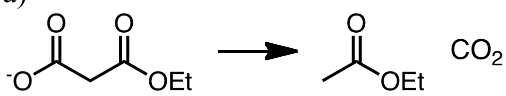
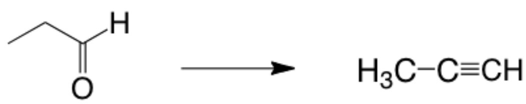
1. State whether each of the following reactions is an oxidation, reduction, or neither *in the direction indicated.* You may find it useful to keep track of how many hydrogens are found at each carbon.

a)



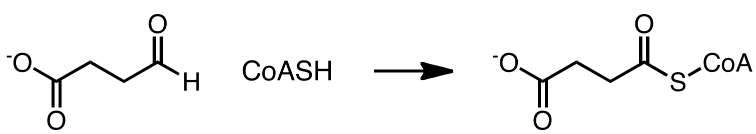
____

b)



____

c)



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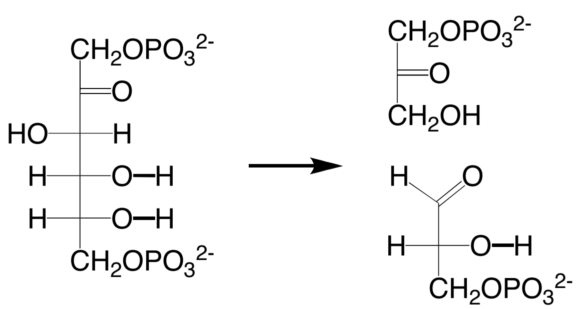
d)



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2. The complete pathways for glycolysis and the citric acid cycle are provided in the supplementary material. If C-5 of glucose is labeled with ^{14}C and then allowed to proceed through these two pathways:

a. Where is the label at the end of glycolysis? If the original glucose was 100 % labeled at C-5, to what extent is each position in pyruvate labeled? Explain your reasoning. You may wish to show the structures of key intermediates for partial credit in case you make a mistake.

b. At which position is citrate labeled when the resulting AcetylCoA molecule is added to oxaloacetate? (Show the structure for clarity).

Continued on next page.

Problem 2 continued.

c. Where is the label found in oxaloacetate after the first round of the citric acid cycle? (Show the structure for clarity).

d. How much of the label remains after the first round of the citric acid cycle? After the second?

3. a. Give the three reasons why ATP hydrolysis is thermodynamically favorable. Each response should be two sentences or less.

1)

2)

3)

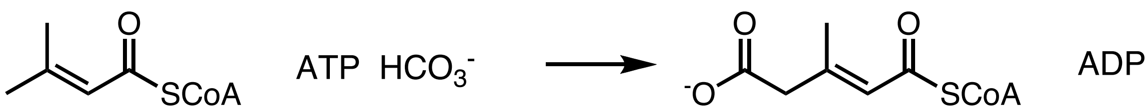
b. Why is it critical that there are molecules in the cell that are more reactive than ATP? Each response should be two sentences or less.

1)

2)

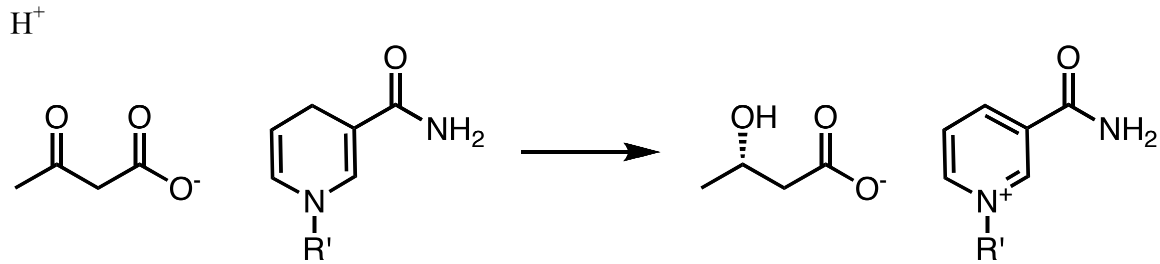
4. a. Which co-factor is required for the following enzyme-catalyzed reaction? (Hint: number your carbons!)

Cofactor:________________



b. Write a complete mechanism for this reaction, using curved arrows to show the flow of electrons. Be sure to show the structures of all intermediates. You may abbreviate the structures of any required co-factors, as long as you are clear. Clearly indicate the roles of any enzyme side chains.

5. Ketone bodies are important in lipid metabolism. Two important ketone body fuels are acetoacetate and β-hydroxybutyrate. Write a complete mechanism for the conversion of acetoacetate into β-hydroxybutyrate, using curved arrows to show the flow of electrons.



6. For the following hypothetical metabolic pathway:

Enzyme	Reactant(s)	Product(s)	ΔG°′(kJ/mol)	ΔG′ (kJ/mol)
1	A	B	+1.6	-15.5
2	B	C	+16.7	-1.2
3	C	D	-18.2	-1.3
4	D	E	+1.7	-0.8

a. Which step is the most likely to be regulated?

b. Which is more abundant under cellular conditions, B or C?

c. What is the ratio of B to A under cellular conditions? Show your work.

7. Regulation of glucose metabolism.

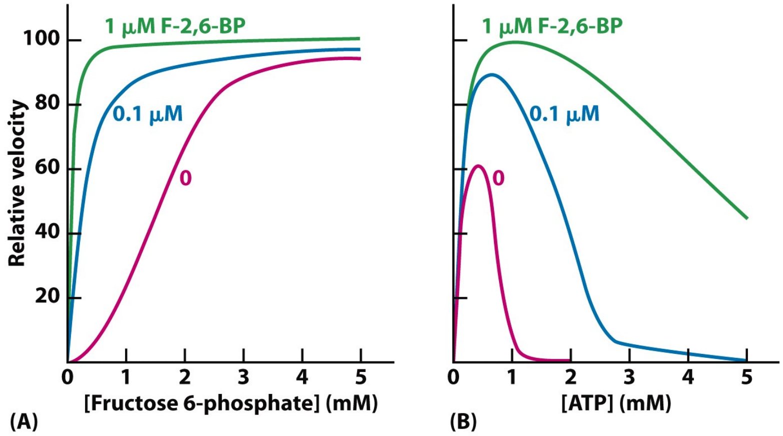


Figure 16-18
Biochemistry, Sixth Edition

a) Consider panel (A) above, which shows the rate of the phosphofructose-catalyzed reaction with respect to fructose-6-phosphate (see supplementary materials). What effect does fructose-2,6-bisphosphate have on phosphofructokinase activity? How does it exert this effect?

b) Consider panel (B). Why is the curve shape different for ATP and fructose-6-phosphate? Why does the curve shape change in the presence of 1 μM fructose-2,6-bisphosphate?

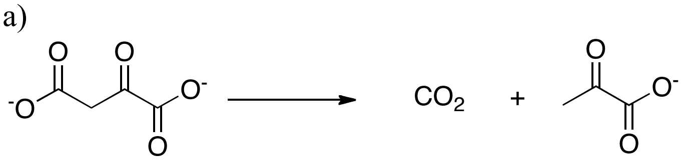
8. a. Consider the table of free energies of the glycolytic reactions that is shown in your supplementary material.

a. Which step(s) in glycolysis would you expect to be regulated? Why?

b. Of these steps, which is the key point for regulation? Explain your reasoning.

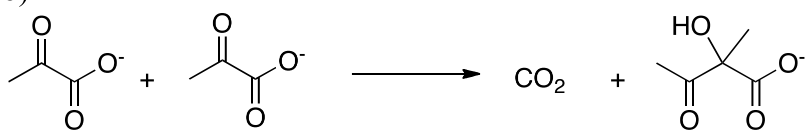
9. Based on the involvement of thiamine pyrophosphate (TPP) in the pyruvate decarboxylase reaction, which of the following reactions, if any, might be expected to utilize TPP as a cofactor? Write hypothetical mechanisms for each reaction showing where TPP is involved or why it is unnecessary. (part b on next page)

a)



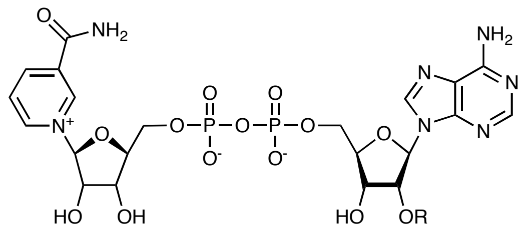
Problem 9 continued.

b)

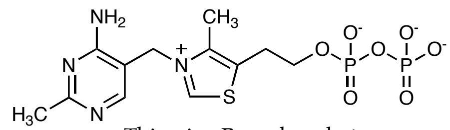


Supplementary Information Section

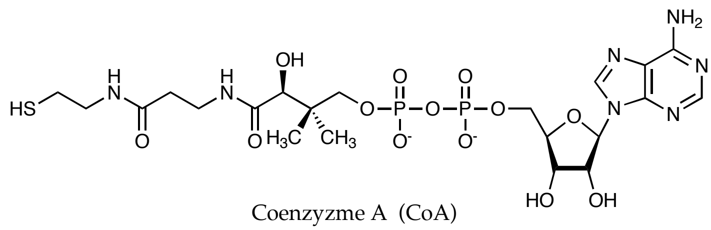
Co-factors



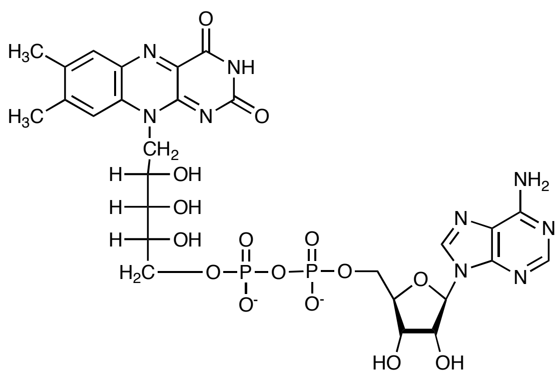
NAD$^+$: R = H
NADP$^+$: R = PO_3^{2-}
(Nicotinamide Adenine Dinucleotide)



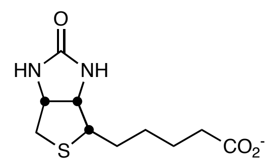
Thiamine Pyrophosphate



Coenzyzme A (CoA)



FAD (Flavin Adenine Dinucleotide)
FMN (no AMP attached)



Biotin

ATP is also a cofactor: you should know its structure

Enzyme	ΔG°′ in kJ mol^{-1} (kcal mol^{-1})	ΔG in kJ mol^{-1} (kcal mol^{-1})
Hexokinase	−16.7 (−4.0)	−33.5 (−8.0)
Phosphoglucose isomerase	+1.7 (+0.4)	−2.5 (−0.6)
Phosphofructokinase	−14.2 (−3.4)	−22.2 (−5.3)
Aldolase	+23.8 (+5.7)	−1.3 (−0.3)
Triose phosphate isomerase	+7.5 (+1.8)	+2.5 (+0.6)
Glyceraldehyde 3-phosphate dehydrogenase	+6.3 (+1.5)	−1.7 (−0.4)
Phosphoglycerate kinase	−18.8 (−4.5)	+1.3 (+0.3)
Phosphoglycerate mutase	+4.6 (+1.1)	+0.8 (+0.2)
Enolase	+1.7 (+0.4)	−3.3 (−0.8)
Pyruvate kinase	−31.4 (−7.5)	−16.7 (−4.0)

Table 16-1 part 2
Biochemistry, Sixth Edition

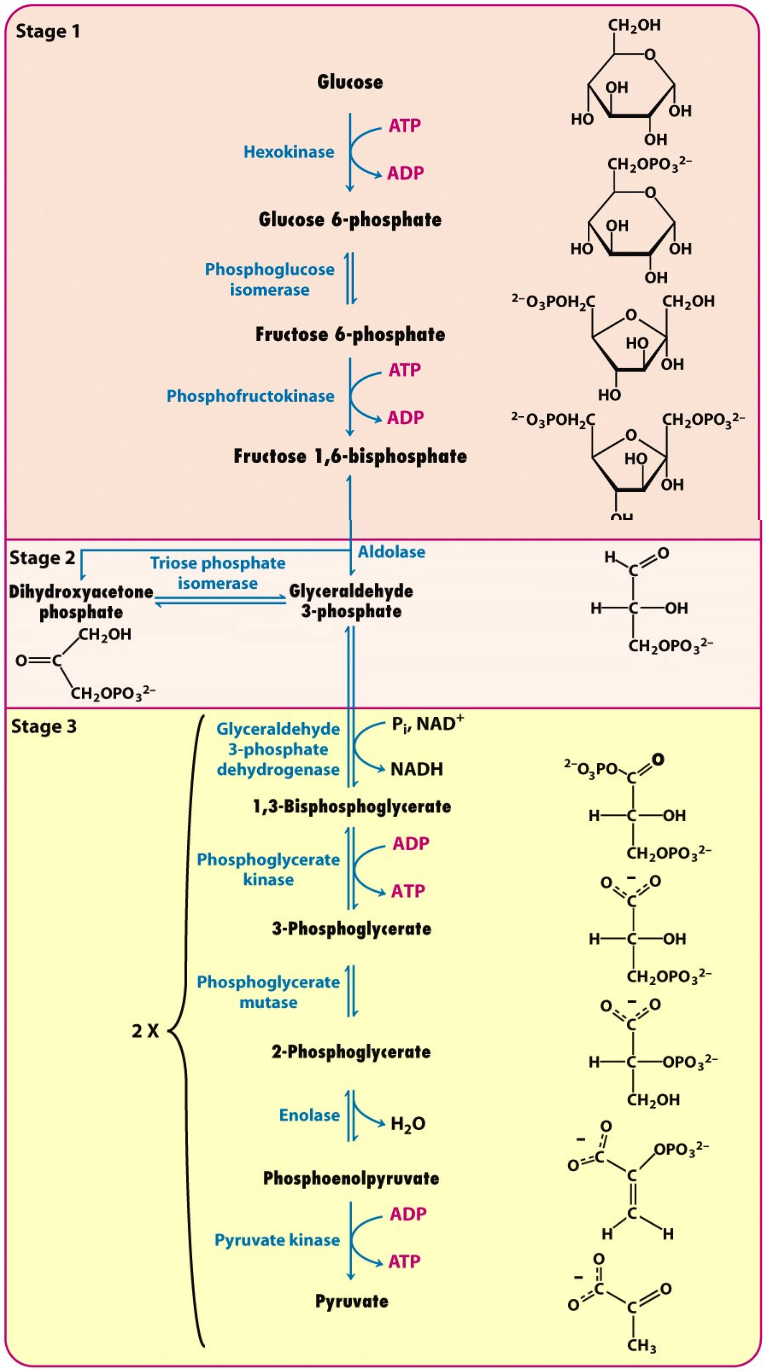
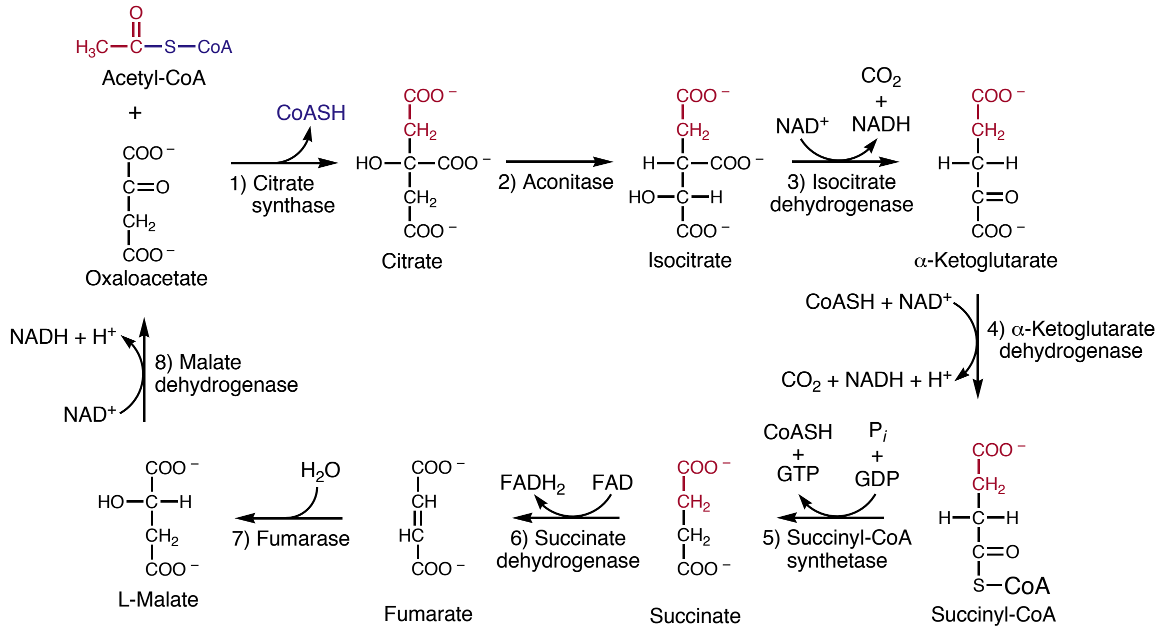


Figure 16-2 part 2
Biochemistry, Sixth Edition



Acetyl-CoA
+
Oxaloacetate
CoASH
1) Citrate synthase
Citrate
2) Aconitase
Isocitrate
NAD+
CO2 + NADH
3) Isocitrate dehydrogenase
α-Ketoglutarate
CoASH + NAD+
4) α-Ketoglutarate dehydrogenase
CO2 + NADH + H+
Succinyl-CoA
CoASH + GTP
Pi + GDP
5) Succinyl-CoA synthetase
Succinate
FADH2
FAD
6) Succinate dehydrogenase
Fumarate
H2O
7) Fumarase
L-Malate
NAD+
NADH + H+
8) Malate dehydrogenase