

# BIOLOGI SEL

## PERTEMUAN 5

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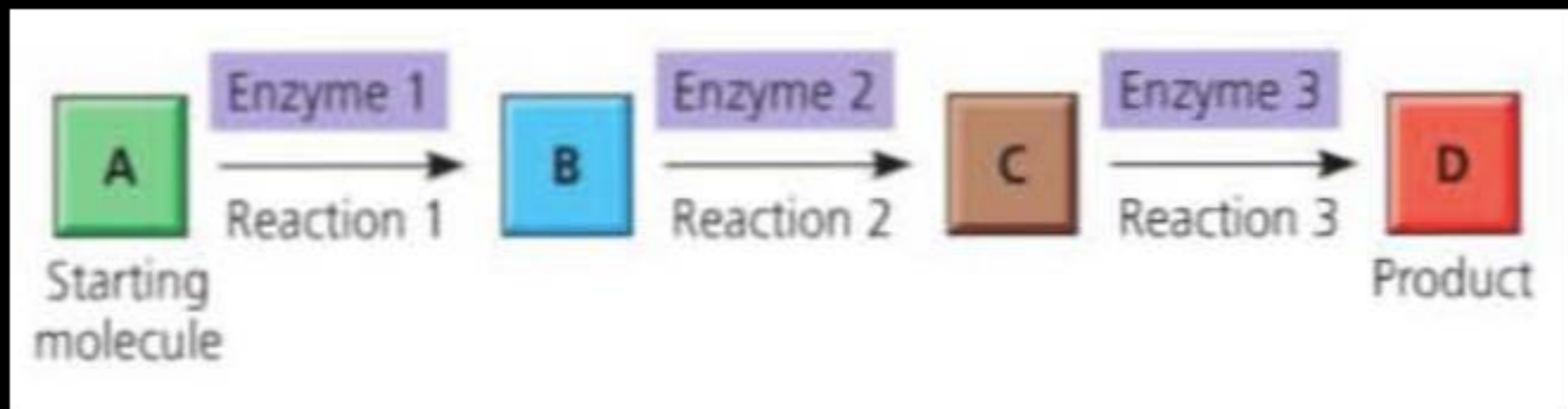
# KONSEP KUNCI

1. Suatu metabolisme organisme men transform materi dan energi, subjek dari hukum termodinamika
2. Energi bebas mengubah suatu reaksi memberi tahu kita apakah reaksi terjadi secara spontan atau tidak
3. Energi selular ATP bekerja dengan mengkopel reaksi eksergonik ke reaksi endergonik
4. Enzim mempercepat reaksi metabolit dengan menurunkan hambatan energi
5. Regulasi aktivitas enzim membantu mengontrol metabolisme



1. Metabolisme suatu organisme mentransnform materi dan energi, sebjek hukum termodinamika

# Organisasi Kimia Kehidupan ke dalam Jalur Metabolisme



# **INTEGRATION OF METABOLISM**

**Metabolism consists of catabolism and anabolism**

**Catabolism: degradative pathways**  
– Usually energy-yielding!

**Anabolism: biosynthetic pathways**  
– energy-requiring!

# Bentuk Energi

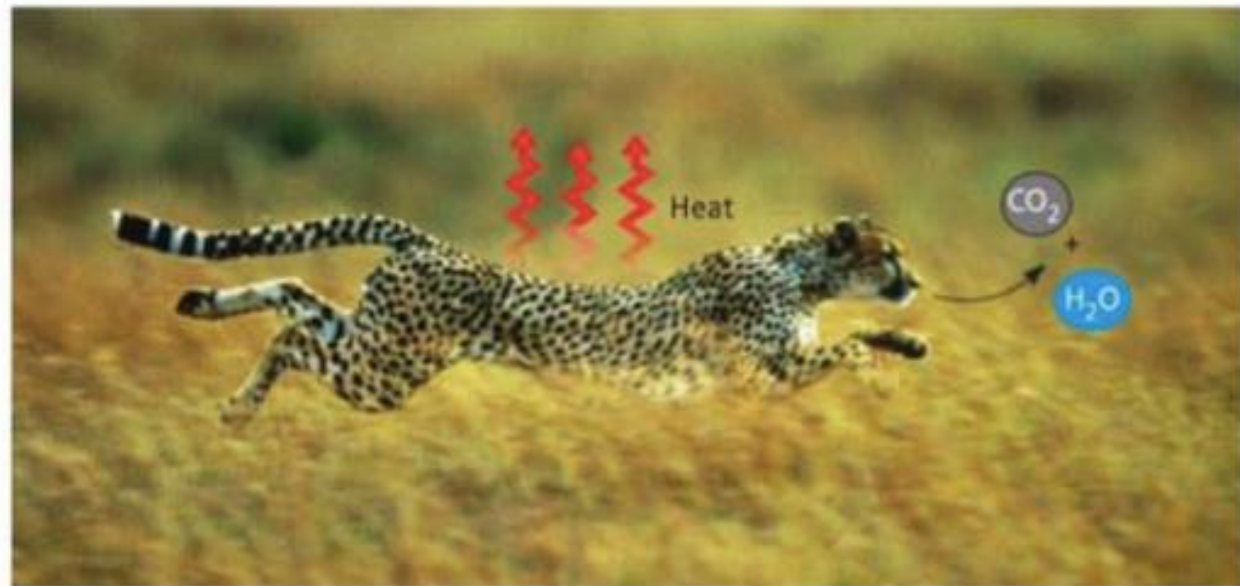


▲ **Figure 8.2** Transformations between potential and kinetic energy.

# Hukum Termodinamika



**(a) First law of thermodynamics:** Energy can be transferred or transformed but neither created nor destroyed. For example, the chemical (potential) energy in food will be converted to the kinetic energy of the cheetah's movement in (b).



**(b) Second law of thermodynamics:** Every energy transfer or transformation increases the disorder (entropy) of the universe. For example, disorder is added to the cheetah's surroundings in the form of heat and the small molecules that are the by-products of metabolism.

**▲ Figure 8.3 The two laws of thermodynamics.**

2. PERUBAHAN ENERGI BEBAS DARI  
SUATU REAKSI MEMBERITAHU KITA  
APAKAH REAKSI TERSEBUT TERJADI  
SECARA SPONTAN ATAU TIDAK



## Perubahan Energi Bebas

$$\Delta G = \Delta H - T\Delta S$$

$\Delta G$  : Perubahan Energi Bebas

$\Delta H$  : Perubahan Entalpi Sistem (Total Energi)

T : Suhu absolut (K)

$\Delta S$  : perubahan Entropi Sistem

# Energi Bebas, Stabilitas & Equilibrium

$$\Delta G = G_{\text{final state}} - G_{\text{initial state}}$$

- More free energy (higher  $G$ )
- Less stable
- Greater work capacity

## In a spontaneous change

- The free energy of the system decreases ( $\Delta G < 0$ )
- The system becomes more stable
- The released free energy can be harnessed to do work

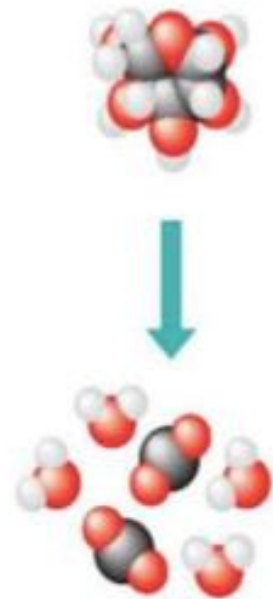
- Less free energy (lower  $G$ )
- More stable
- Less work capacity



**(a) Gravitational motion.** Objects move spontaneously from a higher altitude to a lower one.



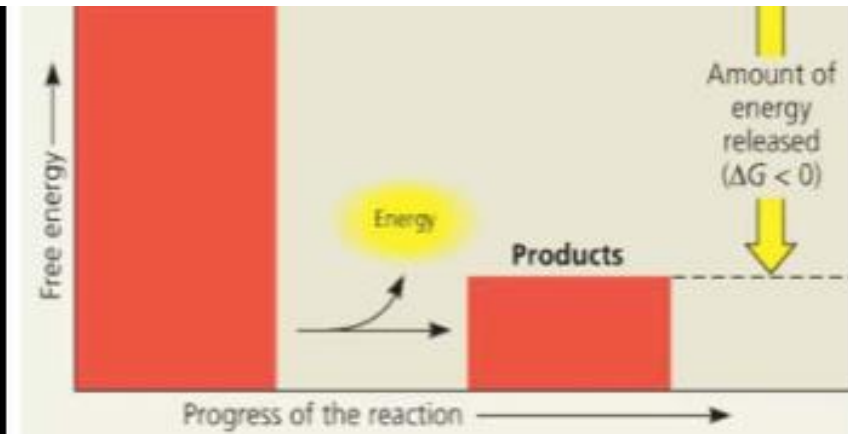
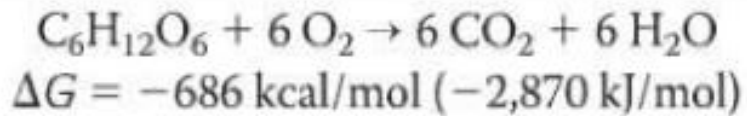
**(b) Diffusion.** Molecules in a drop of dye diffuse until they are randomly dispersed.



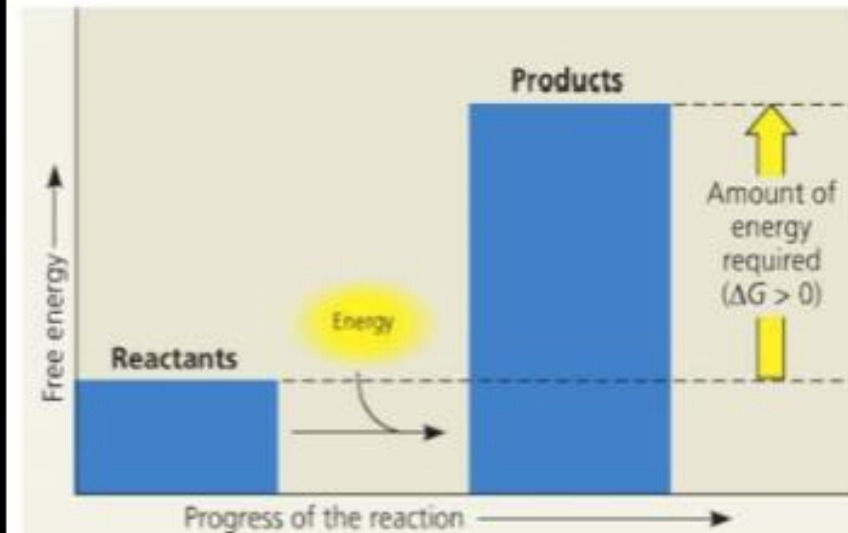
**(c) Chemical reaction.** In a cell, a sugar molecule is broken down into simpler molecules.

# ENERGI BEBAS DAN METABOLISME

## Reaksi Eksergonik & Endergonik dalam Metabolisme



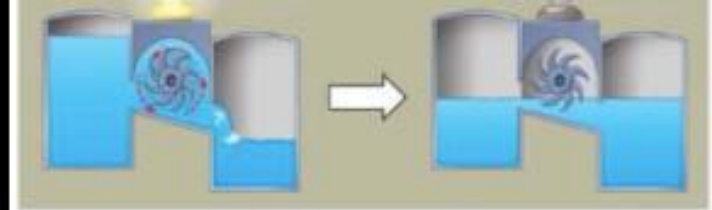
(a) Exergonic reaction: energy released



(b) Endergonic reaction: energy required

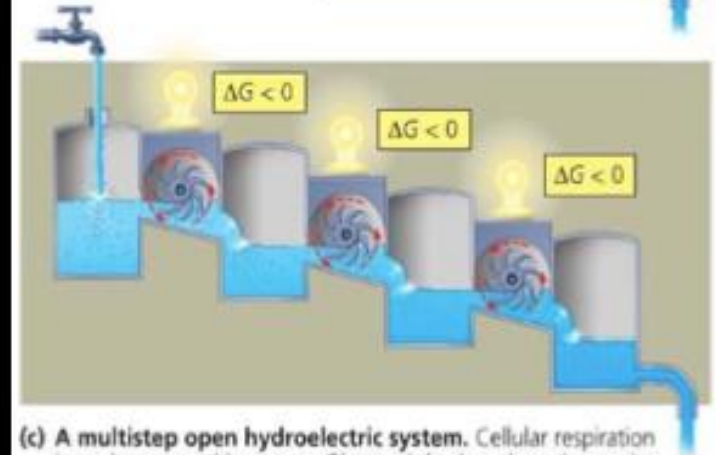
▲ **Figure 8.6** Free energy changes ( $\Delta G$ ) in exergonic and endergonic reactions.

# EKUILIBRIUM DAN METABOLISME



(a) **An isolated hydroelectric system.** Water flowing downhill turns a turbine that drives a generator providing electricity to a light bulb, but only until the system reaches equilibrium.

(b) **An open hydroelectric system.** Flowing water keeps driving the generator because intake and outflow of water keep the system from reaching equilibrium.

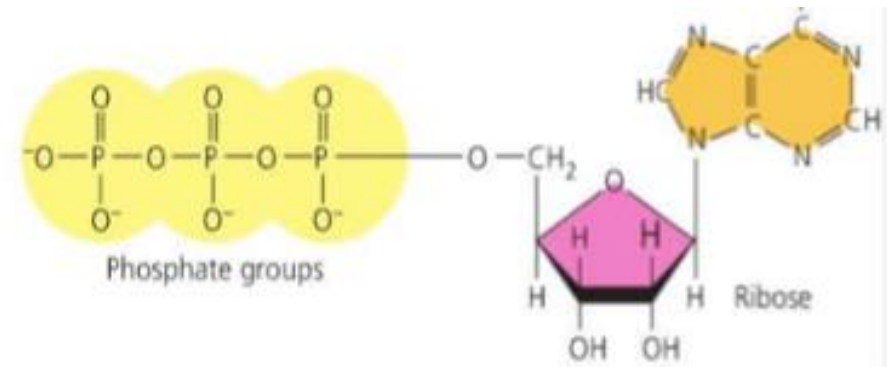


(c) **A multistep open hydroelectric system.** Cellular respiration is analogous to this system: Glucose is broken down in a series of exergonic reactions that power the work of the cell. The product of each reaction becomes the reactant for the next, so no reaction reaches equilibrium.

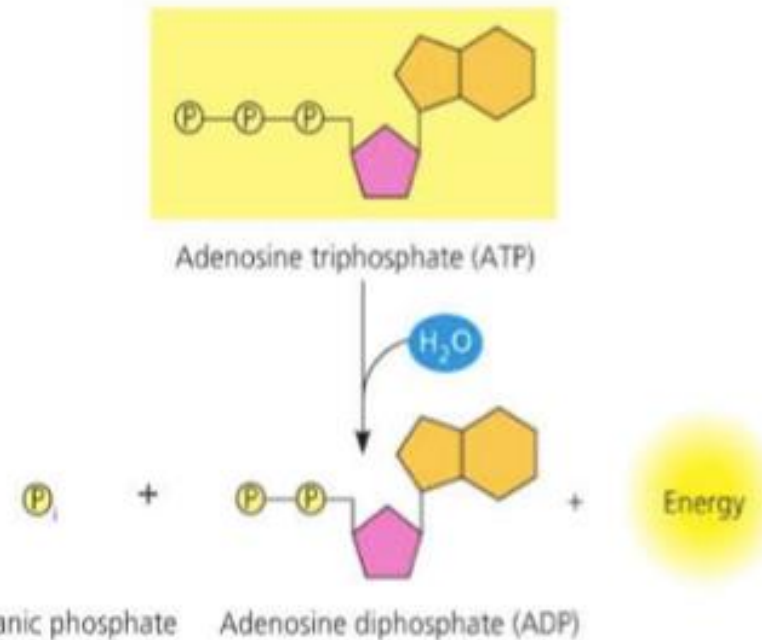
▲ **Figure 8.7** Equilibrium and work in isolated and open systems.

3. ATP MEMBERI TENAGA KERJA  
SELULAR DENGAN MENGGKOPLE  
REAKSI EKSERGONIK KE REAKSI  
ENDERGONIK

# STRUKTUR DAN HIDROLISIS ATP

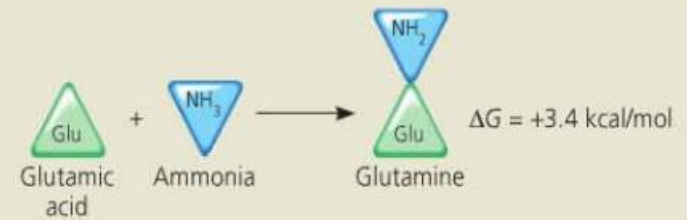


▲ **Figure 8.8** The structure of adenosine triphosphate (ATP). In the cell, most hydroxyl groups of phosphates are ionized ( $\text{—O}^-$ ).

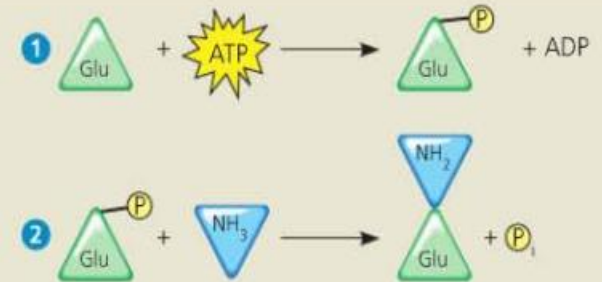


▲ **Figure 8.9** The hydrolysis of ATP. The reaction of ATP and water yields inorganic phosphate ( $\text{P}_i$ ) and ADP and releases energy.

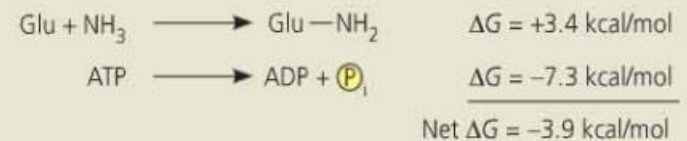
# BAGAIMANA ATP BEKERJA



**(a) Endergonic reaction.** Amino acid conversion by itself is endergonic ( $\Delta G$  is positive), so it is not spontaneous.



**(b) Coupled with ATP hydrolysis, an exergonic reaction.** In the cell, glutamine synthesis occurs in two steps, coupled by a phosphorylated intermediate. **1** ATP phosphorylates glutamic acid, making the amino acid less stable. **2** Ammonia displaces the phosphate group, forming glutamine.

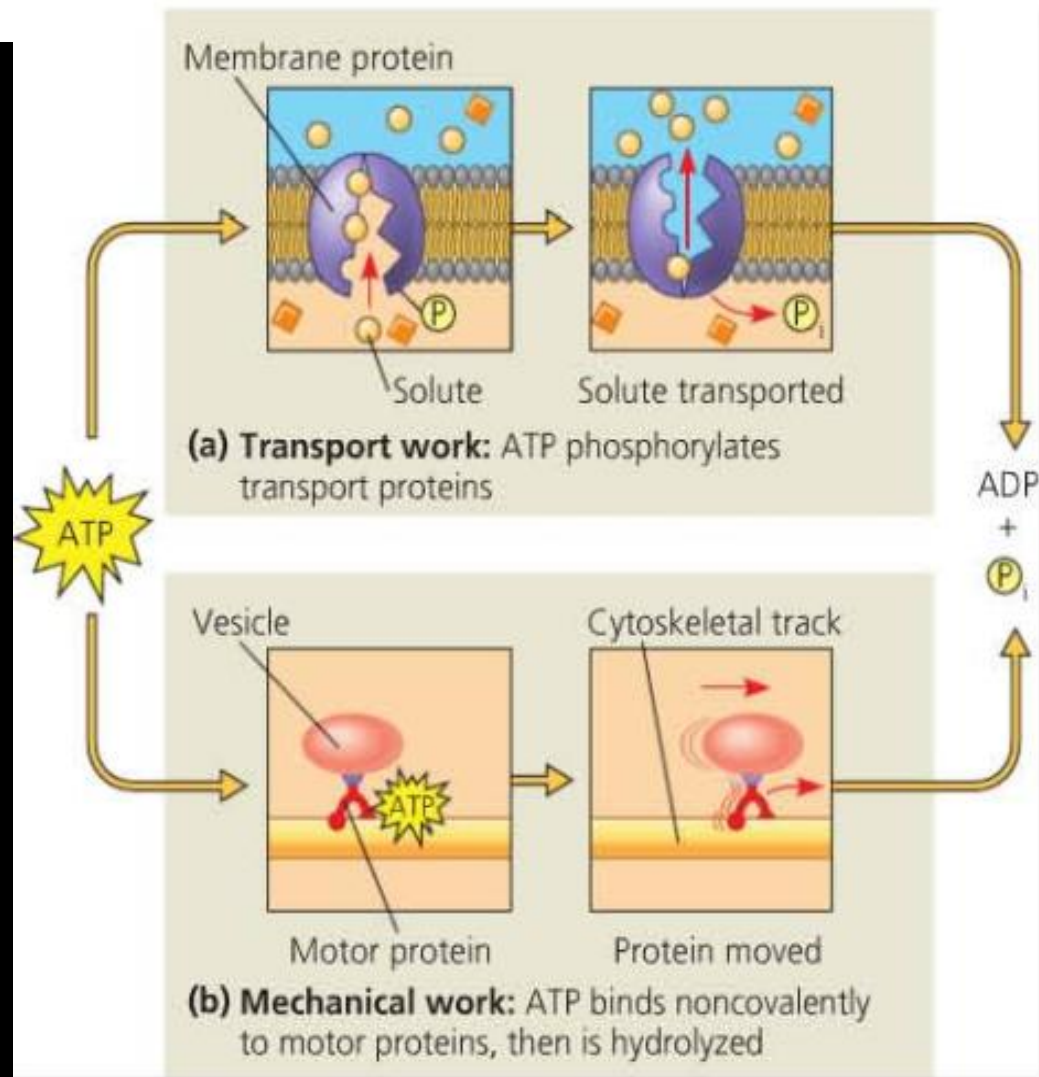


**(c) Overall free-energy change.** Adding the  $\Delta G$  (under standard conditions) for the amino acid conversion to the  $\Delta G$  for ATP hydrolysis gives the free-energy change for the overall reaction. Because the overall process is exergonic ( $\Delta G$  is negative), it occurs spontaneously.

▲ **Figure 8.10 How ATP drives chemical work: Energy coupling using ATP hydrolysis.** In this example, the exergonic process of ATP hydrolysis is used to drive an endergonic process—the cellular synthesis of the amino acid glutamine from glutamic acid and ammonia.



# REGENERASI ATP

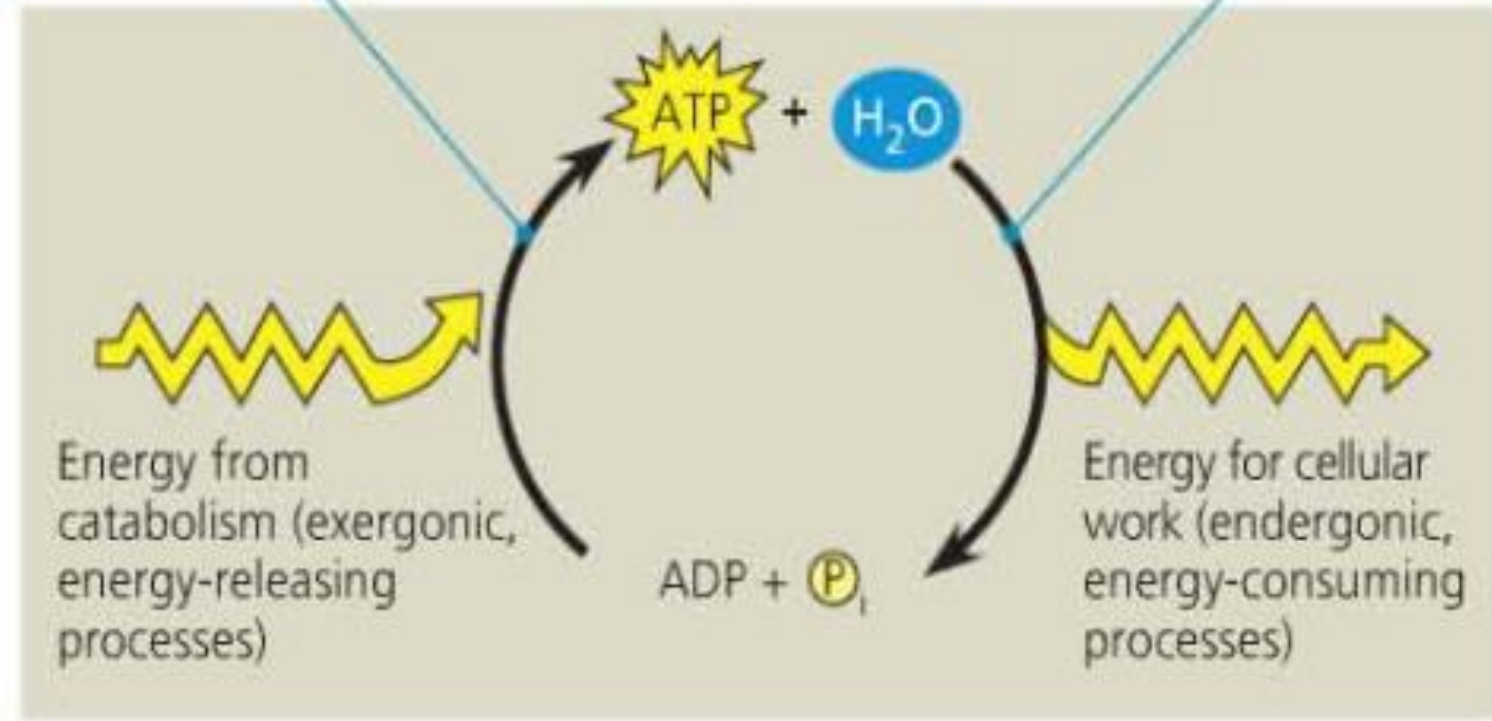


▲ **Figure 8.11 How ATP drives transport and mechanical work.** ATP hydrolysis causes changes in the shapes and binding affinities of proteins. This can occur either **(a)** directly, by phosphorylation, as shown for membrane proteins involved in active transport of solutes, or **(b)** indirectly, via noncovalent binding of ATP and its hydrolytic products, as is the case for motor proteins that move vesicles (and organelles) along cytoskeletal “tracks” in the cell.

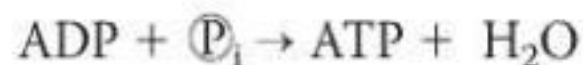


ATP synthesis from  
 $\text{ADP} + \text{P}_i$  requires energy

ATP hydrolysis to  
 $\text{ADP} + \text{P}_i$  yields energy

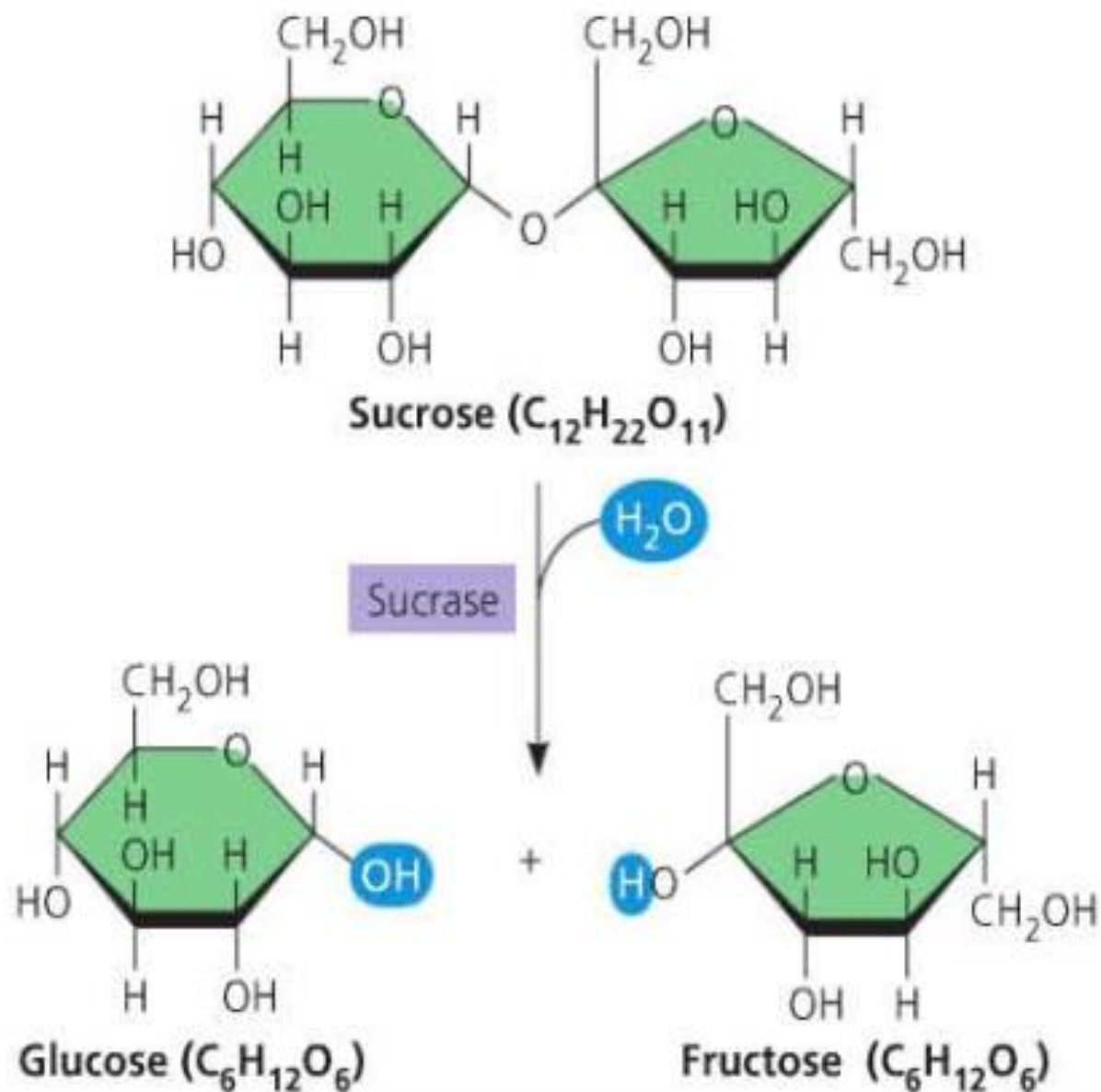


▲ **Figure 8.12 The ATP cycle.** Energy released by breakdown reactions (catabolism) in the cell is used to phosphorylate ADP, regenerating ATP. Chemical potential energy stored in ATP drives most cellular work.

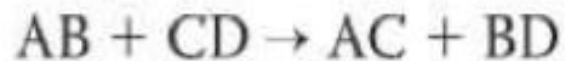


$$\Delta G = +7.3 \text{ kcal/mol } (+30.5 \text{ kJ/mol}) \text{ (standard conditions)}$$

4. ENZIM MEMPERCEPAT REAKSI  
METABOLIT DENGAN  
MENURUNKAN HAMBATAN  
ENERGI

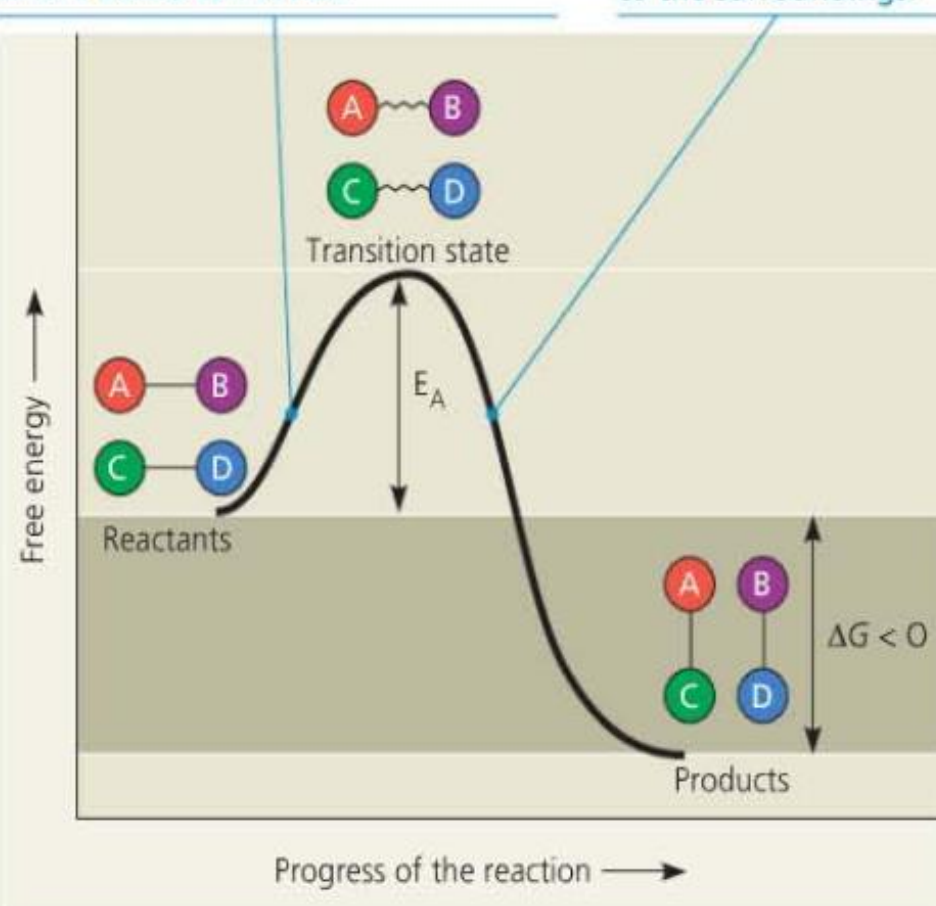


▲ **Figure 8.13** Example of an enzyme-catalyzed reaction: hydrolysis of sucrose by sucrase.

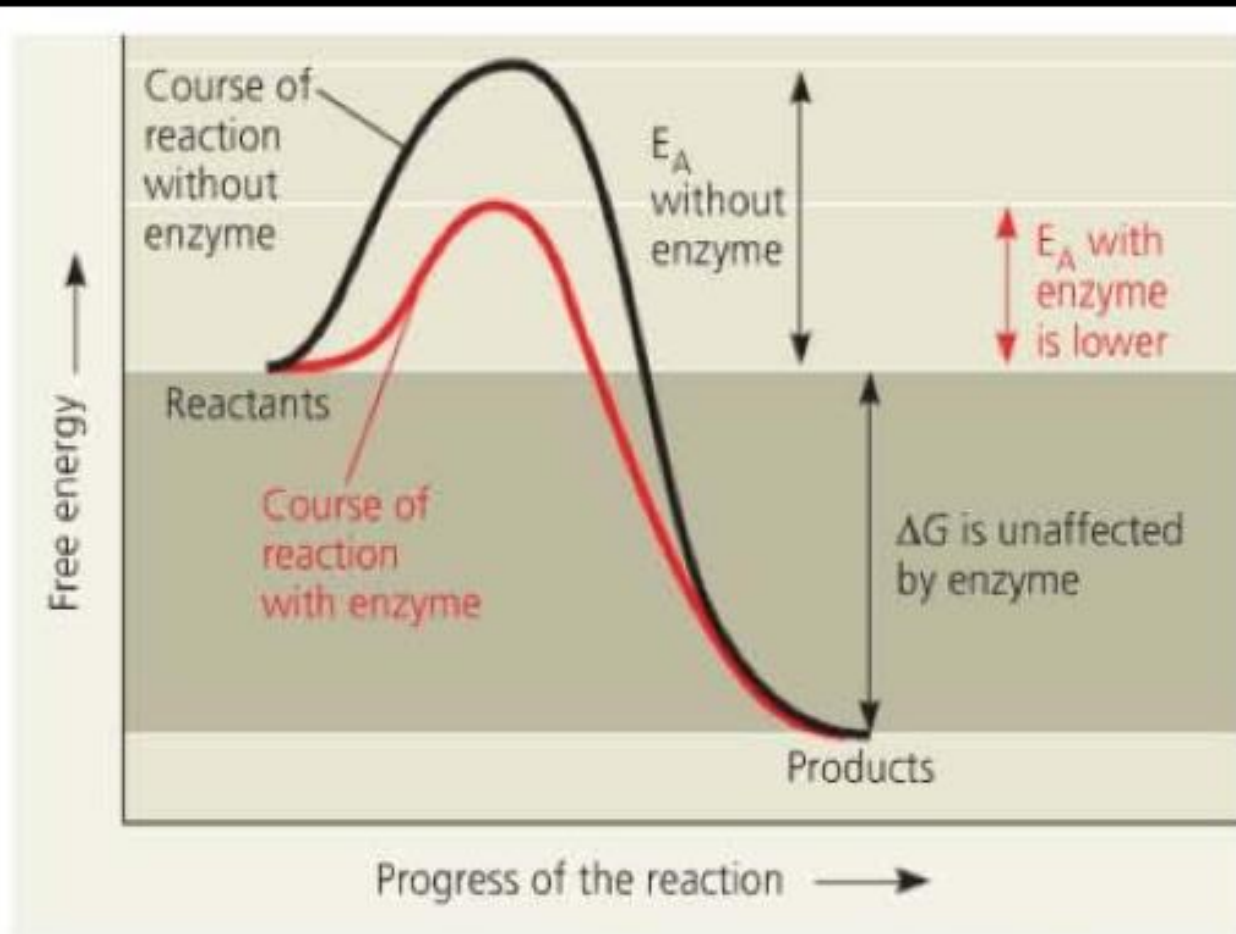


The reactants AB and CD must absorb enough energy from the surroundings to reach the unstable transition state, where bonds can break.

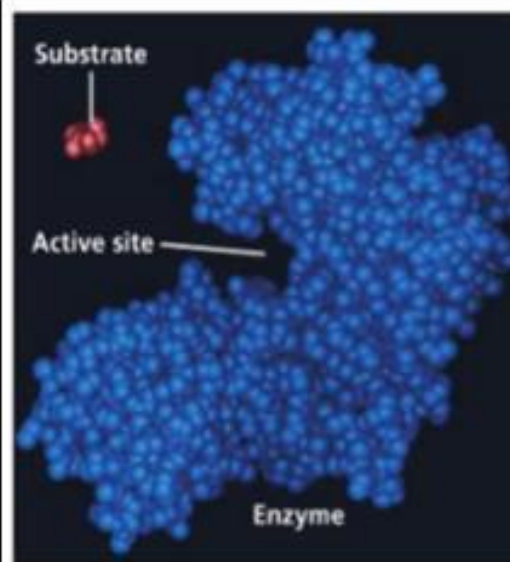
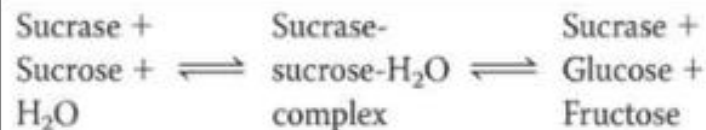
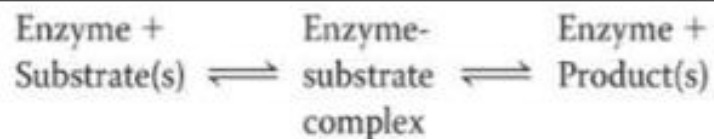
After bonds have broken, new bonds form, releasing energy to the surroundings.



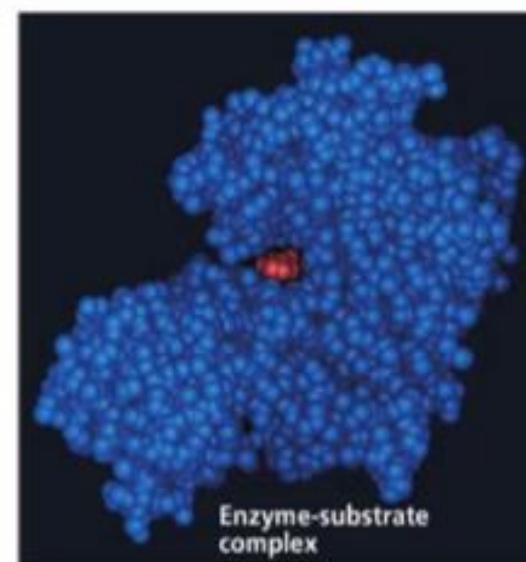
▲ **Figure 8.14 Energy profile of an exergonic reaction.** The “molecules” are hypothetical, with A, B, C, and D representing portions of the molecules. Thermodynamically, this is an exergonic reaction, with a negative  $\Delta G$ , and the reaction occurs spontaneously. However, the activation energy ( $E_A$ ) provides a barrier that determines the rate of the reaction.



▲ **Figure 8.15 The effect of an enzyme on activation energy.** Without affecting the free-energy change ( $\Delta G$ ) for a reaction, an enzyme speeds the reaction by reducing its activation energy ( $E_A$ ).



(a) In this computer graphic model, the active site of this enzyme (hexokinase, shown in blue) forms a groove on its surface. Its substrate is glucose (red).

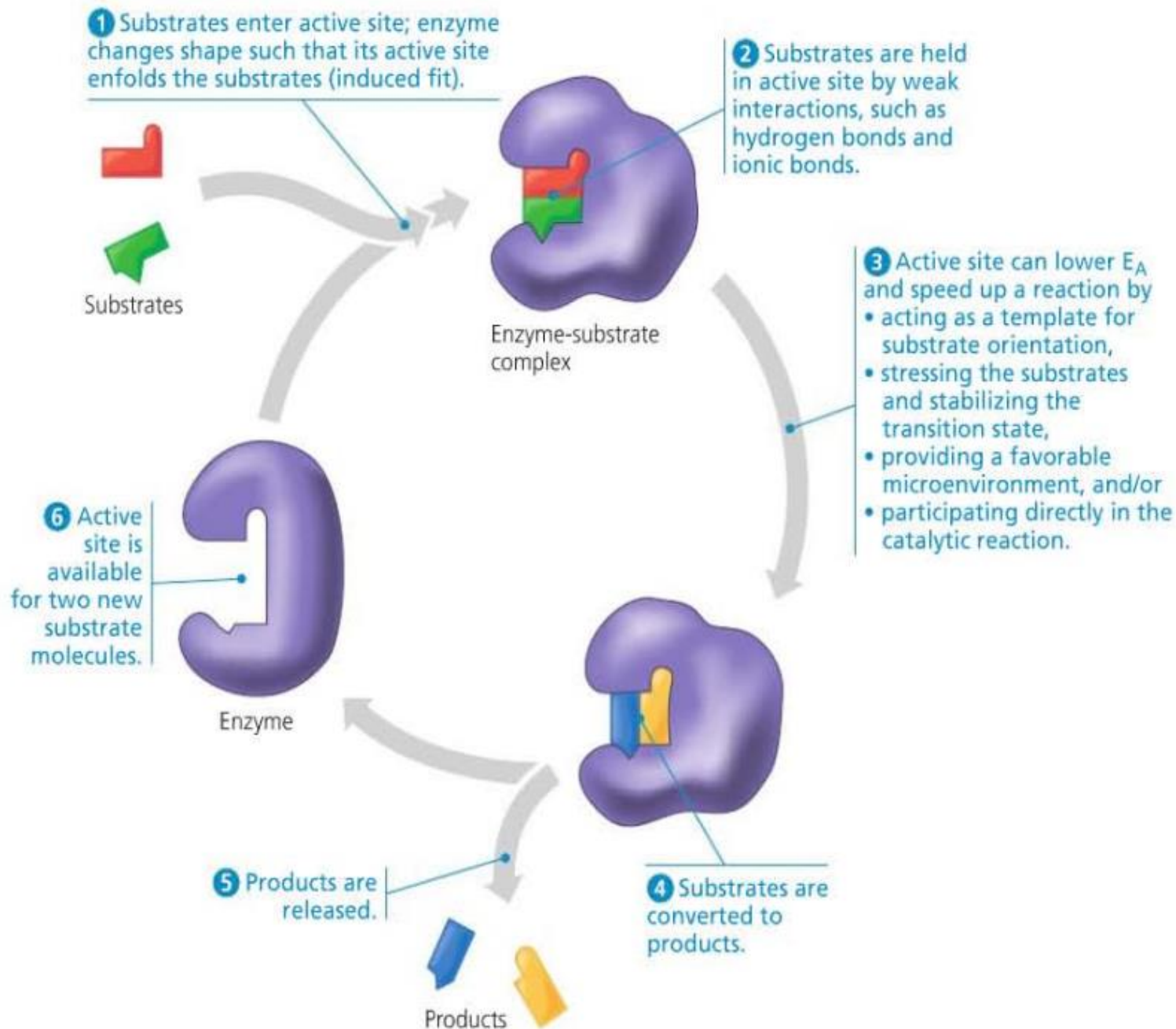


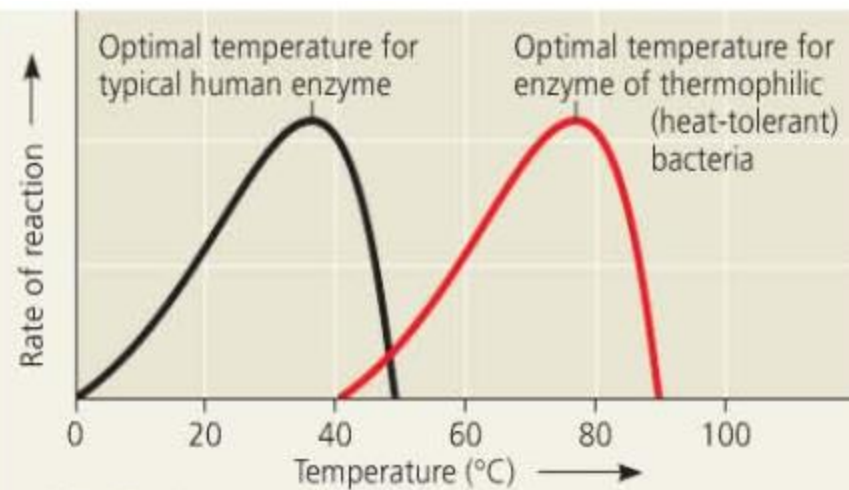
(b) When the substrate enters the active site, it induces a change in the shape of the protein. This change allows more weak bonds to form, causing the active site to enfold the substrate and hold it in place.

▲ **Figure 8.16** Induced fit between an enzyme and its substrate.

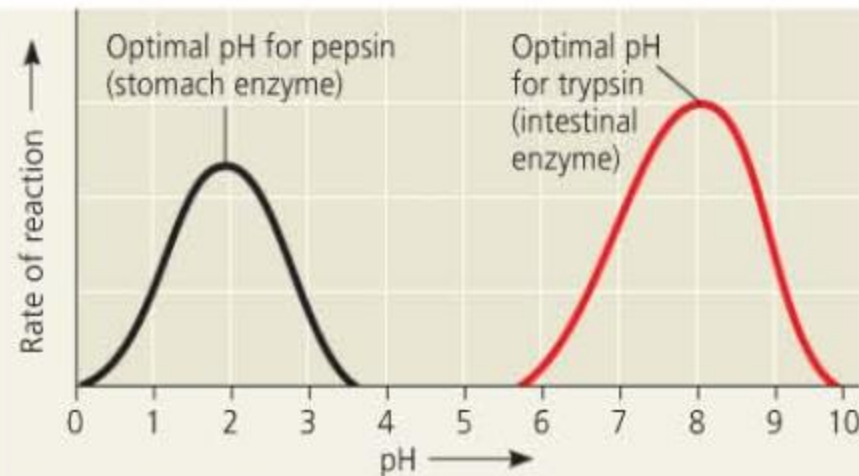


► **Figure 8.17** The active site and catalytic cycle of an enzyme. An enzyme can convert one or more reactant molecules to one or more product molecules. The enzyme shown here converts two substrate molecules to two product molecules.





(a) Optimal temperature for two enzymes



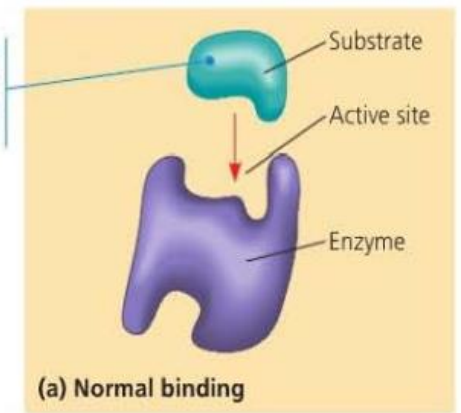
(b) Optimal pH for two enzymes

▲ **Figure 8.18 Environmental factors affecting enzyme activity.** Each enzyme has an optimal (a) temperature and (b) pH that favor the most active shape of the protein molecule.

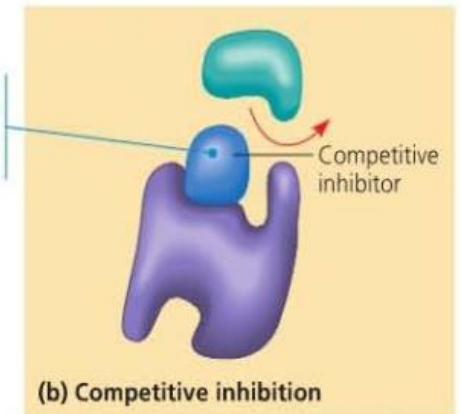
**DRAW IT** Given that a mature lysosome has an internal pH of around 4.5, draw a curve in (b) showing what you would predict for a lysosomal enzyme, labeling its optimal pH.



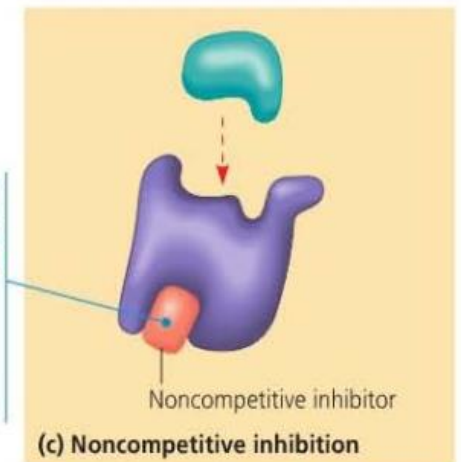
A substrate can bind normally to the active site of an enzyme.



A competitive inhibitor mimics the substrate, competing for the active site.

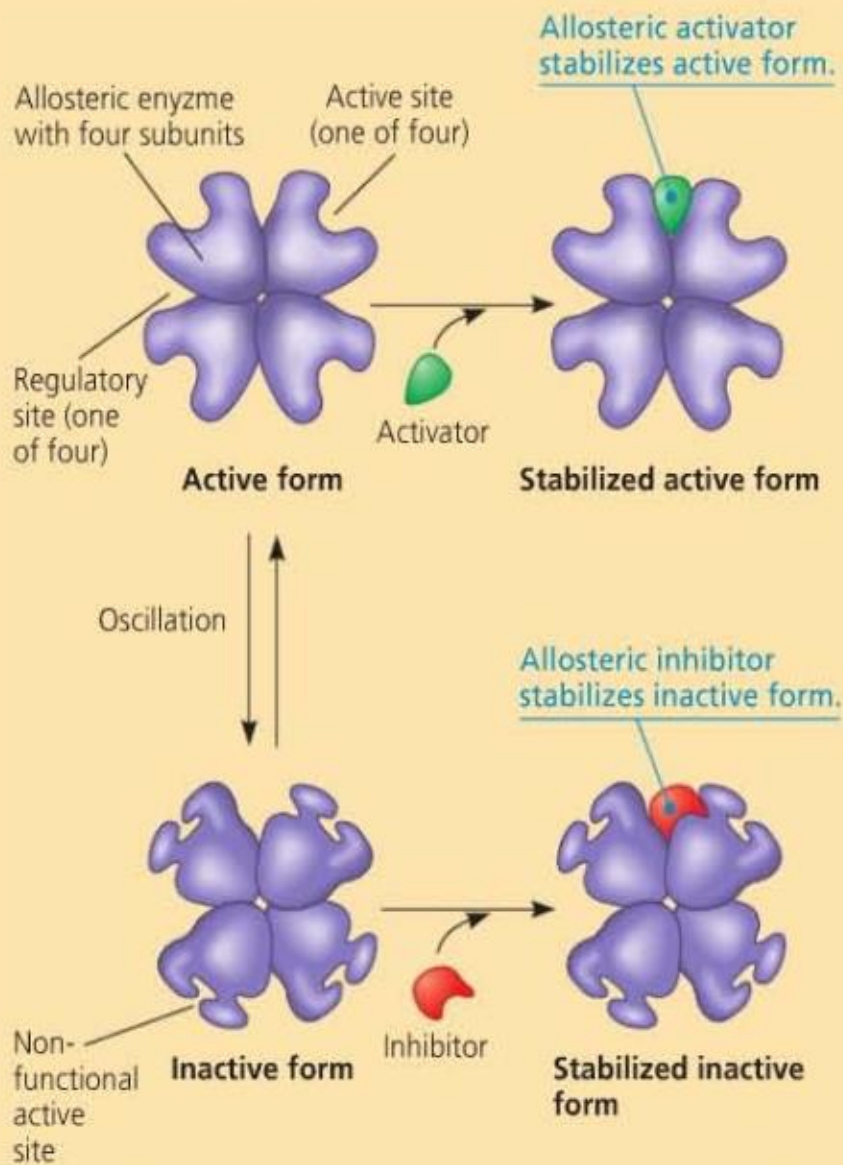


A noncompetitive inhibitor binds to the enzyme away from the active site, altering the shape of the enzyme so that even if the substrate can bind, the active site functions less effectively.

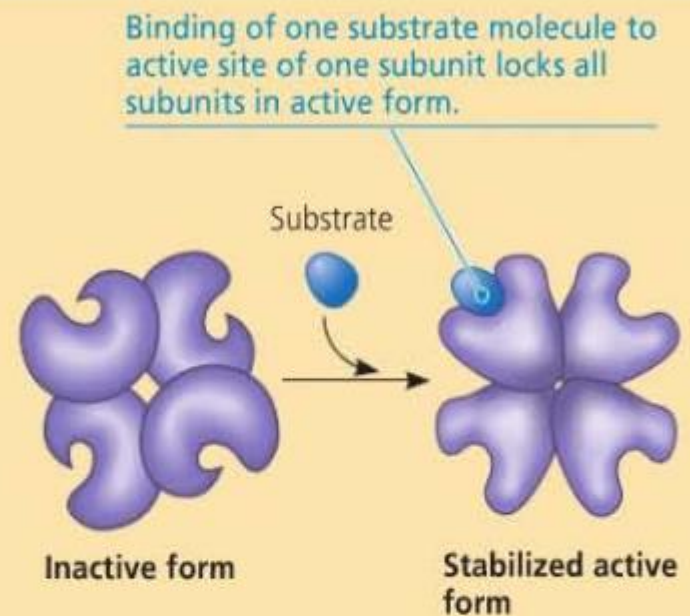


▲ **Figure 8.19** Inhibition of enzyme activity.

# 5. REGULASI AKTIVITAS ENZIM MEMBANTU KONTROL METABOLISME



**(a) Allosteric activators and inhibitors.** In the cell, activators and inhibitors dissociate when at low concentrations. The enzyme can then oscillate again.



**(b) Cooperativity: another type of allosteric activation.** The inactive form shown on the left oscillates back and forth with the active form when the active form is not stabilized by substrate.

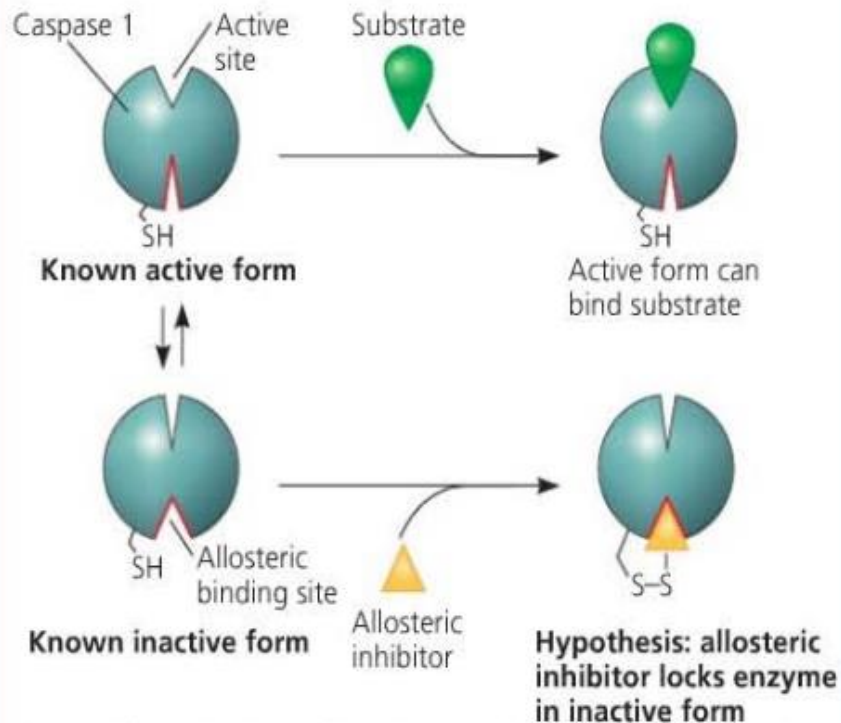
**▲ Figure 8.20 Allosteric regulation of enzyme activity.**

## ▼ Figure 8.21 Inquiry

### Are there allosteric inhibitors of caspase enzymes?

#### EXPERIMENT

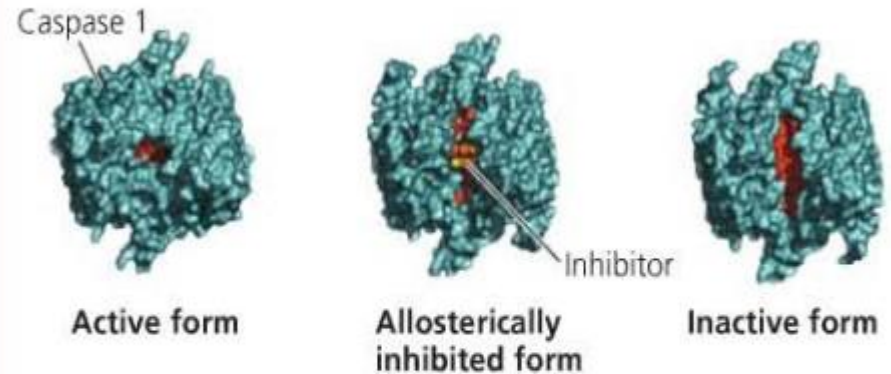
In an effort to identify allosteric inhibitors of caspases, Justin Scheer and co-workers screened close to 8,000 compounds for their ability to bind to a possible allosteric binding site in caspase 1 and inhibit the enzyme's activity. Each compound was designed to form a disulfide bond with a cysteine near the site in order to stabilize the low-affinity interaction that is expected of an allosteric inhibitor. As the caspases are known to exist in both active and inactive forms, the researchers hypothesized that this linkage might lock the enzyme in the inactive form.



To test this model, X-ray diffraction analysis was used to determine the structure of caspase 1 when bound to one of the inhibitors and to compare it with the active and inactive structures.

#### RESULTS

Fourteen compounds were identified that could bind to the proposed allosteric site (red) of caspase 1 and block enzymatic activity. The enzyme's shape when one such inhibitor was bound resembled the inactive caspase 1 more than the active form.



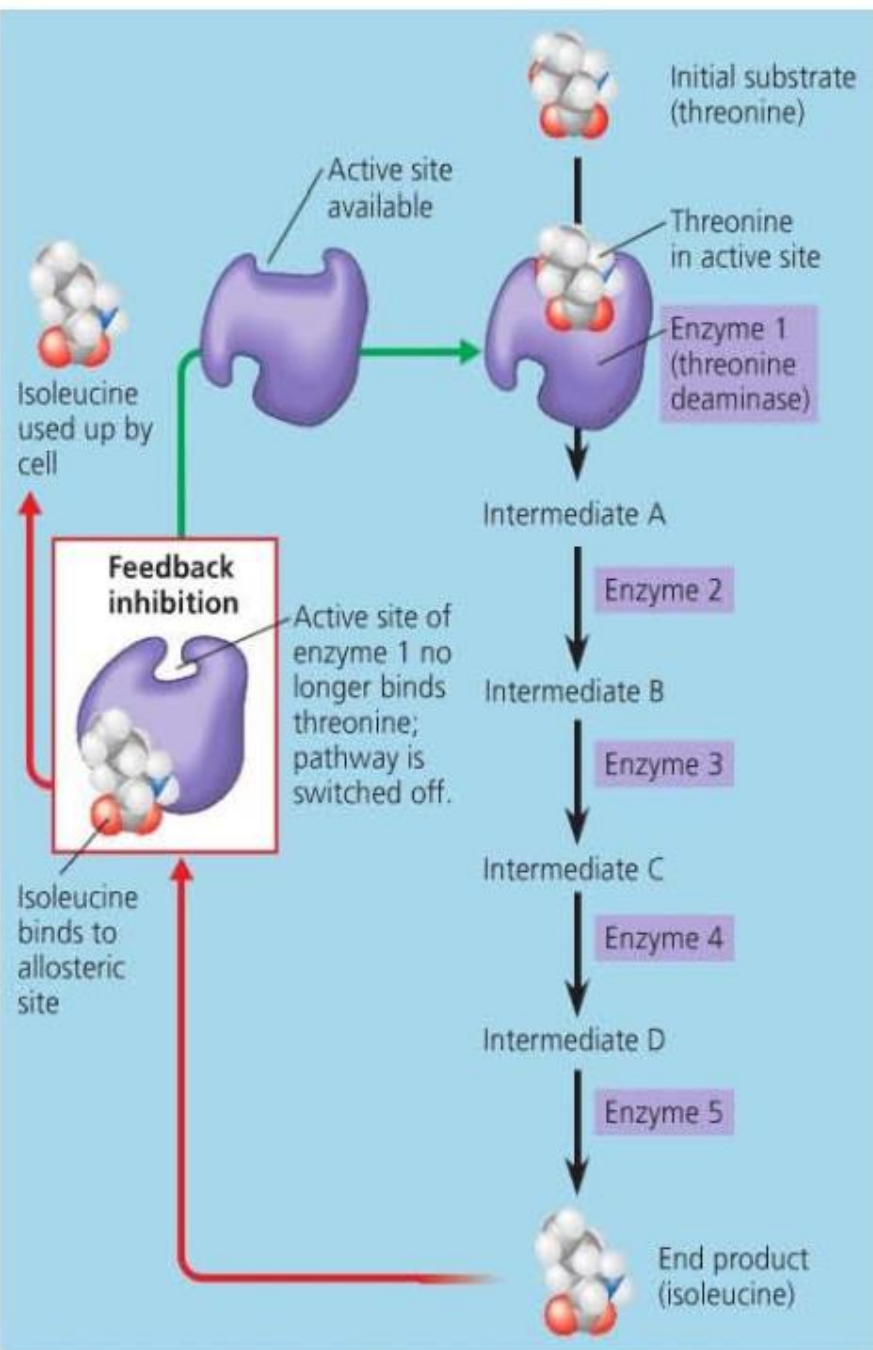
#### CONCLUSION

The inhibitory compound that was studied apparently locks the enzyme in its inactive form, as expected for a true allosteric regulator. The data therefore support the existence of an allosteric inhibitory site on caspase 1, which can be used to control enzymatic activity.

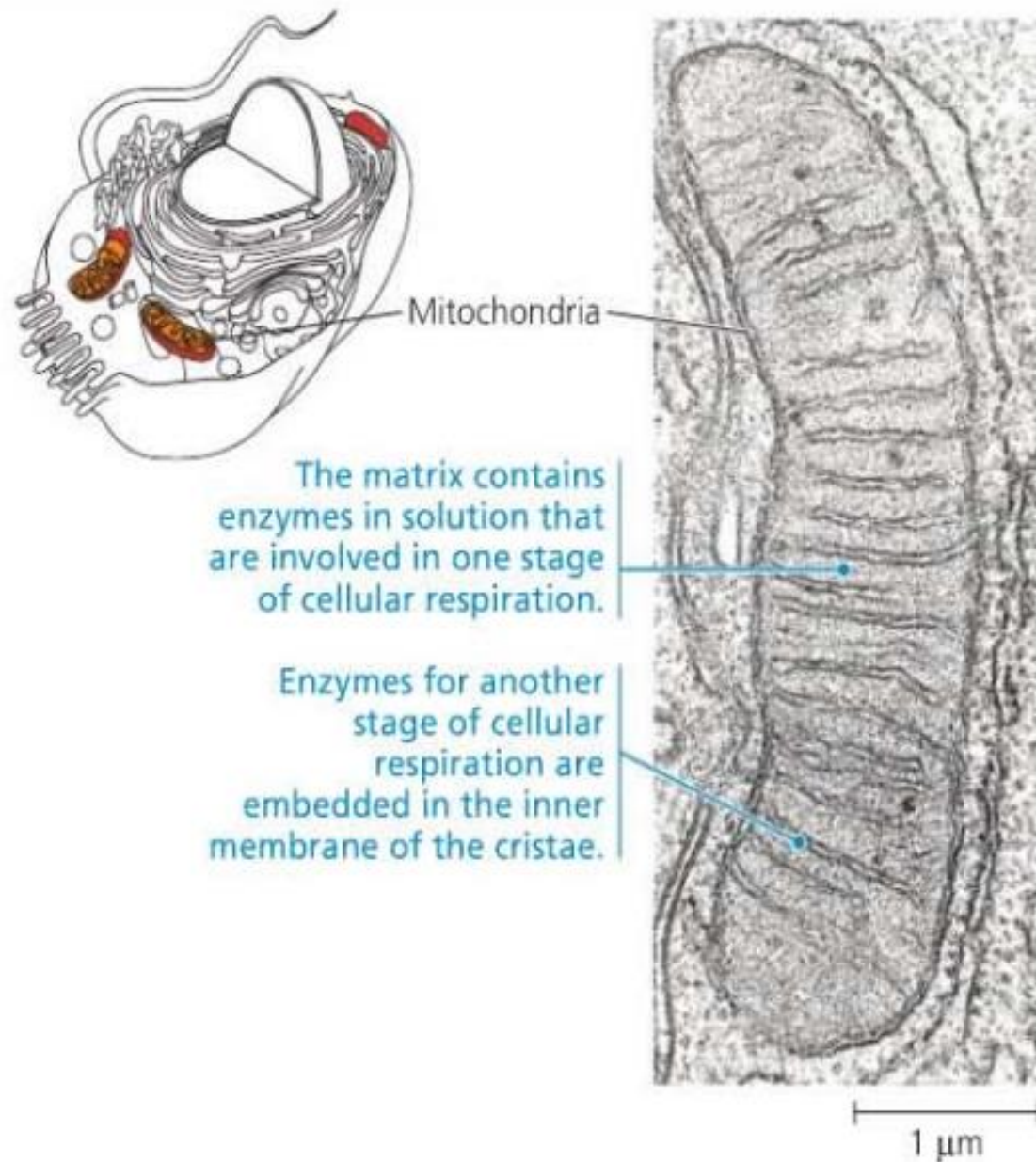
#### SOURCE

J. M. Scheer et al., A common allosteric site and mechanism in caspases, *PNAS* 103:7595-7600 (2006).





▲ **Figure 8.22** Feedback inhibition in isoleucine synthesis.



▲ **Figure 8.23 Organelles and structural order in metabolism.** Organelles such as these mitochondria (TEM) contain enzymes that carry out specific functions. In this case cellular respiration.

# DAFTAR PUSTAKA

- Campbell, Neil A., Jane B. Reece.  
2008. Biology. 8th ed. Pearson  
Benjamin Cummings, San  
Francisco.

