direction a reaction will proceed spontaneously, given a specified pH and $[Mg^{2+}]$, or to calculate the equilibrium constant of such a reaction.

Throughout this book we use biochemical equations, unless the focus is on chemical mechanism, and we use values of $\Delta G'^{\circ}$ and K'_{eq} as determined at pH 7 and 1 mM Mg^{2+} .

SUMMARY 13.2 Phosphoryl Group Transfers and ATP

- ATP is the chemical link between catabolism and anabolism. It is the energy currency of the living cell. The exergonic conversion of ATP to ADP and P_i , or to AMP and PP_i , is coupled to many endergonic reactions and processes.
- Direct hydrolysis of ATP is the source of energy in the conformational changes that produce muscle contraction but, in general, it is not ATP hydrolysis but the transfer of a phosphoryl, pyrophosphoryl, or adenylyl group from ATP to a substrate or enzyme molecule that couples the energy of ATP breakdown to endergonic transformations of substrates.
- Through these group transfer reactions, ATP provides the energy for anabolic reactions, including the synthesis of informational molecules, and for the transport of molecules and ions across membranes against concentration gradients and electrical potential gradients.
- Cells contain other metabolites with large, negative, free energies of hydrolysis, including phosphoenolpyruvate, 1,3-bisphosphoglycerate, and phosphocreatine. These high-energy compounds, like ATP, have a high phosphoryl group transfer potential; they are good donors of the phosphoryl group. Thioesters also have high free energies of hydrolysis.
- Inorganic polyphosphate, present in all cells, may serve as a reservoir of phosphoryl groups with high group transfer potential.

13.3 Biological Oxidation-Reduction Reactions

The transfer of phosphoryl groups is a central feature of metabolism. Equally important is another kind of transfer, electron transfer in oxidation-reduction reactions. These reactions involve the loss of electrons by one chemical species, which is thereby oxidized, and the gain of electrons by another, which is reduced. The flow of electrons in oxidation-reduction reactions is responsible, directly or indirectly, for all work done by living organisms. In nonphotosynthetic organisms, the sources of electrons are reduced compounds (foods); in photosynthetic organisms, the initial electron donor is a chemical species excited by the absorption of light. The path of electron flow in metabolism is complex. Electrons move from various metabolic intermediates to specialized electron carriers in enzyme-catalyzed reactions.

The carriers in turn donate electrons to acceptors with higher electron affinities, with the release of energy. Cells contain a variety of molecular energy transducers, which convert the energy of electron flow into useful work.

We begin our discussion with a description of the general types of metabolic reactions in which electrons are transferred. After considering the theoretical and experimental basis for measuring the energy changes in oxidation reactions in terms of electromotive force, we discuss the relationship between this force, expressed in volts, and the free-energy change, expressed in joules. We conclude by describing the structures and oxidation-reduction chemistry of the most common of the specialized electron carriers, which you will encounter repeatedly in later chapters.

The Flow of Electrons Can Do Biological Work

Every time we use a motor, an electric light or heater, or a spark to ignite gasoline in a car engine, we use the flow of electrons to accomplish work. In the circuit that powers a motor, the source of electrons can be a battery containing two chemical species that differ in affinity for electrons. Electrical wires provide a pathway for electron flow from the chemical species at one pole of the battery, through the motor, to the chemical species at the other pole of the battery. Because the two chemical species differ in their affinity for electrons, electrons flow spontaneously through the circuit, driven by a force proportional to the difference in electron affinity, the **electromotive force (emf)**. The electromotive force (typically a few volts) can accomplish work if an appropriate energy transducer—in this case a motor—is placed in the circuit. The motor can be coupled to a variety of mechanical devices to accomplish useful work.

Living cells have an analogous biological “circuit,” with a relatively reduced compound such as glucose as the source of electrons. As glucose is enzymatically oxidized, the released electrons flow spontaneously through a series of electron-carrier intermediates to another chemical species, such as O_2 . This electron flow is exergonic, because O_2 has a higher affinity for electrons than do the electron-carrier intermediates. The resulting electromotive force provides energy to a variety of molecular energy transducers (enzymes and other proteins) that do biological work. In the mitochondrion, for example, membrane-bound enzymes couple electron flow to the production of a transmembrane pH difference, accomplishing osmotic and electrical work. The proton gradient thus formed has potential energy, sometimes called the proton-motive force by analogy with electromotive force. Another enzyme, ATP synthase in the inner mitochondrial membrane, uses the proton-motive force to do chemical work: synthesis of ATP from ADP and P_i as protons flow spontaneously across the membrane. Similarly, membrane-localized enzymes in

E. coli convert electromotive force to proton-motive force, which is then used to power flagellar motion.

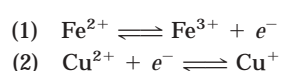
The principles of electrochemistry that govern energy changes in the macroscopic circuit with a motor and battery apply with equal validity to the molecular processes accompanying electron flow in living cells. We turn now to a discussion of those principles.

Oxidation-Reductions Can Be Described as Half-Reactions

Although oxidation and reduction must occur together, it is convenient when describing electron transfers to consider the two halves of an oxidation-reduction reaction separately. For example, the oxidation of ferrous ion by cupric ion,

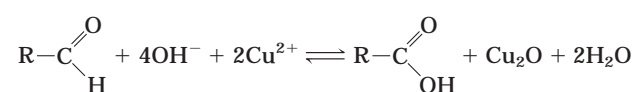


can be described in terms of two half-reactions:

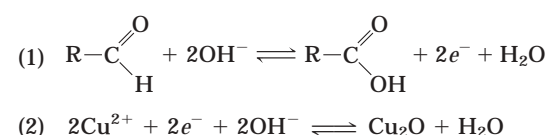


The electron-donating molecule in an oxidation-reduction reaction is called the reducing agent or reductant; the electron-accepting molecule is the oxidizing agent or oxidant. A given agent, such as an iron cation existing in the ferrous (Fe^{2+}) or ferric (Fe^{3+}) state, functions as a conjugate reductant-oxidant pair (redox pair), just as an acid and corresponding base function as a conjugate acid-base pair. Recall from Chapter 2 that in acid-base reactions we can write a general equation: proton donor $\rightleftharpoons \text{H}^+$ + proton acceptor. In redox reactions we can write a similar general equation: electron donor $\rightleftharpoons e^-$ + electron acceptor. In the reversible half-reaction (1) above, Fe^{2+} is the electron donor and Fe^{3+} is the electron acceptor; together, Fe^{2+} and Fe^{3+} constitute a **conjugate redox pair**.

The electron transfers in the oxidation-reduction reactions of organic compounds are not fundamentally different from those of inorganic species. In Chapter 7 we considered the oxidation of a reducing sugar (an aldehyde or ketone) by cupric ion (see Fig. 7-10a):



This overall reaction can be expressed as two half-reactions:



Because two electrons are removed from the aldehyde carbon, the second half-reaction (the one-electron reduction of cupric to cuprous ion) must be doubled to balance the overall equation.

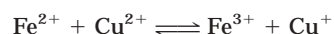
Biological Oxidations Often Involve Dehydrogenation

The carbon in living cells exists in a range of oxidation states (Fig. 13-13). When a carbon atom shares an electron pair with another atom (typically H, C, S, N, or O), the sharing is unequal in favor of the more electronegative atom. The order of increasing electronegativity is $\text{H} < \text{C} < \text{S} < \text{N} < \text{O}$. In oversimplified but useful terms, the more electronegative atom “owns” the bonding electrons it shares with another atom. For example, in methane (CH_4), carbon is more electronegative than the four hydrogens bonded to it, and the C atom therefore “owns” all eight bonding electrons (Fig. 13-13). In ethane, the electrons in the C—C bond are shared equally, so each C atom owns only seven of its eight bonding electrons. In ethanol, C-1 is less electronegative than the oxygen to which it is bonded, and the O atom therefore “owns” both electrons of the C—O bond, leaving C-1 with only five bonding electrons. With each formal loss of electrons, the carbon atom has undergone oxidation—even when no oxygen is involved, as in the conversion of an alkane ($-\text{CH}_2-\text{CH}_2-$) to an alkene ($-\text{CH}=\text{CH}-$). In this case, oxidation (loss of electrons) is coincident with the loss of hydrogen. In biological systems, oxidation is often synonymous with **dehydrogenation**, and many enzymes that catalyze oxidation reactions are **dehydrogenases**. Notice that the more reduced compounds in Figure 13-13 (top) are richer in hydrogen than in oxygen, whereas the more oxidized compounds (bottom) have more oxygen and less hydrogen.

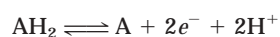
Not all biological oxidation-reduction reactions involve carbon. For example, in the conversion of molecular nitrogen to ammonia, $6\text{H}^+ + 6e^- + \text{N}_2 \rightarrow 2\text{NH}_3$, the nitrogen atoms are reduced.

Electrons are transferred from one molecule (electron donor) to another (electron acceptor) in one of four different ways:

1. Directly as *electrons*. For example, the $\text{Fe}^{2+}/\text{Fe}^{3+}$ redox pair can transfer an electron to the $\text{Cu}^+/\text{Cu}^{2+}$ redox pair:



2. As *hydrogen atoms*. Recall that a hydrogen atom consists of a proton (H^+) and a single electron (e^-). In this case we can write the general equation



where AH_2 is the hydrogen/electron donor.

(Do not mistake the above reaction for an acid dissociation; the H^+ arises from the removal of a hydrogen atom, $\text{H}^+ + e^-$.) AH_2 and A together constitute a conjugate redox pair (A/AH_2), which can reduce another compound B (or redox pair, B/BH_2) by transfer of hydrogen atoms:



- 3. As a *hydride ion* (:H[−]), which has two electrons. This occurs in the case of NAD-linked dehydrogenases, described below.
- 4. Through direct *combination with oxygen*. In this case, oxygen combines with an organic reductant and is covalently incorporated in the product, as in the oxidation of a hydrocarbon to an alcohol:

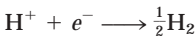


The hydrocarbon is the electron donor and the oxygen atom is the electron acceptor.

All four types of electron transfer occur in cells. The neutral term **reducing equivalent** is commonly used to designate a single electron equivalent participating in an oxidation-reduction reaction, no matter whether this equivalent is an electron per se, a hydrogen atom, or a hydride ion, or whether the electron transfer takes place in a reaction with oxygen to yield an oxygenated product. Because biological fuel molecules are usually enzymatically dehydrogenated to lose *two* reducing equivalents at a time, and because each oxygen atom can accept two reducing equivalents, biochemists by convention regard the unit of biological oxidations as two reducing equivalents passing from substrate to oxygen.

Reduction Potentials Measure Affinity for Electrons

When two conjugate redox pairs are together in solution, electron transfer from the electron donor of one pair to the electron acceptor of the other may proceed spontaneously. The tendency for such a reaction depends on the relative affinity of the electron acceptor of each redox pair for electrons. The **standard reduction potential, E°**, a measure (in volts) of this affinity, can be determined in an experiment such as that described in Figure 13–14. Electrochemists have chosen as a standard of reference the half-reaction



The electrode at which this half-reaction occurs (called a half-cell) is arbitrarily assigned a standard reduction

potential of 0.00 V. When this hydrogen electrode is connected through an external circuit to another half-cell in which an oxidized species and its corresponding reduced species are present at standard concentrations (each solute at 1 M, each gas at 101.3 kPa), electrons tend to flow through the external circuit from the half-cell of

Methane		8
Ethane (alkane)		7
Ethene (alkene)		6
Ethanol (alcohol)		5
Acetylene (alkyne)		5
Formaldehyde		4
Acetaldehyde (aldehyde)		3
Acetone (ketone)		2
Formic acid (carboxylic acid)		2
Carbon monoxide		2
Acetic acid (carboxylic acid)		1
Carbon dioxide		0

FIGURE 13–13 Oxidation states of carbon in the biosphere. The oxidation states are illustrated with some representative compounds. Focus on the red carbon atom and its bonding electrons. When this carbon is bonded to the less electronegative H atom, both bonding electrons (red) are assigned to the carbon. When carbon is bonded to another carbon, bonding electrons are shared equally, so one of the two electrons is assigned to the red carbon. When the red carbon is bonded to the more electronegative O atom, the bonding electrons are assigned to the oxygen. The number to the right of each compound is the number of electrons “owned” by the red carbon, a rough expression of the oxidation state of that carbon. When the red carbon undergoes oxidation (loses electrons), the number gets smaller. Thus the oxidation state increases from top to bottom of the list.

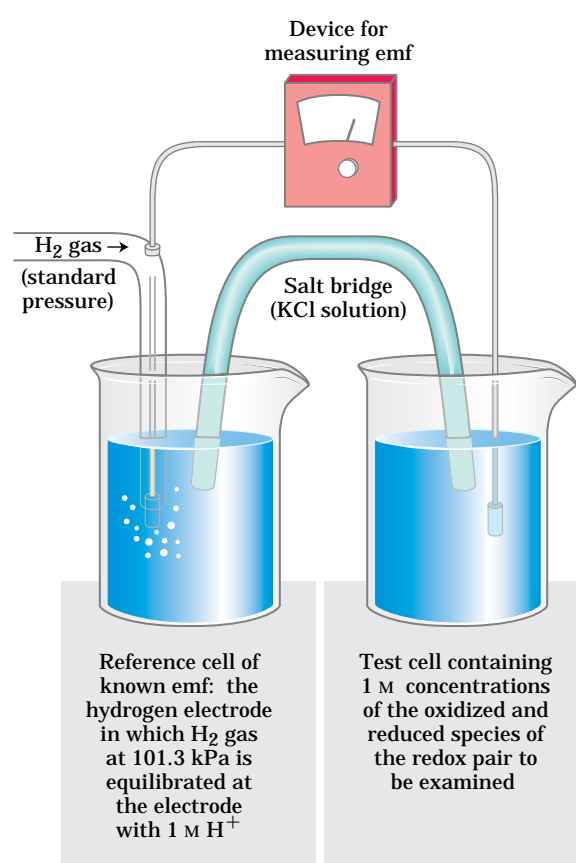


FIGURE 13-14 Measurement of the standard reduction potential (E°) of a redox pair. Electrons flow from the test electrode to the reference electrode, or vice versa. The ultimate reference half-cell is the hydrogen electrode, as shown here, at pH 0. The electromotive force (emf) of this electrode is designated 0.00 V. At pH 7 in the test cell, E° for the hydrogen electrode is -0.414 V. The direction of electron flow depends on the relative electron “pressure” or potential of the two cells. A salt bridge containing a saturated KCl solution provides a path for counter-ion movement between the test cell and the reference cell. From the observed emf and the known emf of the reference cell, the experimenter can find the emf of the test cell containing the redox pair. The cell that gains electrons has, by convention, the more positive reduction potential.

lower standard reduction potential to the half-cell of higher standard reduction potential. By convention, the half-cell with the stronger tendency to acquire electrons is assigned a positive value of E° .

The reduction potential of a half-cell depends not only on the chemical species present but also on their activities, approximated by their concentrations. About a century ago, Walther Nernst derived an equation that relates standard reduction potential (E°) to the reduction potential (E) at any concentration of oxidized and reduced species in the cell:

$$E = E^\circ + \frac{RT}{n\mathcal{F}} \ln \frac{[\text{electron acceptor}]}{[\text{electron donor}]} \quad (13-4)$$

where R and T have their usual meanings, n is the number of electrons transferred per molecule, and \mathcal{F} is the Faraday constant (Table 13-1). At 298 K (25 °C), this expression reduces to

$$E = E^\circ + \frac{0.026 \text{ V}}{n} \ln \frac{[\text{electron acceptor}]}{[\text{electron donor}]} \quad (13-5)$$

Many half-reactions of interest to biochemists involve protons. As in the definition of $\Delta G'^\circ$, biochemists define the standard state for oxidation-reduction reactions as pH 7 and express reduction potential as E'° , the standard reduction potential at pH 7. The standard reduction potentials given in Table 13-7 and used throughout this book are values for E'° and are therefore valid only for systems at neutral pH. Each value represents the potential difference when the conjugate redox pair, at 1 M concentrations and pH 7, is connected with the standard (pH 0) hydrogen electrode. Notice in Table 13-7 that when the conjugate pair $2\text{H}^+/\text{H}_2$ at pH 7 is connected with the standard hydrogen electrode (pH 0), electrons tend to flow from the pH 7 cell to the standard (pH 0) cell; the measured E'° for the $2\text{H}^+/\text{H}_2$ pair is -0.414 V.

Standard Reduction Potentials Can Be Used to Calculate the Free-Energy Change

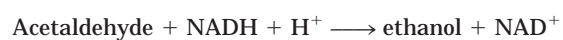
The usefulness of reduction potentials stems from the fact that when E values have been determined for any two half-cells, relative to the standard hydrogen electrode, their reduction potentials relative to each other are also known. We can then predict the direction in which electrons will tend to flow when the two half-cells are connected through an external circuit or when components of both half-cells are present in the same solution. Electrons tend to flow to the half-cell with the more positive E , and the strength of that tendency is proportional to the difference in reduction potentials, ΔE .

The energy made available by this spontaneous electron flow (the free-energy change for the oxidation-reduction reaction) is proportional to ΔE :

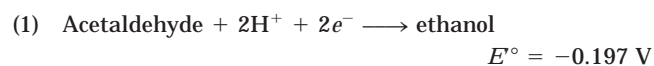
$$\Delta G = -n\mathcal{F} \Delta E \quad \text{or} \quad \Delta G'^\circ = -n\mathcal{F} \Delta E'^\circ \quad (13-6)$$

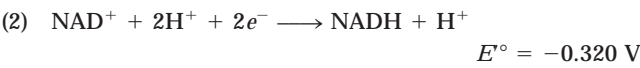
Here n represents the number of electrons transferred in the reaction. With this equation we can calculate the free-energy change for any oxidation-reduction reaction from the values of E'° in a table of reduction potentials (Table 13-7) and the concentrations of the species participating in the reaction.

Consider the reaction in which acetaldehyde is reduced by the biological electron carrier NADH:



The relevant half-reactions and their E'° values are:





By convention, ΔE° is expressed as E° of the electron acceptor minus E° of the electron donor. Because acetaldehyde is accepting electrons from NADH in our example, $\Delta E^\circ = -0.197 \text{ V} - (-0.320 \text{ V}) = 0.123 \text{ V}$, and n is 2. Therefore,

$$\begin{aligned}\Delta G^\circ &= -n\mathcal{F} \Delta E^\circ = -2(96.5 \text{ kJ/V} \cdot \text{mol})(0.123 \text{ V}) \\ &= -23.7 \text{ kJ/mol}\end{aligned}$$

This is the free-energy change for the oxidation-reduction reaction at pH 7, when acetaldehyde, ethanol, NAD^+ , and NADH are all present at 1.00 M concentrations. If, instead, acetaldehyde and NADH were present at 1.00 M but ethanol and NAD^+ were present at 0.100 M, the value for ΔG would be calculated as follows. First,

the values of E for both reductants are determined (Eqn 13-4):

$$\begin{aligned}E_{\text{acetaldehyde}} &= E^\circ + \frac{RT}{n\mathcal{F}} \ln \frac{[\text{acetaldehyde}]}{[\text{ethanol}]} \\ &= -0.197 \text{ V} + \frac{0.026 \text{ V}}{2} \ln \frac{1.00}{0.100} = -0.167 \text{ V} \\ E_{\text{NADH}} &= E^\circ + \frac{RT}{n\mathcal{F}} \ln \frac{[\text{NAD}^+]}{[\text{NADH}]} \\ &= -0.320 \text{ V} + \frac{0.026 \text{ V}}{2} \ln \frac{1.00}{0.100} = -0.350 \text{ V}\end{aligned}$$

Then ΔE is used to calculate ΔG (Eqn 13-5):

$$\begin{aligned}\Delta E &= -0.167 \text{ V} - (-0.350 \text{ V}) = 0.183 \text{ V} \\ \Delta G &= -n\mathcal{F} \Delta E \\ &= -2(96.5 \text{ kJ/V} \cdot \text{mol})(0.183 \text{ V}) \\ &= -35.3 \text{ kJ/mol}\end{aligned}$$

TABLE 13-7 Standard Reduction Potentials of Some Biologically Important Half-Reactions, at pH 7.0 and 25 °C (298 K)

Half-reaction	E° (V)
$\frac{1}{2}\text{O}_2 + 2\text{H}^+ + 2e^- \longrightarrow \text{H}_2\text{O}$	0.816
$\text{Fe}^{3+} + e^- \longrightarrow \text{Fe}^{2+}$	0.771
$\text{NO}_3^- + 2\text{H}^+ + 2e^- \longrightarrow \text{NO}_2^- + \text{H}_2\text{O}$	0.421
Cytochrome <i>f</i> (Fe^{3+}) + $e^- \longrightarrow$ cytochrome <i>f</i> (Fe^{2+})	0.365
$\text{Fe}(\text{CN})_6^{3-}$ (ferricyanide) + $e^- \longrightarrow \text{Fe}(\text{CN})_6^{4-}$	0.36
Cytochrome <i>a</i> ₃ (Fe^{3+}) + $e^- \longrightarrow$ cytochrome <i>a</i> ₃ (Fe^{2+})	0.35
$\text{O}_2 + 2\text{H}^+ + 2e^- \longrightarrow \text{H}_2\text{O}_2$	0.295
Cytochrome <i>a</i> (Fe^{3+}) + $e^- \longrightarrow$ cytochrome <i>a</i> (Fe^{2+})	0.29
Cytochrome <i>c</i> (Fe^{3+}) + $e^- \longrightarrow$ cytochrome <i>c</i> (Fe^{2+})	0.254
Cytochrome <i>c</i> ₁ (Fe^{3+}) + $e^- \longrightarrow$ cytochrome <i>c</i> ₁ (Fe^{2+})	0.22
Cytochrome <i>b</i> (Fe^{3+}) + $e^- \longrightarrow$ cytochrome <i>b</i> (Fe^{2+})	0.077
Ubiquinone + $2\text{H}^+ + 2e^- \longrightarrow$ ubiquinol + H_2	0.045
$\text{Fumarate}^{2-} + 2\text{H}^+ + 2e^- \longrightarrow \text{succinate}^{2-}$	0.031
$2\text{H}^+ + 2e^- \longrightarrow \text{H}_2$ (at standard conditions, pH 0)	0.000
Crotonyl-CoA + $2\text{H}^+ + 2e^- \longrightarrow$ butyryl-CoA	-0.015
$\text{Oxaloacetate}^{2-} + 2\text{H}^+ + 2e^- \longrightarrow \text{malate}^{2-}$	-0.166
$\text{Pyruvate}^- + 2\text{H}^+ + 2e^- \longrightarrow \text{lactate}^-$	-0.185
Acetaldehyde + $2\text{H}^+ + 2e^- \longrightarrow$ ethanol	-0.197
$\text{FAD} + 2\text{H}^+ + 2e^- \longrightarrow \text{FADH}_2$	-0.219*
Glutathione + $2\text{H}^+ + 2e^- \longrightarrow$ 2 reduced glutathione	-0.23
$\text{S} + 2\text{H}^+ + 2e^- \longrightarrow \text{H}_2\text{S}$	-0.243
Lipoic acid + $2\text{H}^+ + 2e^- \longrightarrow$ dihydrolipoic acid	-0.29
$\text{NAD}^+ + \text{H}^+ + 2e^- \longrightarrow \text{NADH}$	-0.320
$\text{NADP}^+ + \text{H}^+ + 2e^- \longrightarrow \text{NADPH}$	-0.324
Acetoacetate + $2\text{H}^+ + 2e^- \longrightarrow \beta$ -hydroxybutyrate	-0.346
α -Ketoglutarate + $\text{CO}_2 + 2\text{H}^+ + 2e^- \longrightarrow$ isocitrate	-0.38
$2\text{H}^+ + 2e^- \longrightarrow \text{H}_2$ (at pH 7)	-0.414
Ferredoxin (Fe^{3+}) + $e^- \longrightarrow$ ferredoxin (Fe^{2+})	-0.432

Source: Data mostly from Loach, P.A. (1976) In *Handbook of Biochemistry and Molecular Biology*, 3rd edn (Fasman, G.D., ed.), Physical and Chemical Data, Vol. I, pp. 122-130, CRC Press, Boca Raton, FL.

* This is the value for free FAD; FAD bound to a specific flavoprotein (for example succinate dehydrogenase) has a different E° that depends on its protein environments.

It is thus possible to calculate the free-energy change for any biological redox reaction at any concentrations of the redox pairs.

Cellular Oxidation of Glucose to Carbon Dioxide Requires Specialized Electron Carriers

The principles of oxidation-reduction energetics described above apply to the many metabolic reactions that involve electron transfers. For example, in many organisms, the oxidation of glucose supplies energy for the production of ATP. The complete oxidation of glucose:



has a ΔG° of $-2,840$ kJ/mol. This is a much larger release of free energy than is required for ATP synthesis (50 to 60 kJ/mol; see Box 13–1). Cells convert glucose to CO_2 not in a single, high-energy-releasing reaction, but rather in a series of controlled reactions, some of which are oxidations. The free energy released in these oxidation steps is of the same order of magnitude as that required for ATP synthesis from ADP, with some energy to spare. Electrons removed in these oxidation steps are transferred to coenzymes specialized for carrying electrons, such as NAD^+ and FAD (described below).

A Few Types of Coenzymes and Proteins Serve as Universal Electron Carriers

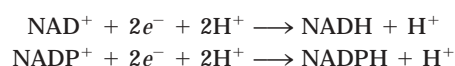
The multitude of enzymes that catalyze cellular oxidations channel electrons from their hundreds of different substrates into just a few types of universal electron carriers. The reduction of these carriers in catabolic processes results in the conservation of free energy released by substrate oxidation. NAD^+ , NADP^+ , FMN, and FAD are water-soluble coenzymes that undergo reversible oxidation and reduction in many of the electron-transfer reactions of metabolism. The nucleotides NAD^+ and NADP^+ move readily from one enzyme to another; the flavin nucleotides FMN and FAD are usually very tightly bound to the enzymes, called flavoproteins, for which they serve as prosthetic groups. Lipid-soluble quinones such as ubiquinone and plastoquinone act as electron carriers and proton donors in the nonaqueous environment of membranes. Iron-sulfur proteins and cytochromes, which have tightly bound prosthetic groups that undergo reversible oxidation and reduction, also serve as electron carriers in many oxidation-reduction reactions. Some of these proteins are water-soluble, but others are peripheral or integral membrane proteins (see Fig. 11–6).

We conclude this chapter by describing some chemical features of nucleotide coenzymes and some of the enzymes (dehydrogenases and flavoproteins) that use them. The oxidation-reduction chemistry of quinones, iron-sulfur proteins, and cytochromes is discussed in Chapter 19.

NADH and NADPH Act with Dehydrogenases as Soluble Electron Carriers

Nicotinamide adenine dinucleotide (NAD^+ in its oxidized form) and its close analog nicotinamide adenine dinucleotide phosphate (NADP^+) are composed of two nucleotides joined through their phosphate groups by a phosphoanhydride bond (Fig. 13–15a). Because the nicotinamide ring resembles pyridine, these compounds are sometimes called **pyridine nucleotides**. The vitamin niacin is the source of the nicotinamide moiety in nicotinamide nucleotides.

Both coenzymes undergo reversible reduction of the nicotinamide ring (Fig. 13–15). As a substrate molecule undergoes oxidation (dehydrogenation), giving up two hydrogen atoms, the oxidized form of the nucleotide (NAD^+ or NADP^+) accepts a hydride ion ($:\text{H}^-$, the equivalent of a proton and two electrons) and is transformed into the reduced form (NADH or NADPH). The second proton removed from the substrate is released to the aqueous solvent. The half-reaction for each type of nucleotide is therefore

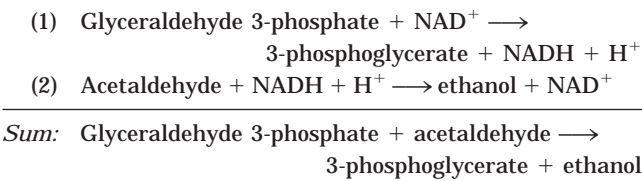


Reduction of NAD^+ or NADP^+ converts the benzenoid ring of the nicotinamide moiety (with a fixed positive charge on the ring nitrogen) to the quinonoid form (with no charge on the nitrogen). Note that the reduced nucleotides absorb light at 340 nm; the oxidized forms do not (Fig. 13–15b). The plus sign in the abbreviations NAD^+ and NADP^+ does *not* indicate the net charge on these molecules (they are both negatively charged); rather, it indicates that the nicotinamide ring is in its oxidized form, with a positive charge on the nitrogen atom. In the abbreviations NADH and NADPH, the “H” denotes the added hydride ion. To refer to these nucleotides without specifying their oxidation state, we use NAD and NADP.

The total concentration of $\text{NAD}^+ + \text{NADH}$ in most tissues is about 10^{-5} M; that of $\text{NADP}^+ + \text{NADPH}$ is about 10^{-6} M. In many cells and tissues, the ratio of NAD^+ (oxidized) to NADH (reduced) is high, favoring hydride transfer from a substrate *to* NAD^+ to form NADH. By contrast, NADPH (reduced) is generally present in greater amounts than its oxidized form, NADP^+ , favoring hydride transfer *from* NADPH to a substrate. This reflects the specialized metabolic roles of the two coenzymes: NAD^+ generally functions in oxidations—usually as part of a catabolic reaction; and NADPH is the usual coenzyme in reductions—nearly always as part of an anabolic reaction. A few enzymes can use either coenzyme, but most show a strong preference for one over the other. The processes in which these two cofactors function are also segregated in specific organelles of eukaryotic cells: oxidations of fuels such as pyruvate, fatty acids, and α -keto acids derived from

TABLE 13–8 Stereospecificity of Dehydrogenases That Employ NAD ⁺ or NADP ⁺ as Coenzymes			
Enzyme	Coenzyme	Stereochemical specificity for nicotinamide ring (A or B)	Text page(s)
Isocitrate dehydrogenase	NAD ⁺	A	XXX–XXX
α-Ketoglutarate dehydrogenase	NAD ⁺	B	XXX
Glucose 6-phosphate dehydrogenase	NADP ⁺	B	XXX
Malate dehydrogenase	NAD ⁺	A	XXX
Glutamate dehydrogenase	NAD ⁺ or NADP ⁺	B	XXX
Glyceraldehyde 3-phosphate dehydrogenase	NAD ⁺	B	XXX
Lactate dehydrogenase	NAD ⁺	A	XXX
Alcohol dehydrogenase	NAD ⁺	A	XXX

carrier of electrons from one metabolite to another. For example, in the production of alcohol during fermentation of glucose by yeast cells, a hydride ion is removed from glyceraldehyde 3-phosphate by one enzyme (glyceraldehyde 3-phosphate dehydrogenase, a type B enzyme) and transferred to NAD⁺. The NADH produced then leaves the enzyme surface and diffuses to another enzyme (alcohol dehydrogenase, a type A enzyme), which transfers a hydride ion to acetaldehyde, producing ethanol:



Notice that in the overall reaction there is no net production or consumption of NAD⁺ or NADH; the coenzymes function catalytically and are recycled repeatedly without a net change in the concentration of NAD⁺ + NADH.

Dietary Deficiency of Niacin, the Vitamin Form of NAD and NADP, Causes Pellagra

The pyridine-like rings of NAD and NADP are derived from the vitamin **niacin** (nicotinic acid; Fig. 13–17), which is synthesized from tryptophan. Humans generally cannot synthesize niacin in sufficient quantities, and this is especially so for those with diets low in tryptophan (maize, for example, has a low tryptophan content). Niacin deficiency, which affects all the NAD(P)-dependent dehydrogenases, causes the serious human disease pellagra (Italian for “rough skin”) and a related disease in dogs, blacktongue. These diseases are characterized by the “three Ds”: dermatitis, diarrhea, and dementia, followed in many cases by death. A century ago, pellagra was a common human disease; in the southern United States, where maize was a dietary staple, about 100,000 people were afflicted and about 10,000 died between 1912 and 1916. In 1920 Joseph Goldberger showed pellagra to be caused by a dietary insufficiency, and in 1937 Frank Strong, D. Wayne Wolley, and Conrad Elvehjem identified niacin as the curative agent for blacktongue. Supplementation of the human diet with this inexpensive compound led to the eradication of pellagra in the populations of the developed world—with one significant exception. Pellagra is still found among alcoholics, whose intestinal absorption of niacin is much

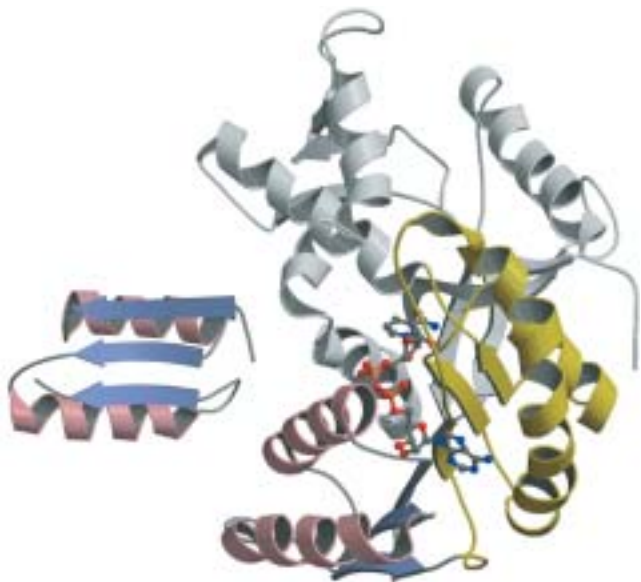


FIGURE 13–16 The nucleotide binding domain of the enzyme lactate dehydrogenase. (a) The Rossmann fold is a structural motif found in the NAD-binding site of many dehydrogenases. It consists of a six-stranded parallel β sheet and four α helices; inspection reveals the arrangement to be a pair of structurally similar β - α - β - α - β motifs. (b) The dinucleotide NAD binds in an extended conformation through hydrogen bonds and salt bridges (derived from PDB ID 3LDH).

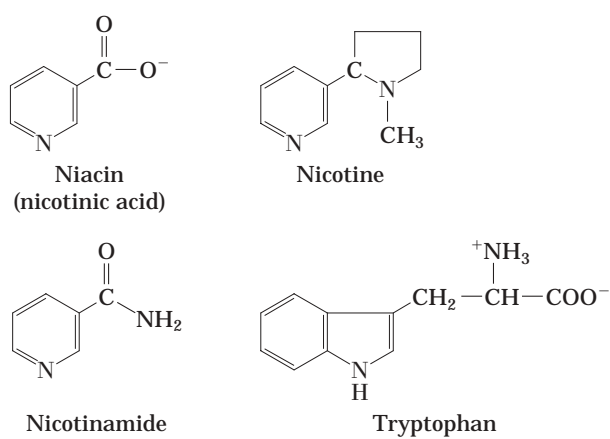


FIGURE 13-17 Structures of niacin (nicotinic acid) and its derivative nicotinamide. The biosynthetic precursor of these compounds is tryptophan. In the laboratory, nicotinic acid was first produced by oxidation of the natural product nicotine—thus the name. Both nicotinic acid and nicotinamide cure pellagra, but nicotine (from cigarettes or elsewhere) has no curative activity.

reduced, and whose caloric needs are often met with distilled spirits that are virtually devoid of vitamins, including niacin. In a few places, including the Deccan Plateau in India, pellagra still occurs, especially among the poor. ■

Flavin Nucleotides Are Tightly Bound in Flavoproteins

Flavoproteins (Table 13-9) are enzymes that catalyze oxidation-reduction reactions using either flavin mononucleotide (FMN) or flavin adenine dinucleotide (FAD) as coenzyme (Fig. 13-18). These coenzymes, the **flavin nucleotides**, are derived from the vitamin riboflavin. The fused ring structure of flavin nucleotides (the isoalloxazine ring) undergoes reversible reduction, accepting either one or two electrons in the form of one or two hydrogen atoms (each atom an electron plus a proton) from a reduced substrate. The fully reduced forms are abbreviated FADH₂ and FMNH₂. When a fully oxidized flavin nucleotide accepts only one electron (one hydrogen atom), the semiquinone form of the isoal-

TABLE 13-9 Some Enzymes (Flavoproteins) That Employ Flavin Nucleotide Coenzymes

Enzyme	Flavin nucleotide	Text page(s)
Acyl-CoA dehydrogenase	FAD	XXX
Dihydrolipoyl dehydrogenase	FAD	XXX
Succinate dehydrogenase	FAD	XXX
Glycerol 3-phosphate dehydrogenase	FAD	XXX
Thioredoxin reductase	FAD	XXX-XXX
NADH dehydrogenase (Complex I)	FMN	XXX
Glycolate oxidase	FMN	XXX

loxazine ring is produced, abbreviated FADH• and FMNH•. Because flavoproteins can participate in either one- or two-electron transfers, this class of proteins is involved in a greater diversity of reactions than the NAD (P)-linked dehydrogenases.

Like the nicotinamide coenzymes (Fig. 13-15), the flavin nucleotides undergo a shift in a major absorption band on reduction. Flavoproteins that are fully reduced (two electrons accepted) generally have an absorption maximum near 360 nm. When partially reduced (one electron), they acquire another absorption maximum at about 450 nm; when fully oxidized, the flavin has maxima at 370 and 440 nm. The intermediate radical form, reduced by one electron, has absorption maxima at 380, 480, 580, and 625 nm. These changes can be used to assay reactions involving a flavoprotein.

The flavin nucleotide in most flavoproteins is bound rather tightly to the protein, and in some enzymes, such as succinate dehydrogenase, it is bound covalently. Such tightly bound coenzymes are properly called prosthetic groups. They do not transfer electrons by diffusing from one enzyme to another; rather, they provide a means by which the flavoprotein can temporarily hold electrons while it catalyzes electron transfer from a reduced substrate to an electron acceptor. One important feature of the flavoproteins is the variability in the standard reduction potential (*E*°) of the bound flavin nucleotide. Tight association between the enzyme and prosthetic group confers on the flavin ring a reduction potential typical of that particular flavoprotein, sometimes quite different from the reduction potential of the free flavin nucleotide. FAD bound to succinate dehydrogenase, for example, has an *E*° close to 0.0 V, compared with -0.219 V for free FAD; *E*° for other flavoproteins ranges from -0.40 V to +0.06 V.



Frank Strong,
1908-1993



D. Wayne Woolley,
1914-1966



Conrad Elvehjem,
1901-1962

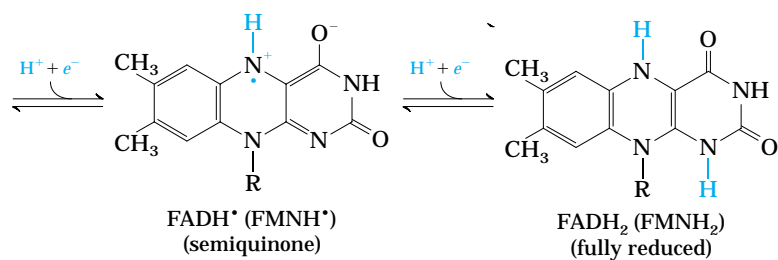
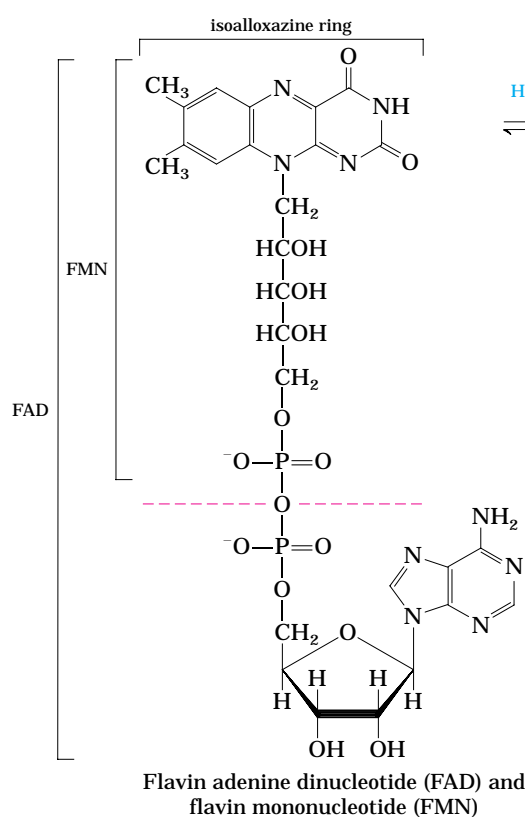


FIGURE 13–18 Structures of oxidized and reduced FAD and FMN. FMN consists of the structure above the dashed line on the FAD (oxidized form). The flavin nucleotides accept two hydrogen atoms (two electrons and two protons), both of which appear in the flavin ring system. When FAD or FMN accepts only one hydrogen atom, the semi-quinone, a stable free radical, forms.

Flavoproteins are often very complex; some have, in addition to a flavin nucleotide, tightly bound inorganic ions (iron or molybdenum, for example) capable of participating in electron transfers.

Certain flavoproteins act in a quite different role as light receptors. **Cryptochromes** are a family of flavoproteins, widely distributed in the eukaryotic phyla, that mediate the effects of blue light on plant development and the effects of light on mammalian circadian rhythms (oscillations in physiology and biochemistry, with a 24-hour period). The cryptochromes are homologs of another family of flavoproteins, the photolyases. Found in both prokaryotes and eukaryotes, **photolyases** use the energy of absorbed light to repair chemical defects in DNA.

We examine the function of flavoproteins as electron carriers in Chapter 19, when we consider their roles in oxidative phosphorylation (in mitochondria) and photophosphorylation (in chloroplasts), and we describe the photolyase reactions in Chapter 25.

SUMMARY 13.3 Biological Oxidation-Reduction Reactions

- In many organisms, a central energy-conserving process is the stepwise oxidation of glucose to CO₂, in which some of the energy of oxidation is conserved in ATP as electrons are passed to O₂.

- Biological oxidation-reduction reactions can be described in terms of two half-reactions, each with a characteristic standard reduction potential, E° .
- When two electrochemical half-cells, each containing the components of a half-reaction, are connected, electrons tend to flow to the half-cell with the higher reduction potential. The strength of this tendency is proportional to the difference between the two reduction potentials (ΔE) and is a function of the concentrations of oxidized and reduced species.
- The standard free-energy change for an oxidation-reduction reaction is directly proportional to the difference in standard reduction potentials of the two half-cells: $\Delta G^\circ = -nF\Delta E^\circ$.
- Many biological oxidation reactions are dehydrogenations in which one or two hydrogen atoms ($H^+ + e^-$) are transferred from a substrate to a hydrogen acceptor. Oxidation-reduction reactions in living cells involve specialized electron carriers.
- NAD and NADP are the freely diffusible coenzymes of many dehydrogenases. Both NAD⁺ and NADP⁺ accept two electrons and

one proton. NAD and NADP are bound to dehydrogenases in a widely conserved structural motif called the Rossmann fold.

- FAD and FMN, the flavin nucleotides, serve as tightly bound prosthetic groups of

flavoproteins. They can accept either one or two electrons. Flavoproteins also serve as light receptors in cryptochromes and photolyases.

Key Terms

Terms in bold are defined in the glossary.

autotroph XXX	thioester XXX	dehydrogenation XXX
heterotroph XXX	adenylation XXX	dehydrogenases XXX
metabolism XXX	inorganic pyrophosphatase XXX	reducing equivalent XXX
metabolic pathways XXX	nucleoside diphosphate	standard reduction potential
metabolite XXX	kinase XXX	(E°) XXX
intermediary metabolism XXX	adenylate kinase XXX	pyridine nucleotide XXX
catabolism XXX	creatine kinase XXX	oxidoreductase XXX
anabolism XXX	phosphagens XXX	flavoprotein XXX
standard transformed constants XXX	polyphosphate kinase-1, -2 XXX	flavin nucleotides XXX
phosphorylation potential	electromotive force (emf) XXX	cryptochrome XXX
(ΔG_p) XXX	conjugate redox pair XXX	photolyase XXX

Further Reading

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Bergethon, P.R. (1998) *The Physical Basis of Biochemistry*, Springer Verlag, New York.
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Problems

- 1. Entropy Changes during Egg Development** Consider a system consisting of an egg in an incubator. The white and yolk of the egg contain proteins, carbohydrates, and lipids. If fertilized, the egg is transformed from a single cell to a complex organism. Discuss this irreversible process in terms of the entropy changes in the system, surroundings, and universe. Be sure that you first clearly define the system and surroundings.
- 2. Calculation of ΔG° from an Equilibrium Constant** Calculate the standard free-energy changes of the following metabolically important enzyme-catalyzed reactions at 25 °C and pH 7.0, using the equilibrium constants given.
- (a) $\text{Glutamate} + \text{oxaloacetate} \xrightleftharpoons[\text{aspartate aminotransferase}]{} \text{aspartate} + \alpha\text{-ketoglutarate}$ $K'_{\text{eq}} = 6.8$

(b) $\text{Dihydroxyacetone phosphate} \xrightleftharpoons[\text{triose phosphate isomerase}]{} \text{glyceraldehyde 3-phosphate}$ $K'_{\text{eq}} = 0.0475$

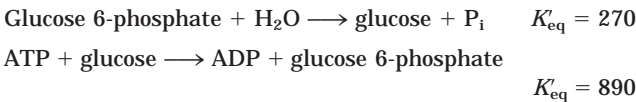
(c) $\text{Fructose 6-phosphate} + \text{ATP} \xrightleftharpoons[\text{phosphofructokinase}]{} \text{fructose 1,6-bisphosphate} + \text{ADP}$ $K'_{\text{eq}} = 254$
- 3. Calculation of the Equilibrium Constant from ΔG°** Calculate the equilibrium constants K'_{eq} for each of the fol-

- lowing reactions at pH 7.0 and 25 °C, using the ΔG° values in Table 13–4.
- (a) $\text{Glucose 6-phosphate} + \text{H}_2\text{O} \xrightleftharpoons[\text{glucose 6-phosphatase}]{} \text{glucose} + \text{P}_i$

(b) $\text{Lactose} + \text{H}_2\text{O} \xrightleftharpoons[\beta\text{-galactosidase}]{} \text{glucose} + \text{galactose}$

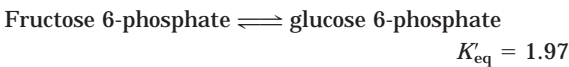
(c) $\text{Malate} \xrightleftharpoons[\text{fumarase}]{} \text{fumarate} + \text{H}_2\text{O}$
- 4. Experimental Determination of K'_{eq} and ΔG°** If a 0.1 M solution of glucose 1-phosphate is incubated with a catalytic amount of phosphoglucomutase, the glucose 1-phosphate is transformed to glucose 6-phosphate. At equilibrium, the concentrations of the reaction components are
- $$\begin{array}{ccc} \text{Glucose 1-phosphate} & \rightleftharpoons & \text{glucose 6-phosphate} \\ 4.5 \times 10^{-3} \text{ M} & & 9.6 \times 10^{-2} \text{ M} \end{array}$$
- Calculate K'_{eq} and ΔG° for this reaction at 25 °C.
- 5. Experimental Determination of ΔG° for ATP Hydrolysis** A direct measurement of the standard free-energy change associated with the hydrolysis of ATP is technically demanding because the minute amount of ATP remaining at equilibrium is difficult to measure accurately. The value of ΔG° can be calculated indirectly, however, from the equilib-

rium constants of two other enzymatic reactions having less favorable equilibrium constants:



Using this information, calculate the standard free energy of hydrolysis of ATP at 25 °C.

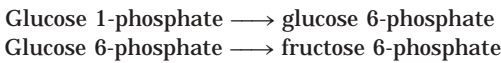
6. Difference between $\Delta G'^{\circ}$ and ΔG Consider the following interconversion, which occurs in glycolysis (Chapter 14):



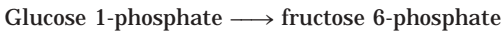
- (a) What is $\Delta G'^{\circ}$ for the reaction (at 25 °C)?
(b) If the concentration of fructose 6-phosphate is adjusted to 1.5 M and that of glucose 6-phosphate is adjusted to 0.50 M, what is ΔG ?
(c) Why are $\Delta G'^{\circ}$ and ΔG different?

7. Dependence of ΔG on pH The free energy released by the hydrolysis of ATP under standard conditions at pH 7.0 is −30.5 kJ/mol. If ATP is hydrolyzed under standard conditions but at pH 5.0, is more or less free energy released? Explain.

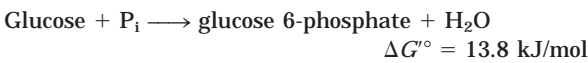
8. The $\Delta G'^{\circ}$ for Coupled Reactions Glucose 1-phosphate is converted into fructose 6-phosphate in two successive reactions:



Using the $\Delta G'^{\circ}$ values in Table 13–4, calculate the equilibrium constant, K'_{eq} , for the sum of the two reactions at 25 °C:

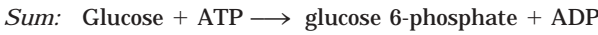
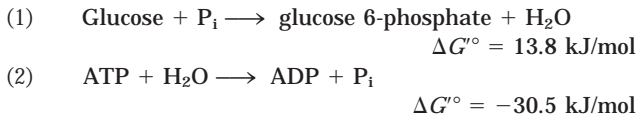


9. Strategy for Overcoming an Unfavorable Reaction: ATP-Dependent Chemical Coupling The phosphorylation of glucose to glucose 6-phosphate is the initial step in the catabolism of glucose. The direct phosphorylation of glucose by P_i is described by the equation



- (a) Calculate the equilibrium constant for the above reaction. In the rat hepatocyte the physiological concentrations of glucose and P_i are maintained at approximately 4.8 mM. What is the equilibrium concentration of glucose 6-phosphate obtained by the direct phosphorylation of glucose by P_i? Does this reaction represent a reasonable metabolic step for the catabolism of glucose? Explain.
(b) In principle, at least, one way to increase the concentration of glucose 6-phosphate is to drive the equilibrium reaction to the right by increasing the intracellular concentrations of glucose and P_i. Assuming a fixed concentration of P_i at 4.8 mM, how high would the intracellular concentration of glucose have to be to give an equilibrium concentration of glucose 6-phosphate of 250 μM (the normal physiological concentration)? Would this route be physiologically reasonable, given that the maximum solubility of glucose is less than 1 M?

(c) The phosphorylation of glucose in the cell is coupled to the hydrolysis of ATP; that is, part of the free energy of ATP hydrolysis is used to phosphorylate glucose:



Calculate K'_{eq} for the overall reaction. For the ATP-dependent phosphorylation of glucose, what concentration of glucose is needed to achieve a 250 μM intracellular concentration of glucose 6-phosphate when the concentrations of ATP and ADP are 3.38 mM and 1.32 mM, respectively? Does this coupling process provide a feasible route, at least in principle, for the phosphorylation of glucose in the cell? Explain.

(d) Although coupling ATP hydrolysis to glucose phosphorylation makes thermodynamic sense, we have not yet specified how this coupling is to take place. Given that coupling requires a common intermediate, one conceivable route is to use ATP hydrolysis to raise the intracellular concentration of P_i and thus drive the unfavorable phosphorylation of glucose by P_i. Is this a reasonable route? (Think about the solubility products of metabolic intermediates.)

(e) The ATP-coupled phosphorylation of glucose is catalyzed in hepatocytes by the enzyme glucokinase. This enzyme binds ATP and glucose to form a glucose-ATP-enzyme complex, and the phosphoryl group is transferred directly from ATP to glucose. Explain the advantages of this route.

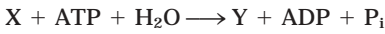
10. Calculations of $\Delta G'^{\circ}$ for ATP-Coupled Reactions From data in Table 13–6 calculate the $\Delta G'^{\circ}$ value for the reactions

- (a) Phosphocreatine + ADP → creatine + ATP
(b) ATP + fructose → ADP + fructose 6-phosphate

11. Coupling ATP Cleavage to an Unfavorable Reaction

To explore the consequences of coupling ATP hydrolysis under physiological conditions to a thermodynamically unfavorable biochemical reaction, consider the hypothetical transformation X → Y, for which $\Delta G'^{\circ} = 20 \text{ kJ/mol}$.

- (a) What is the ratio [Y]/[X] at equilibrium?
(b) Suppose X and Y participate in a sequence of reactions during which ATP is hydrolyzed to ADP and P_i. The overall reaction is



Calculate [Y]/[X] for this reaction at equilibrium. Assume that the equilibrium concentrations of ATP, ADP, and P_i are 1 M.

(c) We know that [ATP], [ADP], and [P_i] are *not* 1 M under physiological conditions. Calculate [Y]/[X] for the ATP-coupled reaction when the values of [ATP], [ADP], and [P_i] are those found in rat myocytes (Table 13–5).

12. Calculations of ΔG at Physiological Concentrations Calculate the physiological ΔG (not $\Delta G'^{\circ}$) for the reaction



at 25 °C, as it occurs in the cytosol of neurons, with phosphocreatine at 4.7 mM, creatine at 1.0 mM, ADP at 0.73 mM, and ATP at 2.6 mM.

13. Free Energy Required for ATP Synthesis under Physiological Conditions In the cytosol of rat hepatocytes, the mass-action ratio, Q , is

$$\frac{[\text{ATP}]}{[\text{ADP}][\text{P}_i]} = 5.33 \times 10^2 \text{ M}^{-1}$$

Calculate the free energy required to synthesize ATP in a rat hepatocyte.

14. Daily ATP Utilization by Human Adults

(a) A total of 30.5 kJ/mol of free energy is needed to synthesize ATP from ADP and P_i when the reactants and products are at 1 M concentrations (standard state). Because the actual physiological concentrations of ATP, ADP, and P_i are not 1 M, the free energy required to synthesize ATP under physiological conditions is different from ΔG° . Calculate the free energy required to synthesize ATP in the human hepatocyte when the physiological concentrations of ATP, ADP, and P_i are 3.5, 1.50, and 5.0 mM, respectively.

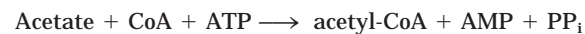
(b) A 68 kg (150 lb) adult requires a caloric intake of 2,000 kcal (8,360 kJ) of food per day (24 h). The food is metabolized and the free energy is used to synthesize ATP, which then provides energy for the body's daily chemical and mechanical work. Assuming that the efficiency of converting food energy into ATP is 50%, calculate the weight of ATP used by a human adult in 24 h. What percentage of the body weight does this represent?

(c) Although adults synthesize large amounts of ATP daily, their body weight, structure, and composition do not change significantly during this period. Explain this apparent contradiction.

15. Rates of Turnover of γ and β Phosphates of ATP

If a small amount of ATP labeled with radioactive phosphorus in the terminal position, $[\gamma\text{-}^{32}\text{P}]\text{ATP}$, is added to a yeast extract, about half of the ^{32}P activity is found in P_i within a few minutes, but the concentration of ATP remains unchanged. Explain. If the same experiment is carried out using ATP labeled with ^{32}P in the central position, $[\beta\text{-}^{32}\text{P}]\text{ATP}$, the ^{32}P does not appear in P_i within such a short time. Why?

16. Cleavage of ATP to AMP and PP_i during Metabolism The synthesis of the activated form of acetate (acetyl-CoA) is carried out in an ATP-dependent process:



(a) The ΔG° for the hydrolysis of acetyl-CoA to acetate and CoA is -32.2 kJ/mol and that for hydrolysis of ATP to AMP and PP_i is -30.5 kJ/mol. Calculate ΔG° for the ATP-dependent synthesis of acetyl-CoA.

(b) Almost all cells contain the enzyme inorganic pyrophosphatase, which catalyzes the hydrolysis of PP_i to P_i . What effect does the presence of this enzyme have on the synthesis of acetyl-CoA? Explain.

17. Energy for H^+ Pumping The parietal cells of the stomach lining contain membrane "pumps" that transport hydrogen ions from the cytosol of these cells (pH 7.0) into the stomach, contributing to the acidity of gastric juice (pH 1.0). Calculate the free energy required to transport 1 mol of hydrogen ions through these pumps. (Hint: See Chapter 11.) Assume a temperature of 25 °C.

18. Standard Reduction Potentials The standard reduction potential, E° , of any redox pair is defined for the half-cell reaction:



The E° values for the NAD^+/NADH and pyruvate/lactate conjugate redox pairs are -0.32 V and -0.19 V, respectively.

(a) Which conjugate pair has the greater tendency to lose electrons? Explain.

(b) Which is the stronger oxidizing agent? Explain.

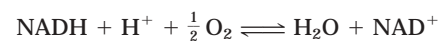
(c) Beginning with 1 M concentrations of each reactant and product at pH 7, in which direction will the following reaction proceed?



(d) What is the standard free-energy change (ΔG°) at 25 °C for the conversion of pyruvate to lactate?

(e) What is the equilibrium constant (K_{eq}) for this reaction?

19. Energy Span of the Respiratory Chain Electron transfer in the mitochondrial respiratory chain may be represented by the net reaction equation



(a) Calculate the value of ΔE° for the net reaction of mitochondrial electron transfer. Use E° values from Table 13-7.

(b) Calculate ΔG° for this reaction.

(c) How many ATP molecules can *theoretically* be generated by this reaction if the free energy of ATP synthesis under cellular conditions is 52 kJ/mol?

20. Dependence of Electromotive Force on Concentrations Calculate the electromotive force (in volts) registered by an electrode immersed in a solution containing the following mixtures of NAD^+ and NADH at pH 7.0 and 25 °C, with reference to a half-cell of E° 0.00 V.

- (a) 1.0 mM NAD^+ and 10 mM NADH
- (b) 1.0 mM NAD^+ and 1.0 mM NADH
- (c) 10 mM NAD^+ and 1.0 mM NADH

21. Electron Affinity of Compounds List the following substances in order of increasing tendency to accept electrons: (a) α -ketoglutarate + CO_2 (yielding isocitrate); (b) oxaloacetate; (c) O_2 ; (d) NADP^+ .

22. Direction of Oxidation-Reduction Reactions Which of the following reactions would you expect to proceed in the direction shown, under standard conditions, assuming that the appropriate enzymes are present to catalyze them?

