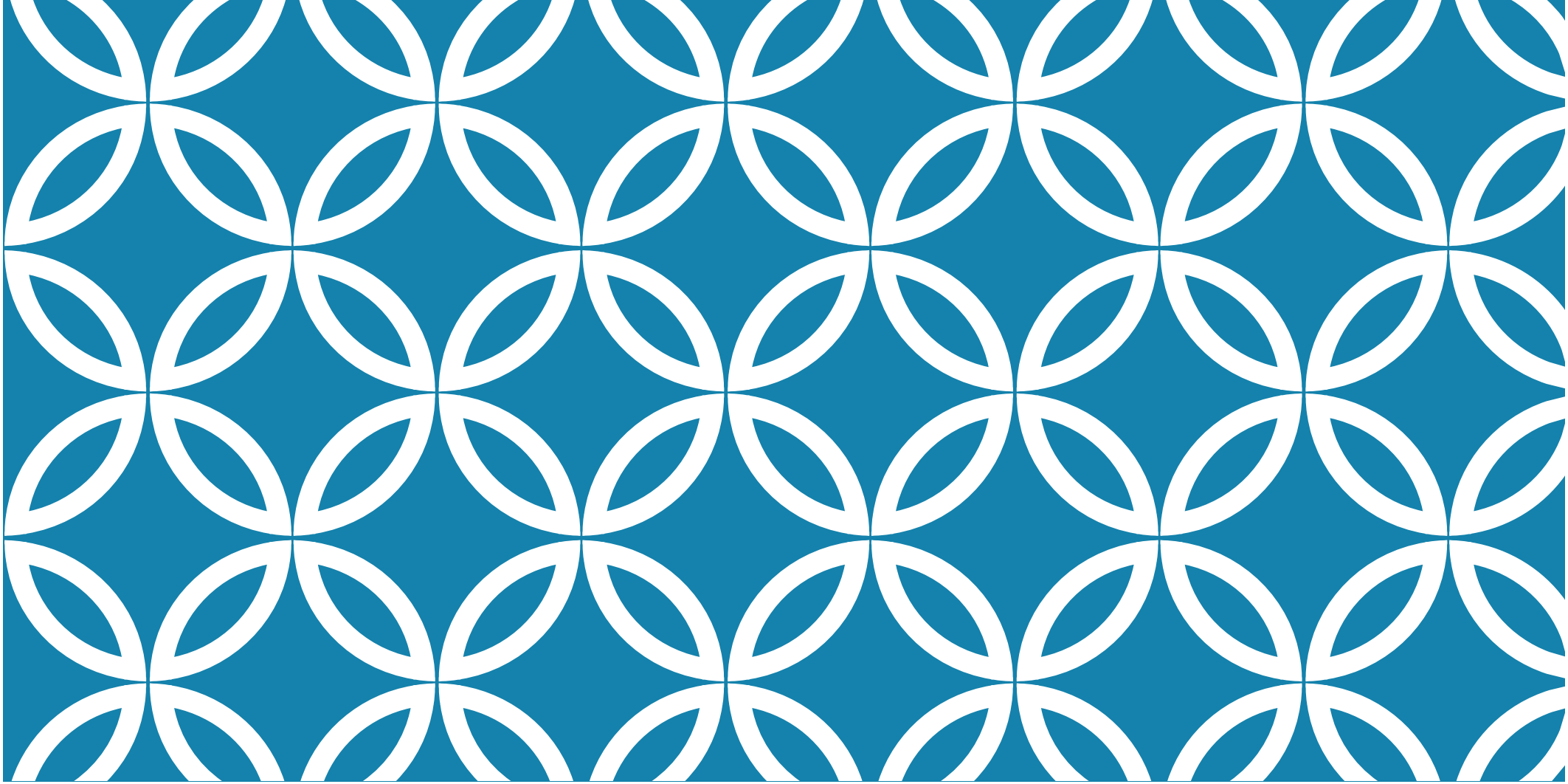
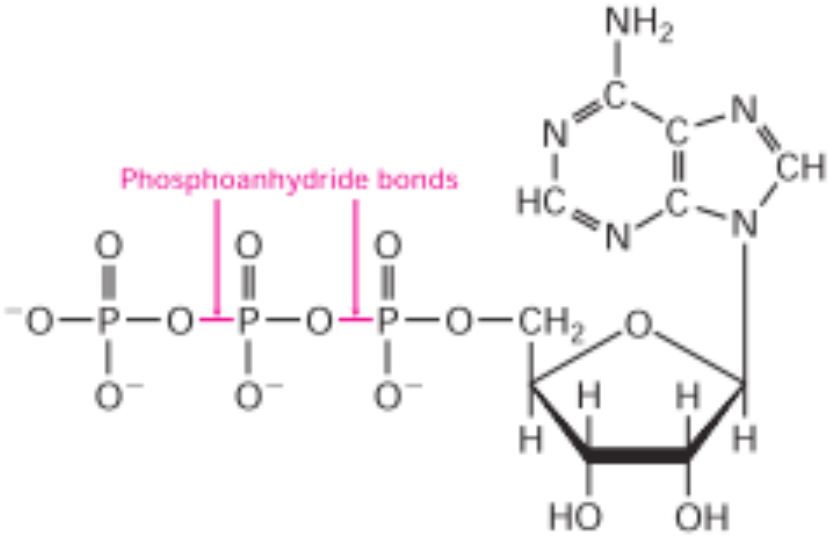


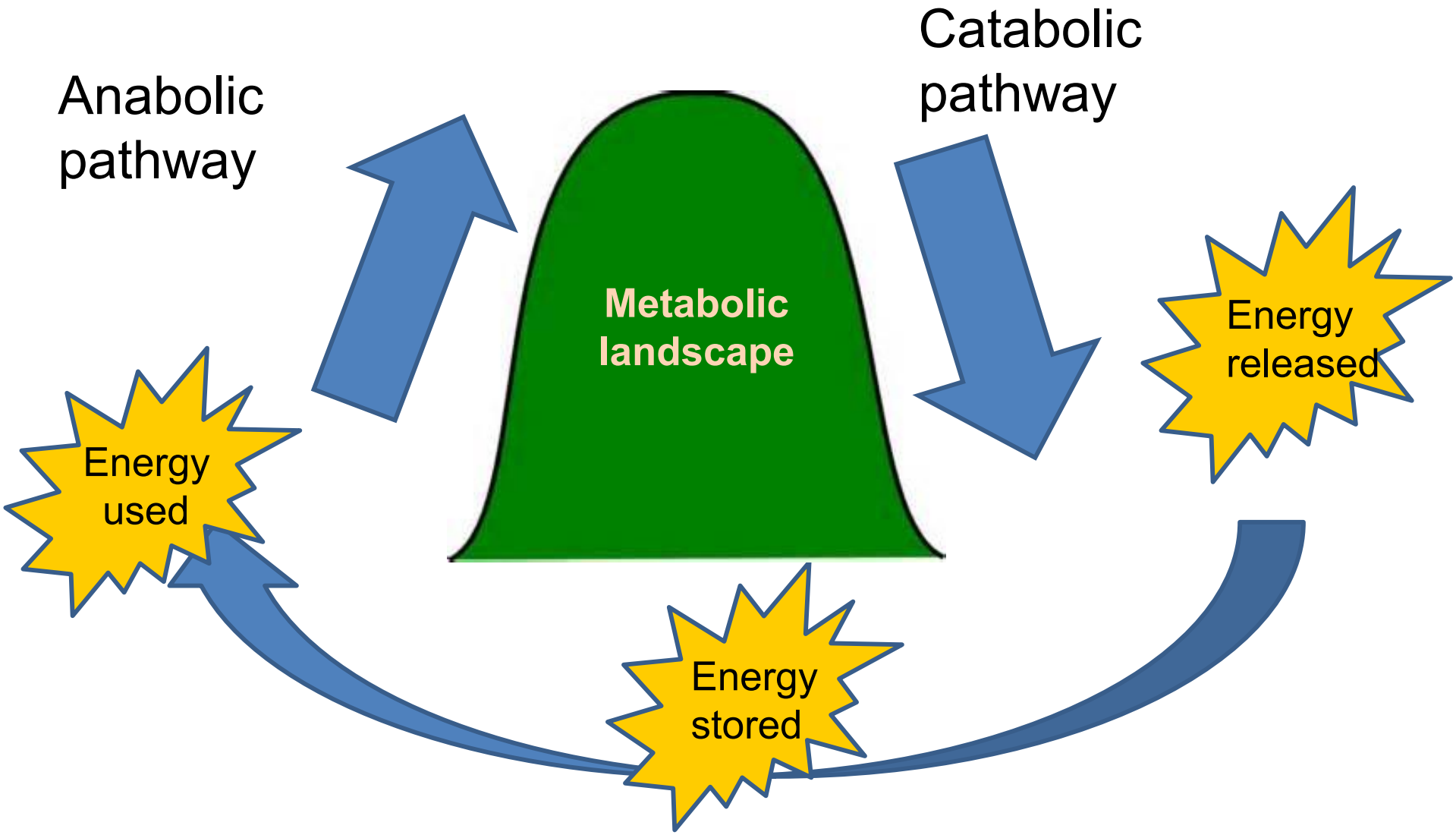
ENERGI DAN METABOLISME

ATP

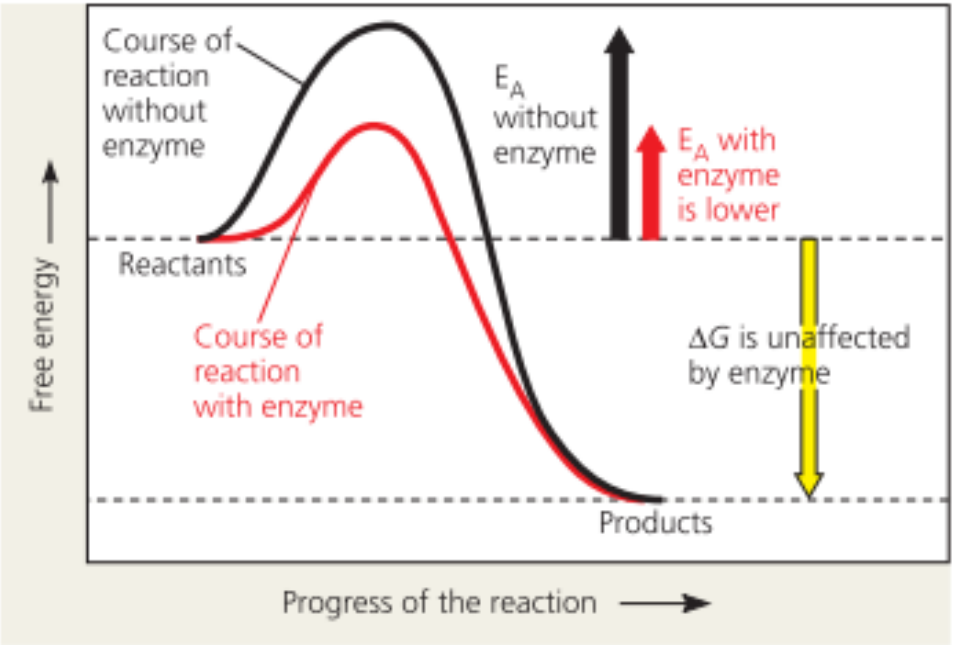


Adenosine triphosphate (ATP)

▲ **FIGURE 2-24 Adenosine triphosphate (ATP).** The two phosphoanhydride bonds (red) in ATP, which link the three phosphate groups, each has a $\Delta G''$ of −7.3 kcal/mol for hydrolysis. Hydrolysis of these bonds, especially the terminal one, drives many energy-requiring reactions in biological systems.

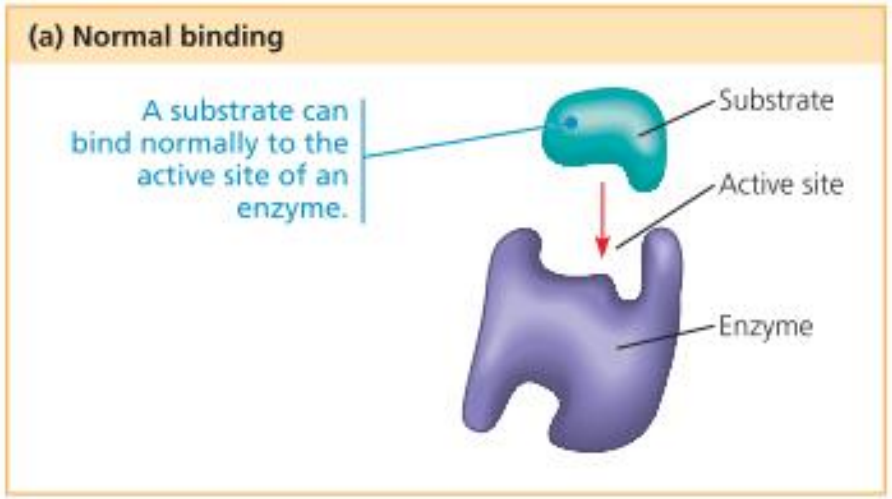

Anabolic pathway
Catabolic pathway
Metabolic landscape
Energy released
Energy used
Energy stored

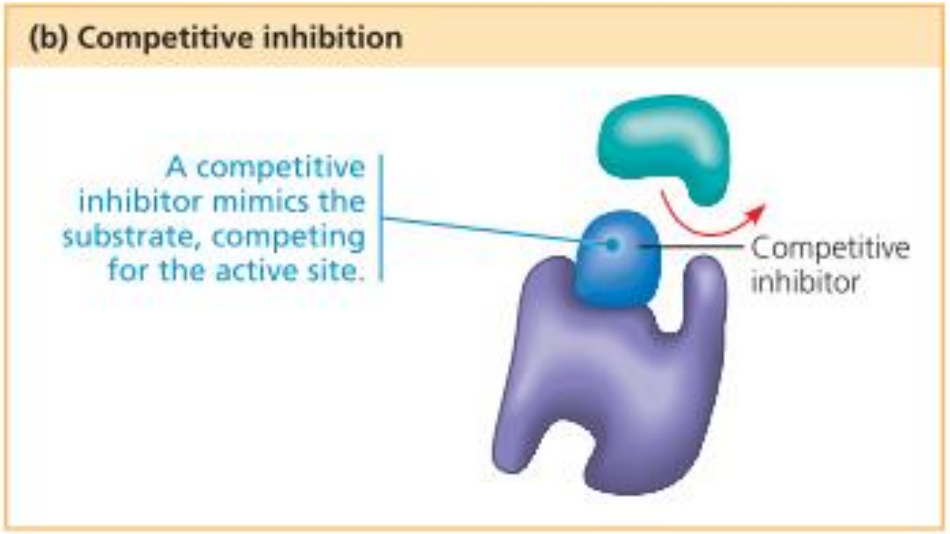
MEKANISME KERJA ENZIM



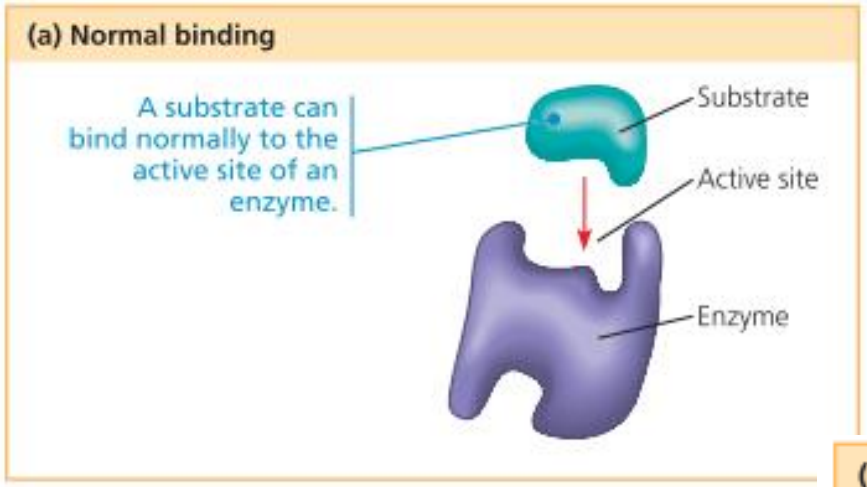
▲ **Figure 8.13 The effect of an enzyme on activation energy.** Without affecting the free-energy change (ΔG) for a reaction, an enzyme speeds the reaction by reducing its activation energy (E_A).

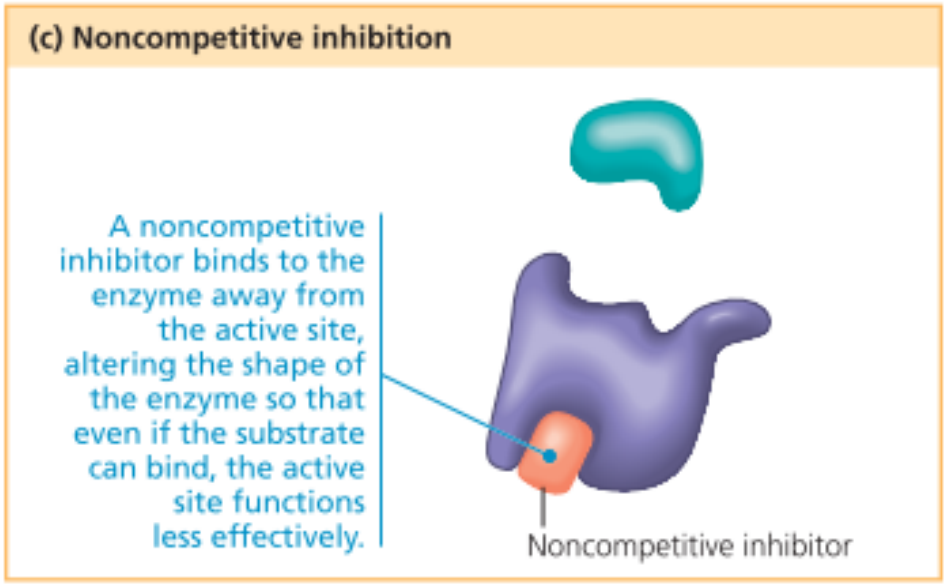
INHIBITOR

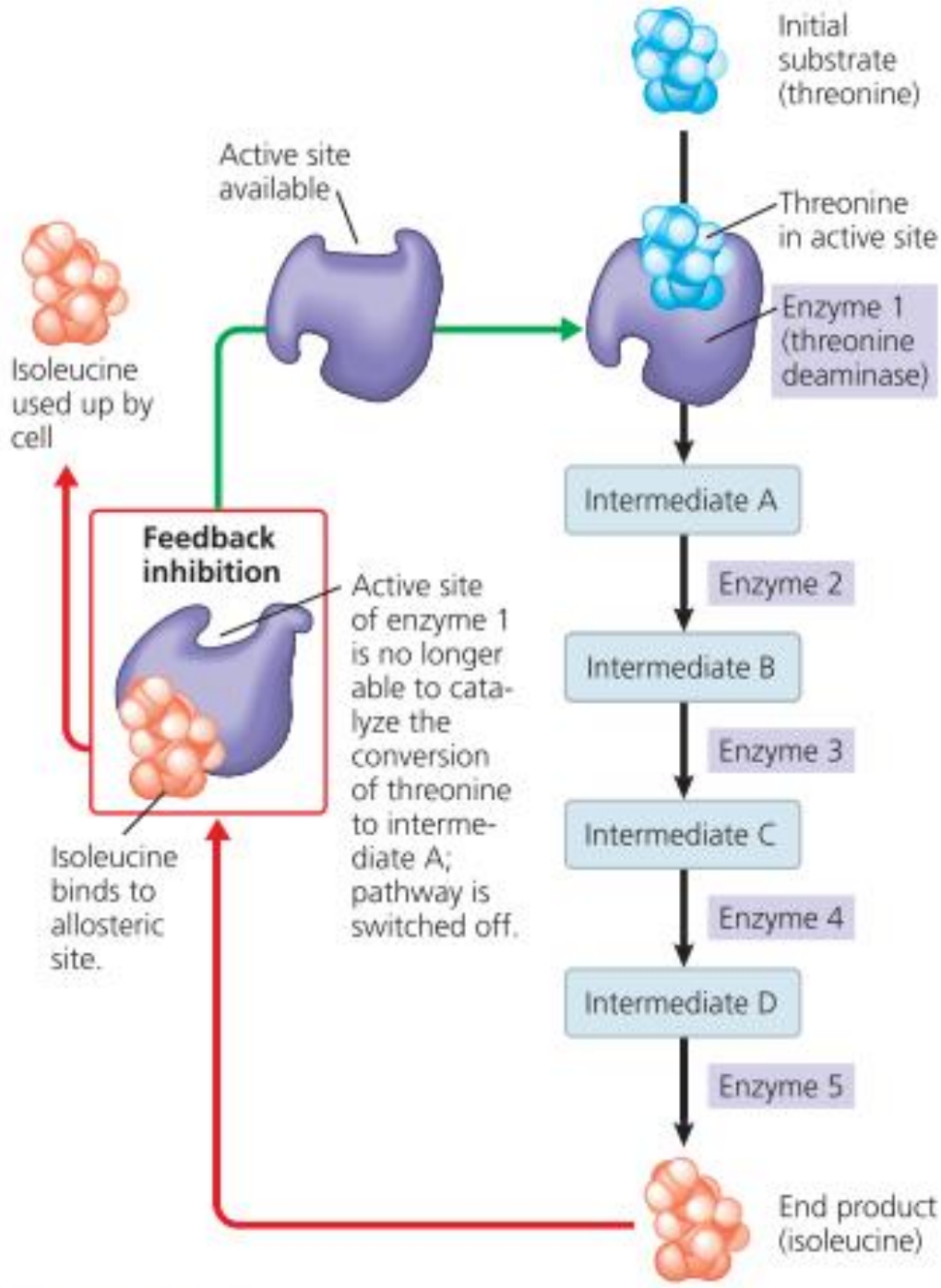

(a) Normal binding
A substrate can bind normally to the active site of an enzyme.
Substrate
Active site
Enzyme


(b) Competitive inhibition
A competitive inhibitor mimics the substrate, competing for the active site.
Competitive inhibitor

INHIBITOR

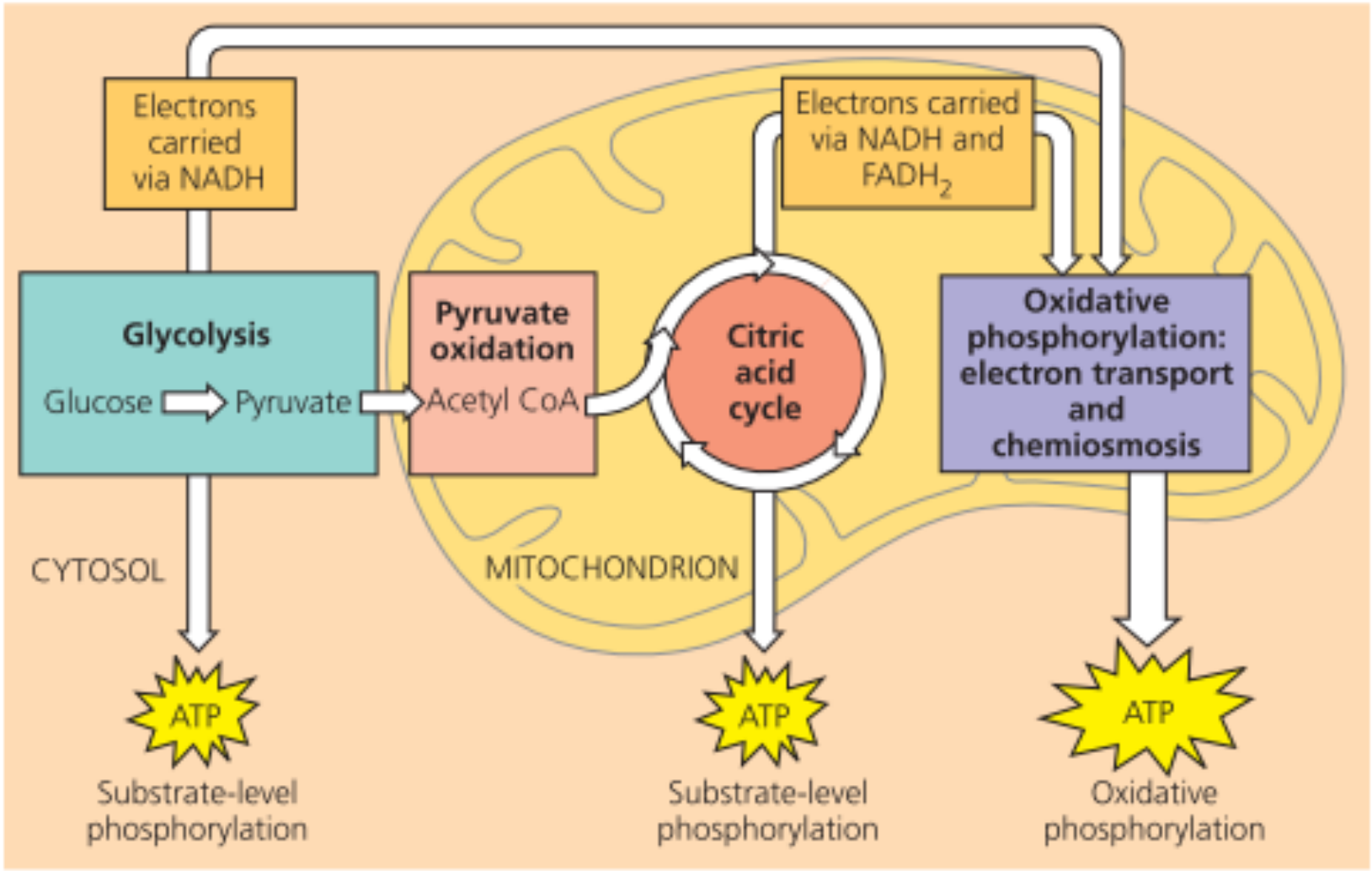

(a) Normal binding
A substrate can bind normally to the active site of an enzyme.
Substrate
Active site
Enzyme

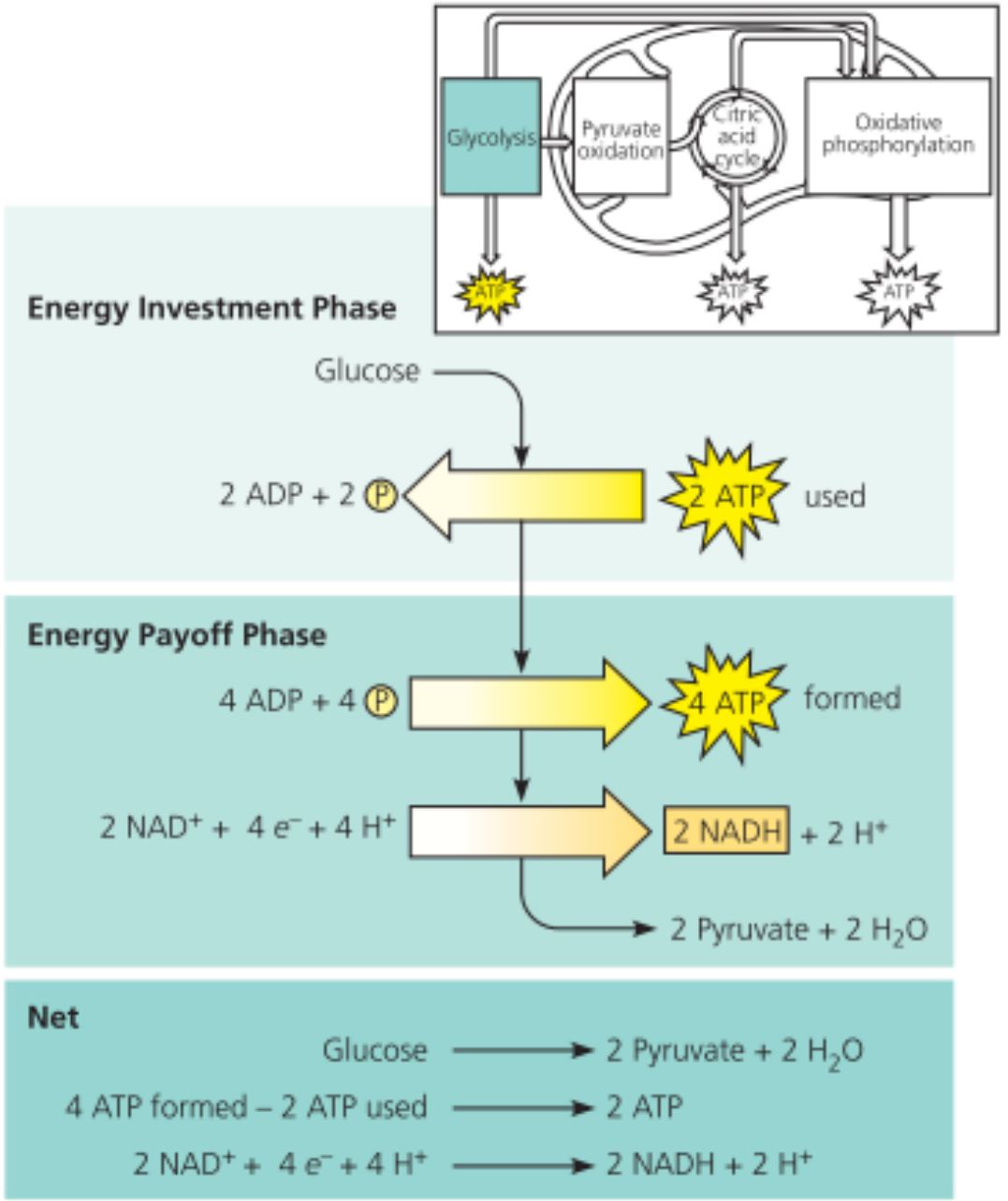

(c) Noncompetitive inhibition
A noncompetitive inhibitor binds to the enzyme away from the active site, altering the shape of the enzyme so that even if the substrate can bind, the active site functions less effectively.
Noncompetitive inhibitor



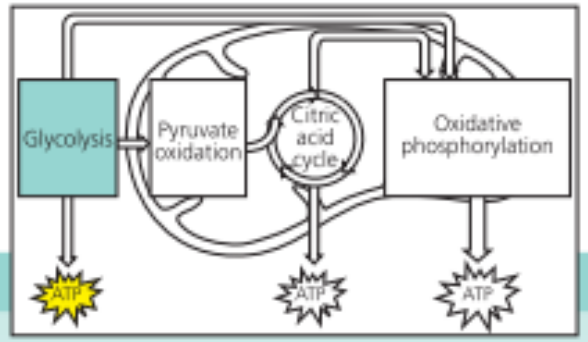
▲ **Figure 8.21 Feedback inhibition in isoleucine synthesis.**

RESPIRASI SELULER





▲ **Figure 9.8 The energy input and output of glycolysis.**



▼ Figure 9.9 A closer look at glycolysis. The orientation diagram on the left relates glycolysis to the entire process of respiration. Note that glycolysis is a source of ATP and NADH.

WHAT IF? *What would happen if you removed the dihydroxyacetone phosphate generated in step 4 as fast as it was produced?*

Glycolysis: Energy Investment Phase

Glucose → (ATP → ADP) Hexokinase → **Glucose 6-phosphate** → Phosphoglucoisomerase → **Fructose 6-phosphate** → (ATP → ADP) Phosphofructokinase → **Fructose 1,6-bisphosphate** → Aldolase 4 → **Dihydroxyacetone phosphate** ⇄ **Glyceraldehyde 3-phosphate** → To step 6

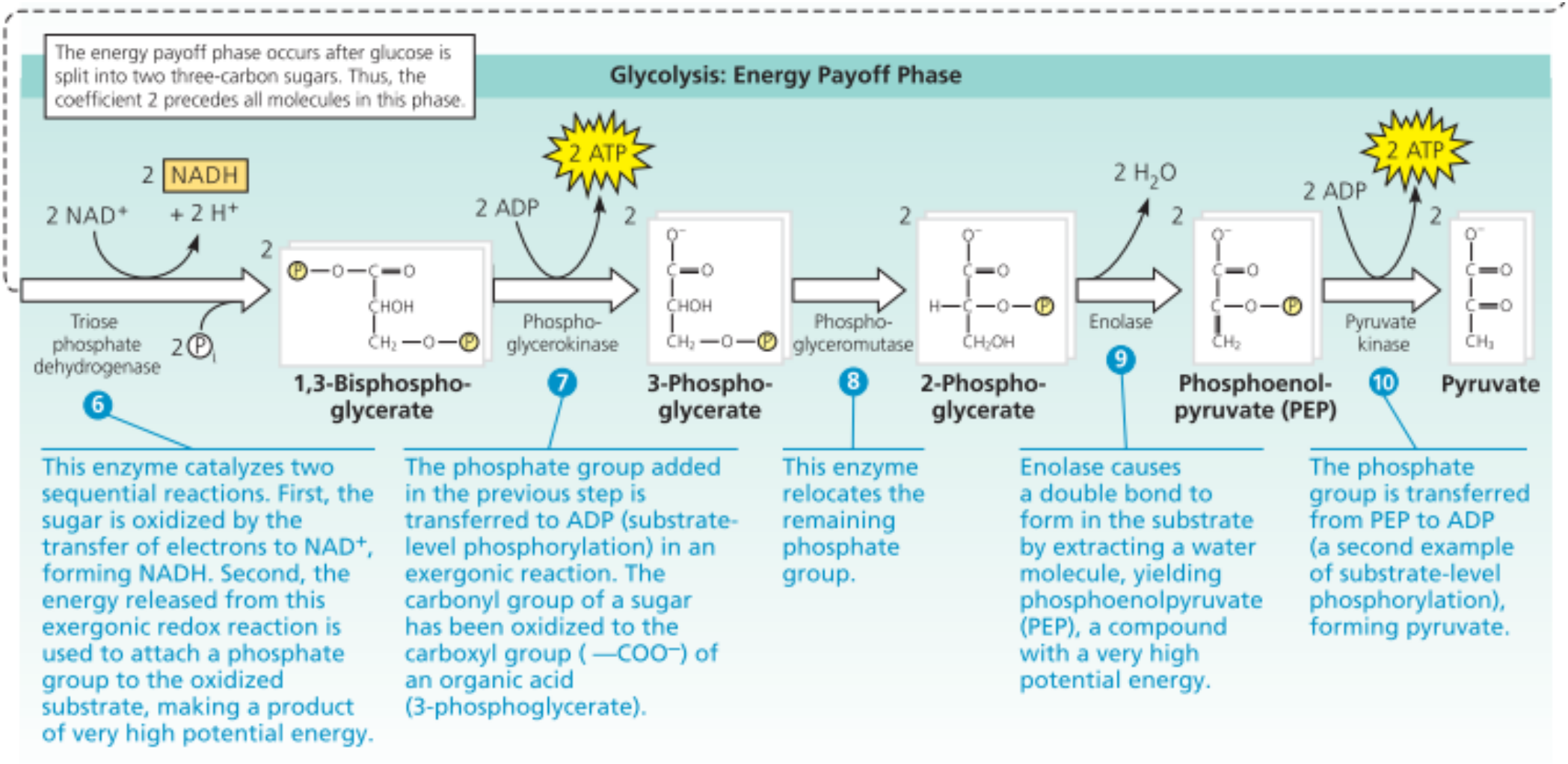
1 Hexokinase transfers a phosphate group from ATP to glucose, making it more chemically reactive. The charge on the phosphate also traps the sugar in the cell.

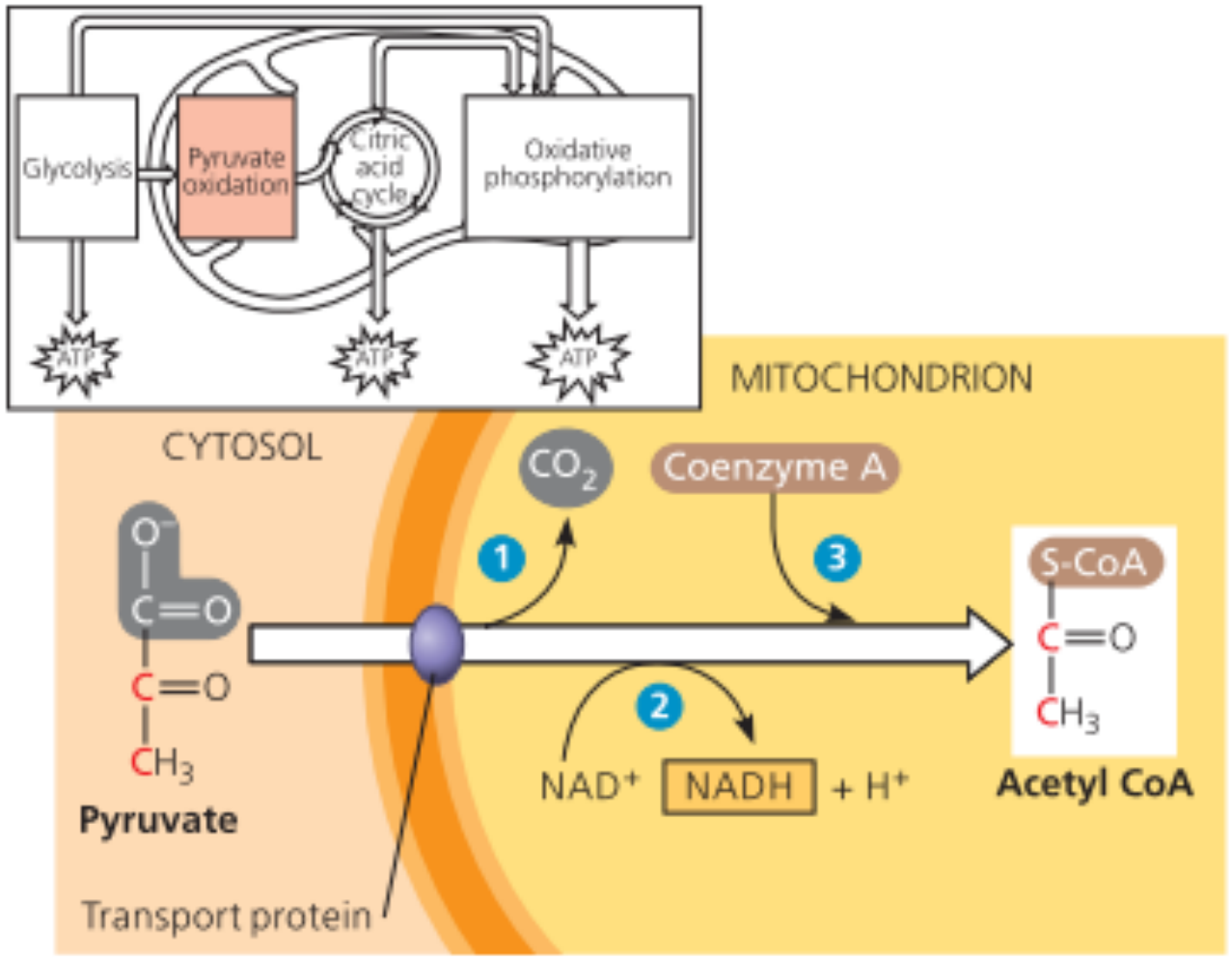
2 Glucose 6-phosphate is converted to its isomer, fructose 6-phosphate.

3 Phosphofructokinase transfers a phosphate group from ATP to the opposite end of the sugar, investing a second molecule of ATP. This is a key step for regulation of glycolysis.

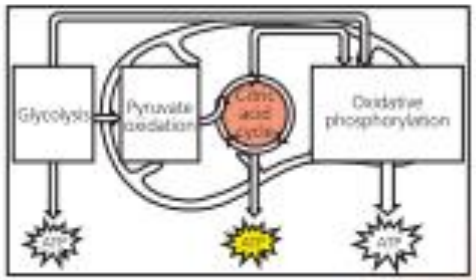
Aldolase cleaves the sugar molecule into two different three-carbon sugars (isomers).

5 Isomerase catalyzes the reversible conversion between the two isomers. This reaction never reaches equilibrium: Glyceraldehyde 3-phosphate is used as the substrate of the next reaction (step 6) as fast as it forms.


The energy payoff phase occurs after glucose is split into two three-carbon sugars. Thus, the coefficient 2 precedes all molecules in this phase.
Glycolysis: Energy Payoff Phase
2 NADH
2 NAD+ + 2 H+
2 ATP
2 ADP
2 H2O
2 ATP
2 ADP
2
Triose phosphate dehydrogenase
2 Pi
1,3-Bisphospho-glycerate
Phospho-glycerokinase
3-Phospho-glycerate
Phospho-glyceromutase
2-Phospho-glycerate
Enolase
Phosphoenol-pyruvate (PEP)
Pyruvate kinase
Pyruvate
6
7
8
9
10
This enzyme catalyzes two sequential reactions. First, the sugar is oxidized by the transfer of electrons to NAD+, forming NADH. Second, the energy released from this exergonic redox reaction is used to attach a phosphate group to the oxidized substrate, making a product of very high potential energy.
The phosphate group added in the previous step is transferred to ADP (substrate-level phosphorylation) in an exergonic reaction. The carbonyl group of a sugar has been oxidized to the carboxyl group (—COO−) of an organic acid (3-phosphoglycerate).
This enzyme relocates the remaining phosphate group.
Enolase causes a double bond to form in the substrate by extracting a water molecule, yielding phosphoenolpyruvate (PEP), a compound with a very high potential energy.
The phosphate group is transferred from PEP to ADP (a second example of substrate-level phosphorylation), forming pyruvate.



▲ **Figure 9.10 Oxidation of pyruvate to acetyl CoA, the step before the citric acid cycle.** Pyruvate is a charged molecule, so in eukaryotic cells it must enter the mitochondrion via active transport, with the help of a transport protein. Next, a complex of several enzymes (the pyruvate dehydrogenase complex) catalyzes the three numbered steps, which are described in the text. The acetyl group of acetyl CoA will enter the citric acid cycle. The CO_2 molecule will diffuse out of the cell. By convention, coenzyme A is abbreviated S-CoA when it is attached to a molecule, emphasizing the sulfur atom (S).



Citric acid cycle

Acetyl CoA

1 Acetyl CoA (from oxidation of pyruvate) adds its two-carbon acetyl group to oxaloacetate, producing citrate.

2 Citrate is converted to its isomer, isocitrate, by removal of one water molecule and addition of another.

3 Isocitrate is oxidized, reducing NAD^+ to NADH. Then the resulting compound loses a CO_2 molecule.

4 Another CO_2 is lost, and the resulting compound is oxidized, reducing NAD^+ to NADH. The remaining molecule is then attached to coenzyme A by an unstable bond.

5 CoA is displaced by a phosphate group, which is transferred to GDP, forming GTP, a molecule with functions similar to ATP. GTP can also be used, as shown, to generate ATP.

6 Two hydrogens are transferred to FAD, forming $FADH_2$ and oxidizing succinate.

7 Addition of a water molecule rearranges bonds in the substrate.

8 The substrate is oxidized, reducing NAD^+ to NADH and regenerating oxaloacetate.

Oxaloacetate

Citrate

Isocitrate

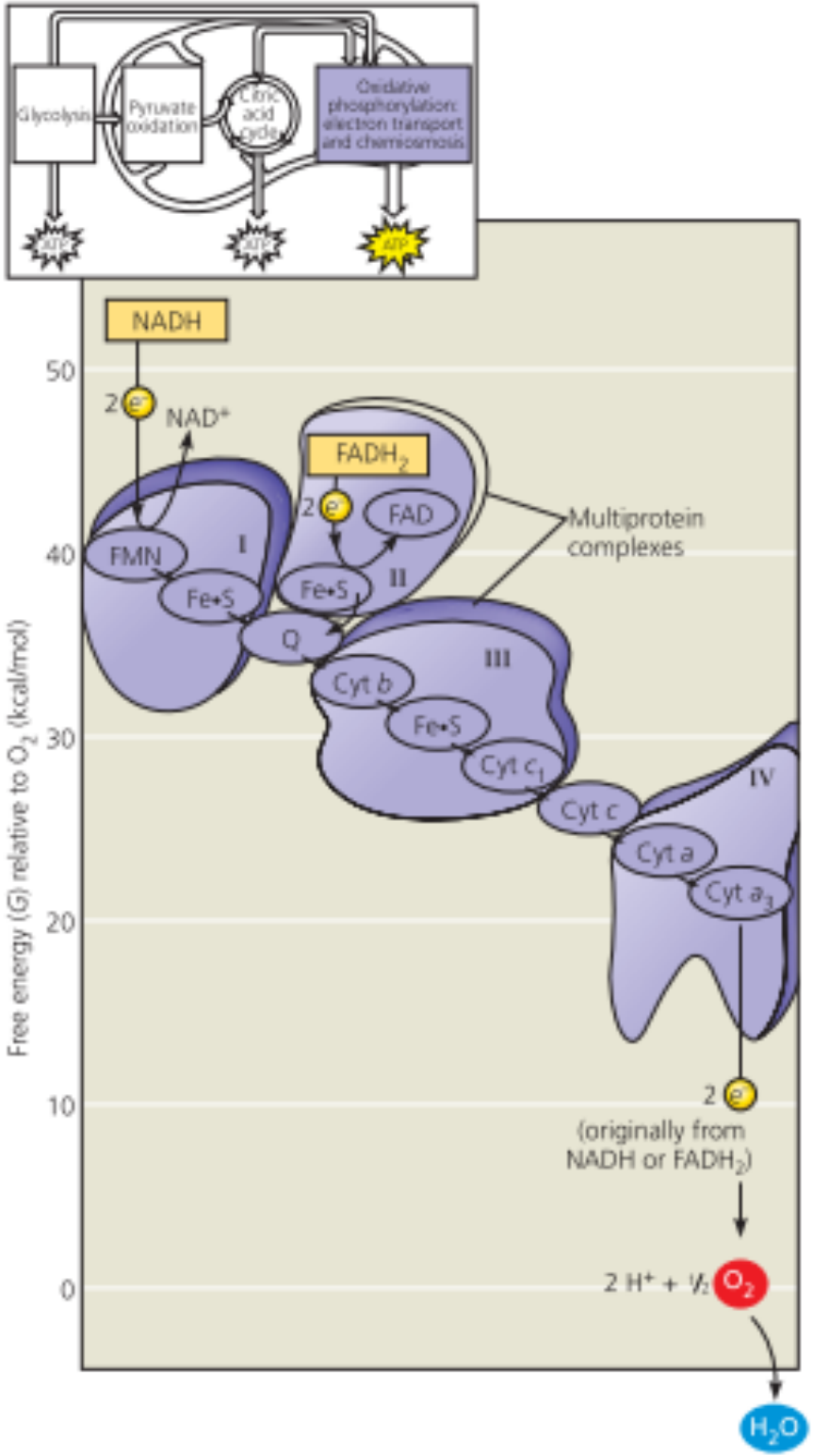
α-Ketoglutarate

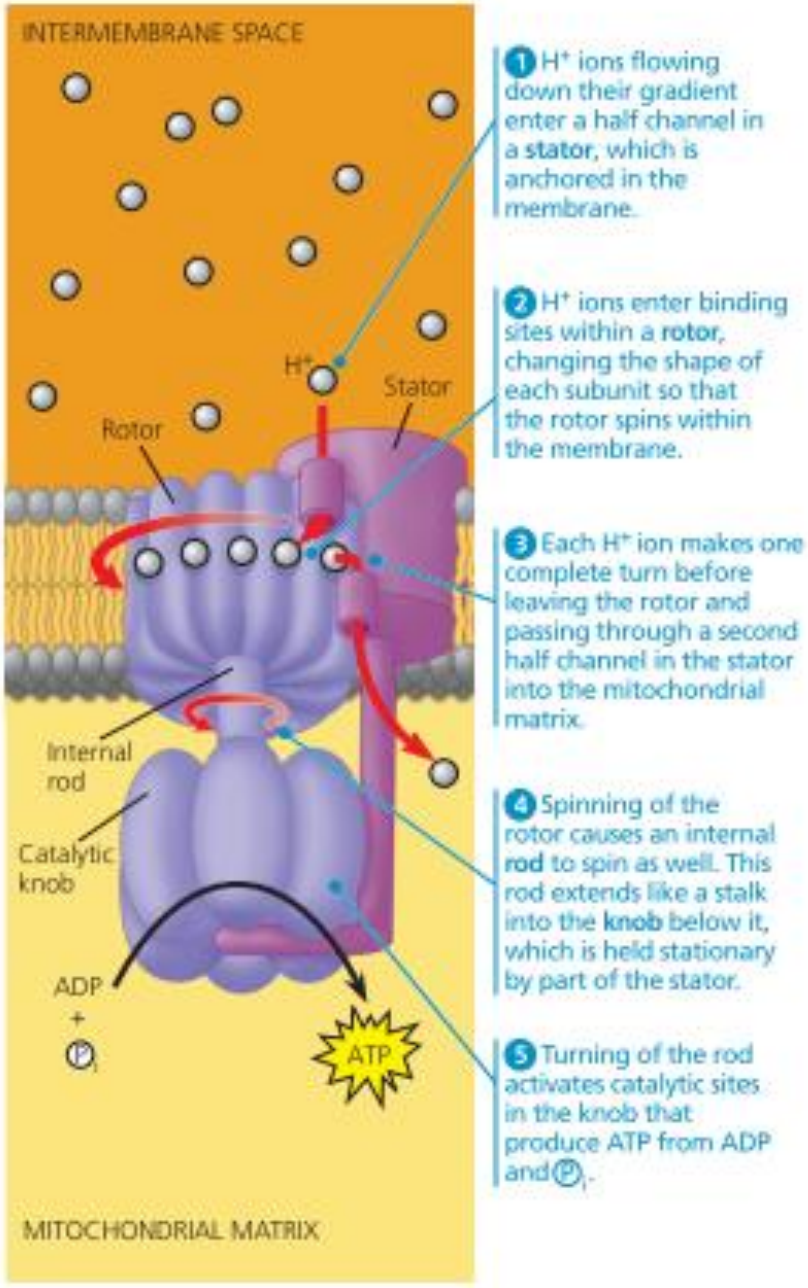
Succinyl CoA

Succinate

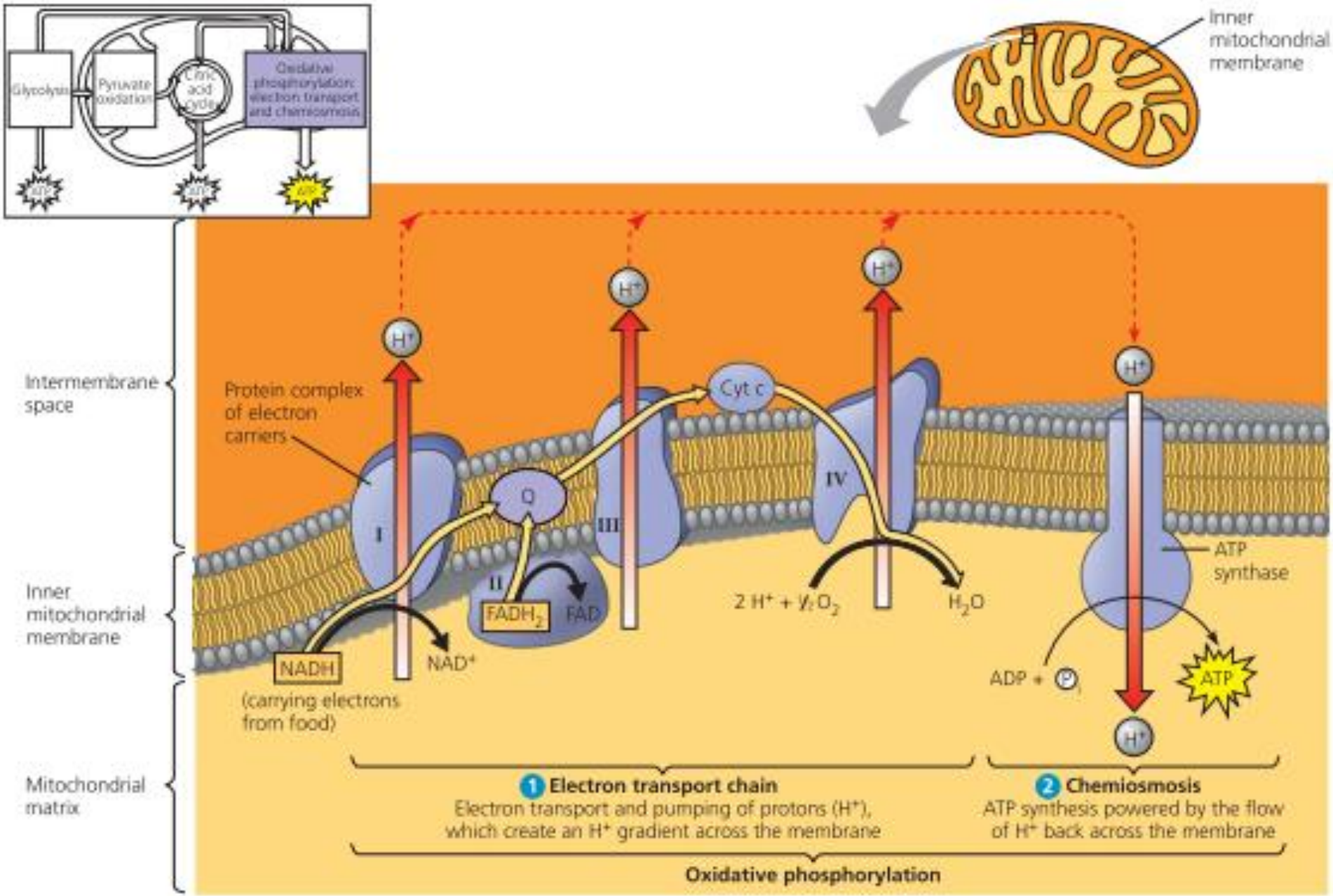
Fumarate

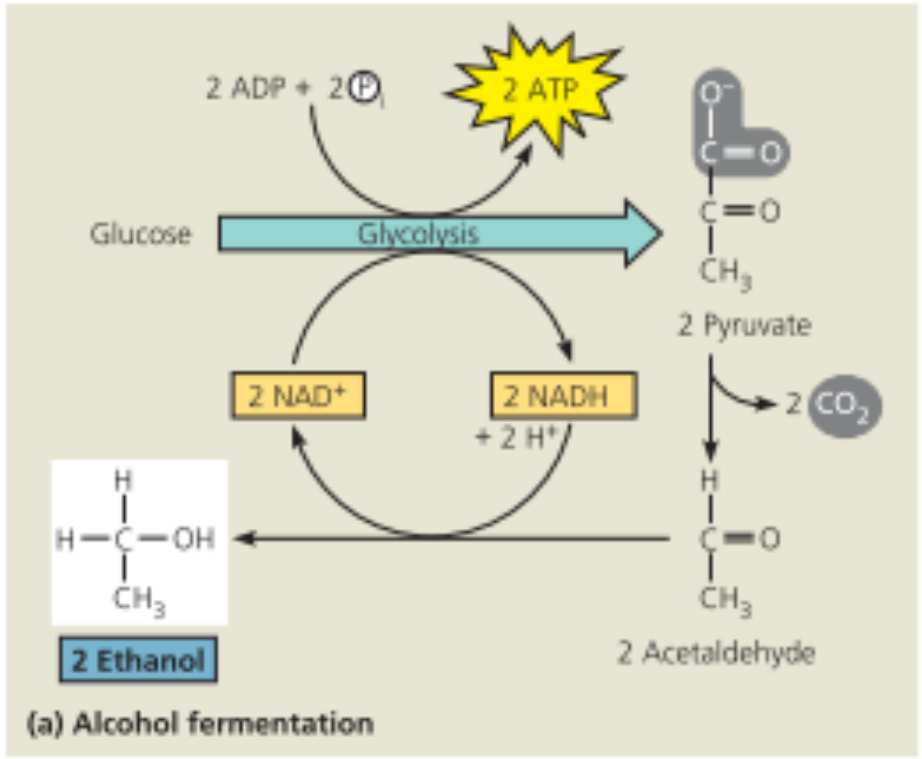
Malate


Glycolysis
Pyruvate oxidation
Citric acid cycle
Oxidative phosphorylation: electron transport and chemiosmosis
ATP
ATP
ATP
NADH
2 e⁻
NAD⁺
FADH₂
2 e⁻
FAD
Multiprotein complexes
FMN
I
Fe•S
Fe•S
II
Q
III
Cyt b
Fe•S
Cyt c₁
IV
Cyt c
Cyt a
Cyt a₃
2 e⁻
(originally from NADH or FADH₂)
2 H⁺ + ½ O₂
H₂O
Free energy (G) relative to O₂ (kcal/mol)
50
40
30
20
10
0

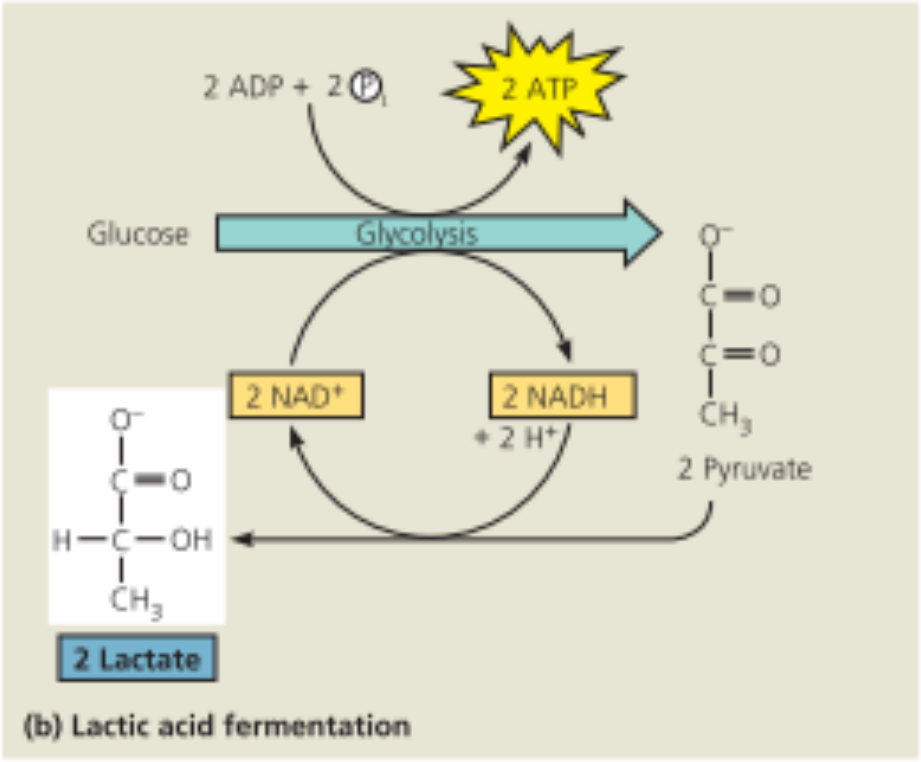


▲ **Figure 9.14 ATP synthase, a molecular mill.** The ATP synthase protein complex functions as a mill, powered by the flow of hydrogen ions. Multiple copies of this complex reside in mitochondrial and chloroplast membranes of eukaryotes and in the plasma membranes of prokaryotes. Each of the four parts of ATP synthase consists of a number of polypeptide subunits.

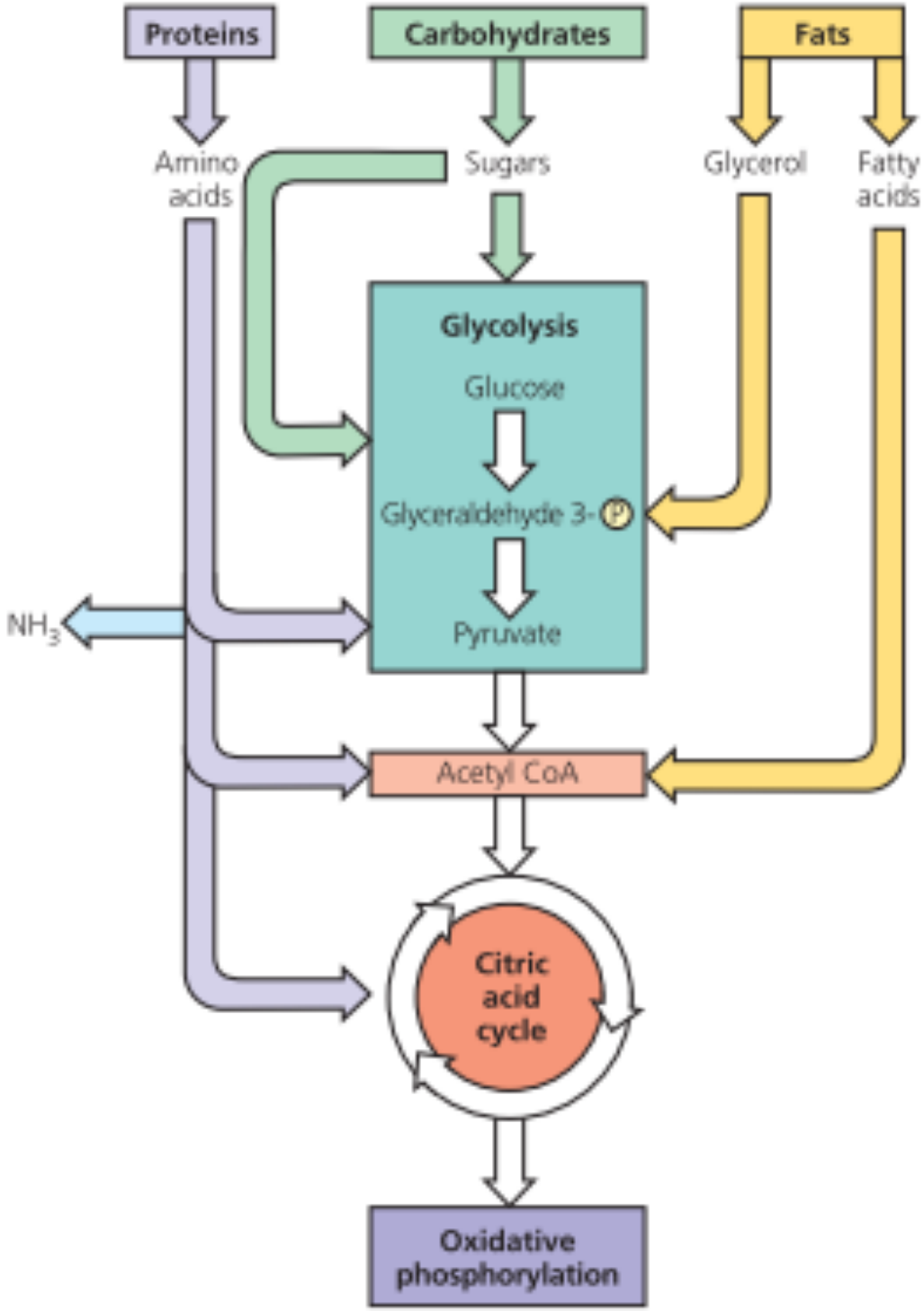

Glycolysis
Pyruvate oxidation
Citric acid cycle
Oxidative phosphorylation: electron transport and chemiosmosis
ATP
ATP
ATP
Inner mitochondrial membrane
Intermembrane space
Inner mitochondrial membrane
Mitochondrial matrix
Protein complex of electron carriers
H+
Q
Cyt c
I
II
III
IV
FADH2
FAD
NADH
(carrying electrons from food)
NAD+
2 H+ + ½ O2
H2O
ATP synthase
ADP + P
ATP
1 Electron transport chain
Electron transport and pumping of protons (H+), which create an H+ gradient across the membrane
2 Chemiosmosis
ATP synthesis powered by the flow of H+ back across the membrane
Oxidative phosphorylation



(a) Alcohol fermentation



(b) Lactic acid fermentation


Proteins
Carbohydrates
Fats
Amino acids
Sugars
Glycerol
Fatty acids
Glycolysis
Glucose
Glyceraldehyde 3-P
Pyruvate
NH3
Acetyl CoA
Citric acid cycle
Oxidative phosphorylation